GenCore version 5.1.8

protein - nucleic search, using frame_plus_p2n model

n on: May 31, 2006, 22:52:13 ; Search time 9316.63 Seconds
(without alignments)
5096.366 Million cell updates/sec

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rfect score: 2660
quence: 1 MPCSRALILGVLALNTMLSL.....VHEGLHNHHTTKSFSRTPGK 495

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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arched: 6366136 seqs, 31973710525 residues

tal number of hits satisfying chosen parameters: 12732272

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st-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	Query Match	Length	DB	ID	Description
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4	1328.5	49.9	3973	2	CQ897414	CQ897414 Sequence
5	1324.5	49.8	1581	2	A78881	A78881 Sequence 1
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ALIGNMENTS

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RESULT 1
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LOCUS       AX081280               1484 bp    DNA     linear   PAT 27-FEB-2001
DEFINITION  Sequence 1 from Patent WO0109194.
ACCESSION   AX081280
VERSION     AX081280.1  GI:13170129
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Glaichenhaus,N. and Malherbe,L.
  TITLE     Recombinant proteins and molecular complexes derived therefrom,
            analogous to molecules involved in immune responses
  JOURNAL   Patent: WO 0109194-A 1 08-FEB-2001;
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GIN

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         21 CysGlyGlyGluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrThrValTyr 40
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Qy      261 AlaSerGluProArgGlyProThrIleLysProCysProProCysLysCysProAlaPro 280
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RESULT 2
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DEFINITION  Monovalent MHC-binding domain fused proteins and conjugates,
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            polymer MHC-binding domain fused proteins and conjugates, and
            utilization therefor.
ACCESSION   BD137962
VERSION     BD137962.1  GI:23232907
KEYWORDS    JP 2002504342-A/7.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 1446)
  AUTHORS   Wucherpfennig,K.W. and Strominger,J.L.
  TITLE     Monovalent MHC-binding domain fused proteins and conjugates,
            polyvalent MHC-binding domain fused proteins and conjugates,
            polymer MHC-binding domain fused proteins and conjugates, and
            utilization
  JOURNAL   Patent: JP 2002504342-A 7 12-FEB-2002;
            PRESIDENT AND FELLOWS OF HARVARD COLLEGE
COMMENT     OS   Artificial Sequence
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            PD   12-FEB-2002
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PR   19-FEB-1998 US    60/075351
PI   KAI W WUCHERPFENNIG,JACK L STROMINGER
PC   C12N15/09,A61K35/14,A61K47/48,C07K14/705,C07K16/00,C07K19/00,
PC   C12Q1/02;
PC   G01N33/53,C12N15/00
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CC   DRA*0101 extracellular domain
CC   Linker
CC   Fos leucine zipper domain
CC   IgG domain
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  126 LeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePheProProValIleAsn 145
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  206 GluProGluIleProAlaProMetSerGluLeuThrGluThr---GlyGlyGlyGlySer 224
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Qy    280 ProAsnLeuLeuGlyGlyProSerValPheIlePheProProLysIleLysAspValLeu 299
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Qy    340 HisArgGluAspTyrAsnSerThrLeuArgValValSerAlaLeuProIleGlnHisGln 359
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Qy    400 ProProProGluGluGluMetThrLysLysGlnValThrLeuThrCysMetValThrAsp 419
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Db   1150 CCTCCACCAGAAGAAGAGATGACTAAGAAACAGGTCACTCTGACCTGCATGGTCACAGAC 1209

Qy    420 PheMetProGluAspIleTyrValGluTrpThrAsnAsnGlyLysThrGluLeuAsnTyr 439
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1210 TTCATGCCTGAAGACATTTACGTGGAGTGGACCAACAACGGGAAAACAGAGCTAAACTAC 1269

Qy    440 LysAsnThrGluProValLeuAspSerAspGlySerTyrPheMetTyrSerLysLeuArg 459
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1270 AAGAACACTGAACCAGTCCTGGACTCTGATGGTTCTTACTTCATGTACAGCAAGCTGAGA 1329

Qy    460 ValGluLysLysAsnTrpValGluArgAsnSerTyrSerCysSerValValHisGluGly 479
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1330 GTGGAAAAGAAGAACTGGGTGGAAAGAAATAGCTACTCCTGTTCAGTGGTCCACGAGGGT 1389

Qy    480 LeuHisAsnHisHisThrThrLysSerPheSerArgThrProGlyLys 495
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1390 CTGCACAATCACCACACGACTAAGAGCTTCTCCCGGACTCCGGGTAAA 1437

RESULT 3
AX080953
LOCUS       AX080953            7528 bp    DNA     linear   PAT 27-FEB-2001
DEFINITION  Sequence 3 from Patent WO0109303.
ACCESSION   AX080953
VERSION     AX080953.1  GI:13169890
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Hermanson,G.G.
  TITLE     Flt-3 ligand-encoding polynucleotide as a polynucleotide-based
            vaccine enhancer
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'OURNAL   Patent: WO 0109303-A 3 08-FEB-2001;
          VICAL INCORPORATED (US)
\TURES             Location/Qualifiers
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'd. No.:              4.04e-123      Length:         7528
)re:                  1332.00        Matches:        290
'cent Similarity:     64.8%          Conservative:   42
t Local Similarity:   56.6%          Mismatches:     89
:y Match:             50.1%          Indels:         92
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:0-048-116B-2 (1-495) x AX080953 (1-7528)

        10 GlyValLeuAlaLeuAsnThrMetLeuSerLeu---CysGlyGlyGluAspAspIleGlu 28
           |||:::|||      :::      |||||||||   ||||||
      1322 GGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCGGT---------GTTTATGGT 1372

        29 AlaAspHisValGlyPheTyrGlyThrThrValTyrGlnSerProGlyAsp--------- 45
                   |||:::|||   :::   :::   |||   ||||||
      1373 GGGTCCTTCAGTGGTTACTACTGGAGCTGGATCCGCCAGCCCCCAGGGAAGGGGCTGGAG 1432

        46 ---IleGlyGlnTyrThrHis-----------------------GluPheAspGlyAsp 56
              ||||||:::      |||
      1433 TGGATTGGGGAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGA 1492

        57 GluLeuPheTyrValAspLeuAspLysLysLysThrValTrpArgLeuProGlu------ 74
                  ||||||      ||||||:::         :::|||
      1493 GTCACCATATCAGTAGACACGTCCAAGAAGCAGCTCTCCCTGAAGTTGAGCTCTGTGAAC 1552

        75 --------------------PheGlyGlnLeuIleLeuPheGluProGlnGlyGlyLeu 87
                             :::         ::::::                  |||
      1553 GCCGCGGACACGGCTGTGTATTACTGTGCGAGAGTTATTACTAGGGCGAGTCCTGGCACA 1612

        88 GlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeuThrLysArgSerAsnPheThr 107
                           ::::::   :::   :::       :::   :::      |||
      1613 GACGGG-----------AGGTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACG 1660

       108 ProAlaThrAsnGluAlaProGlnAlaThrValPheProLysSerProVal--------- 124
              ::::::   :::           :::|||:::|||   :::||||||
      1661 GTCTCCTCGGCCAAAACGGCCGCCCCATCGGTCTATCCACTGGCCCCTGTGTGTGGAGAT 1720

       125 LeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePheProProValIle 144
                 |||         ||||||   |||   |||         ||||||      :::
      1721 ACAAGTGGCTCCTCGGTGACTCTAGGATGCCTGGTCAAGGGTTATTTCCCTGAGCCAGTG 1780

       145 AsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyrGluThrSerPhe 164
              :::||||||      ||||||   |||:::::   |||||||:::
      1781 ACCTTGACCTGG------AACTCTGGATCCCTGTCCAGTGGTGTGCACACCTTCCCAGCT 1834

       165 LeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPheIleProSerAsp 184
              ::::::      |||         :::   ||||||   |||:::
      1835 GTCCTGCAGTCTGAC------CTCTACACCCTCAGCAG-CTCAGT--------------- 1872

       185 AspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluProValLeuLysHis 204
                        ||||||   :::||||||      |||   :::||||||      |||
      1873 ------------GACTGTAACCTCGAGCAC------CTGGCCCAGCCAGTC------CAT 1908

       205 TrpGluProGluIleProAlaProMetSerGluLeuThrGluThrGlyGlyGlyGly-Se 224
              :::                                    :::   |||      ||| ||
      1909 TAC--------------------------------CTGCAATGTGGCCCACCCGGCAAG 1935

       224 rThrThrAlaProSerAlaGlnLeuGluLysGluLeuGlnAlaLeuGluLysGluAsnAl 244
           |:::|||           :::::::::|||::::::
      1936 CAGCACC------------AAGGTGGACAAGAAAATT---------------------- 1960

       244 aGlnLeuGluTrpGluLeuGlnAlaLeuGluLysGluLeuAlaGlnAlaAlaSerGluPr 264
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                                                                    |||||
Db      1961 ----------------------------------------------------GAGCC 1965

Qy       264 oArgGlyProThrIleLysProCysProProCysLysCysProAlaProAsnLeuLeuGl 284
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1966 CAGAGGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCAGCACCTAACCTCTTGGG 2025

Qy       284 yGlyProSerValPheIlePheProProLysIleLysAspValLeuMetIleSerLeuSe 304
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Db      2026 TGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTCCCTGAG 2085

Qy       304 rProIleValThrCysValValValAspValSerGluAspAspProAspValGlnIleSe 324
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Db      2086 CCCCATAGTCACATGTGTGGTGGTGGATGTGAGCGAGGATGACCCAGATGTCCAGATCAG 2145

Qy       324 rTrpPheValAsnAsnValGluValHisThrAlaGlnThrGlnThrHisArgGluAspTy 344
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2146 CTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAAACCCATAGAGAGGATTA 2205

Qy       344 rAsnSerThrLeuArgValValSerAlaLeuProIleGlnHisGlnAspTrpMetSerGl 364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2206 CAACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGACTGGATGAGTGG 2265

Qy       364 yLysGluPheLysCysLysValAsnAsnLysAspLeuProAlaProIleGluArgThrIl 384
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2266 CAAGGAGTTCAAATGCAAGGTCAACAACAAAGACCTCCCAGCGCCCATCGAGAGAACCAT 2325

Qy       384 eSerLysProLysGlySerValArgAlaProGlnValTyrValLeuProProProGluGl 404
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Db      2326 CTCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACCAGAAGA 2385

Qy       404 uGluMetThrLysLysGlnValThrLeuThrCysMetValThrAspPheMetProGluAs 424
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Db      2386 AGAGATGACTAAGAAACAGGTCACTCTGACCTGCATGGTCACAGACTTCATGCCTGAAGA 2445

Qy       424 pIleTyrValGluTrpThrAsnAsnGlyLysThrGluLeuAsnTyrLysAsnThrGluPr 444
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2446 CATTTACGTGGAGTGGACCAACAACGGGAAAACAGAGCTAAACTACAAGAACACTGAACC 2505

Qy       444 oValLeuAspSerAspGlySerTyrPheMetTyrSerLysLeuArgValGluLysLysAs 464
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2506 AGTCCTGGACTCTGATGGTTCTTACTTCATGTACAGCAAGCTGAGAGTGGAAAAGAAGAA 2565

Qy       464 nTrpValGluArgAsnSerTyrSerCysSerValValHisGluGlyLeuHisAsnHisHi 484
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2566 CTGGGTGGAAAGAAATAGCTACTCCTGTTCAGTGGTCCACGAGGGTCTGCACAATCACCA 2625

Qy       484 sThrThrLysSerPheSerArgThrProGlyLys 495
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Db      2626 CACGACTAAGAGCTTCTCCCGGACTCCGGGTAAA 2659
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RESULT 4
CQ897414
LOCUS       CQ897414               3973 bp    DNA     linear   PAT 08-NOV-2004
DEFINITION  Sequence 1 from Patent WO2004091655.
ACCESSION   CQ897414
VERSION     CQ897414.1  GI:55582199
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Loibner,H., Himmler,G., Waxenecker,G., Schuster,M. and Putz,T.
  TITLE     Immunogenic recombinant antibody
  JOURNAL   Patent: WO 2004091655-A 1 28-OCT-2004;
            Igeneon Krebs-Immuntherapie Forschungs- und Entwicklungs- AG (AT)
FEATURES             Location/Qualifiers
     source          1. .3973
                     /organism="synthetic construct"
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ORIGIN
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ed. No.:              3.68e-123      Length:        3973
ore:                  1328.50        Matches:       281
rcent Similarity:     65.0%          Conservative:  26
st Local Similarity:  59.5%          Mismatches:    71
ery Match:            49.9%          Indels:        95
:                     2              Gaps:          11

-10-048-116B-2 (1-495) x CQ897414 (1-3973)

        42 SerProGlyAspIleGly---GlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr 60
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      1567 AATCCTGGAAGTGGTGGTACTAACTACAATGAGAAGTTCAAGGGCAAGGCAACACTGACT 1626

        61 ValAspLeuAspLysLysLysThrValTrpArgLeuProGluPhe--------------- 75
              |||                    :::|||
      1627 GCAGACAAATCCTCCAGCACTGCCTACATGCAGCTCAGCAGCCTGACATCTGATGACTCT 1686

        76 ------------------------GlyGlnLeuIleLeuPheGluProGlnGlyGlyLeu 87
                                   |||          :::      ||||||   |||
      1687 GCGGTCTATTTCTGTGCAAGAGATGGTCCCTGGTTTGCTTACTGGGGCCAAGGGACTCTG 1746

        88 GlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeuThrLysArgSerAsnPheThr 107
              ::::::|||   |||
      1747 GTCACTGTCTCTGCAGCCAAA------------------------------------- 1767

       108 ProAlaThrAsnGluAlaProGlnAlaThrValPheProLysSerProVal--------- 124
                   ||||||      :::|||:::|||   :::||||||
      1768 ---------ACAACAGCCCCA------TCGGTCTATCCACTGGCCCCTGTGTGTGGAGAT 1812

       125 LeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePheProProValIle 144
              |||          ||||||   |||   |||          ||||||      :::
      1813 ACAACTGGCTCCTCGGTGACTCTAGGATGCCTGGTCAAGGGTTATTTCCCTGAGCCAGTG 1872

       145 AsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyrGluThrSerPhe 164
           :::||||||       ||||||   |||::::::   |||||||:::
      1873 ACCTTGACCTGG------AACTCTGGATCCCTGTCCAGTGGTGTGCACACCTTCCCAGCT 1926

       165 LeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPheIleProSerAsp 184
           ::::::      |||          :::   ||||||   |||:::
      1927 GTCCTGCAGTCTGAC------CTCTACACCCTCAGCAG-CTCAGT--------------- 1964

       185 AspAspIleTyrAspCysLysValGluHis-TrpGlyLeuGluGluProValLeuLysHi 204
                     ||||||   :::|||||| |||
      1965 -----------GACTGTAACCTCGAGCACCTGG------------------------- 1986

       204 sTrpGluProGluIleProAlaProMetSerGluLeuThrGluThrGlyGlyGlyGlySe 224
                                 |||          :::|||                ::
      1987 ---------------------CCCAGCCAGTCCATCACC---------TGCAATGTGGC 2015

       224 rThrThrAlaProSerAlaGlnLeuGluLysGluLeuGlnAlaLeuGluLysGluAsnAl 244
           :      |||    |||    :::::::::|||::::::
      2016 CCACCCGGCAAGCAGCACCAAGGTGGACAAGAAAATT---------------------- 2052

       244 aGlnLeuGluTrpGluLeuGlnAlaLeuGluLysGluLeuAlaGlnAlaAlaSerGluPr 264
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       264 oArgGlyProThrIleLysProCysProProCysLysCysProAlaProAsnLeuLeuGl 284
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      2058 CAGAGGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCAGCACCTAACCTCTTGGG 2117

       284 yGlyProSerValPheIlePheProProLysIleLysAspValLeuMetIleSerLeuSe 304
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      2118 TGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTCCCTGAG 2177

       304 rProIleValThrCysValValValAspValSerGluAspAspProAspValGlnIleSe 324
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      2178 CCCCATAGTCACATGTGTGGTGGTGGATGTGAGCGAGGATGACCCAGATGTCCAGATCAG 2237

       324 rTrpPheValAsnAsnValGluValHisThrAlaGlnThrGlnThrHisArgGluAspTy 344
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db      2238 CTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAAACCCATAGAGAGGATTA 2297

Qy       344 rAsnSerThrLeuArgValValSerAlaLeuProIleGlnHisGlnAspTrpMetSerGl 364
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Qy       364 yLysGluPheLysCysLysValAsnAsnLysAspLeuProAlaProIleGluArgThrIl 384
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2358 CAAGGAGTTCAAATGCAAGGTCAACAACAAAGACCTCCCAGCGCCCATCGAGAGAACCAT 2417

Qy       384 eSerLysProLysGlySerValArgAlaProGlnValTyrValLeuProProProGluGl 404
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Db      2418 CTCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACCAGAAGA 2477

Qy       404 uGluMetThrLysLysGlnValThrLeuThrCysMetValThrAspPheMetProGluAs 424
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Db      2478 AGAGATGACTAAGAAACAGGTCACTCTGACCTGCATGGTCACAGACTTCATGCCTGAAGA 2537

Qy       424 pIleTyrValGluTrpThrAsnAsnGlyLysThrGluLeuAsnTyrLysAsnThrGluPr 444
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2538 CATTTACGTGGAGTGGACCAACAACGGGAAAACAGAGCTAAACTACAAGAACACTGAACC 2597

Qy       444 oValLeuAspSerAspGlySerTyrPheMetTyrSerLysLeuArgValGluLysLysAs 464
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Qy       464 nTrpValGluArgAsnSerTyrSerCysSerValValHisGluGlyLeuHisAsnHisHi 484
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Qy       484 sThrThrLysSerPheSerArgThrProGlyLys 495
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Db      2718 CACGACTAAGAGCTTCTCCCGGACTCCGGGTAAA 2751

RESULT 5
A78881
LOCUS       A78881                1581 bp    DNA     linear   PAT 19-OCT-1999
DEFINITION  Sequence 1 from Patent EP0556111.
ACCESSION   A78881
VERSION     A78881.1  GI:6090456
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 1581)
  AUTHORS   Boulain,J. and Ducancel,F.
  TITLE     HYBRID PROTEIN COMPLEXES, THEIR PROCESS OF PREPARATION, AND THEIR
            APPLICATIONS AS AN AGENT IN DIAGNOSTIC AND IN THE THERAPEUTIC FIELD
            OR AS A REAGENT RELEVANT IN MEDICAL APPROACHES
  JOURNAL   Patent: EP 0556111-A 1 18-AUG-1993;
            COMMISSARIAT ENERGIE ATOMIQUE (FR)
FEATURES             Location/Qualifiers
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                     SVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQS
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GIN

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d. No.:              2.52e-123      Length:        1581
re:                  1324.50        Matches:       286
cent Similarity:     65.4%          Conservative:  31
t Local Similarity:  59.0%          Mismatches:    81
y Match:             49.8%          Indels:        89
                     2              Gaps:          11

:0-048-116B-2 (1-495) x A78881 (1-1581)

        34 PheTyrGlyThrThrValTyrGlnSerProGlyAsp------------IleGly------ 47
           :::|||          |||   |||   ||||||              ||||||
       211 TACTATATAAACTGGGTGAAGCAGAAGCCTGGACAGGGACTTAAATGGATTGGATGGATT 270

        48 --------------------GlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr 60
                              :::|||         |||   |||
       271 TATCCTGCAAGCGGTAATACTAAGTACAATGAGAACTTCAAGGGCAAGGCCACATTGACT 330

        61 ValAspLeuAspLysLysLysThrValTrpArgLeu---------------ProGluPhe 75
           ||||||                    :::|||                  :::
       331 GTAGACACATCCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACACT 390

        76 GlyGlnLeuIleLeuPheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHis 95
              |||   |||   :::      ||||||                      :::
       391 GCTGT-CTATTTCTGTGCAAGAGCTATGGGGGCTAC-----------------GGCTAC 431

        96 AsnLeuGlyIleLeuThrLysArg-SerAsnPheThrProAlaThrAsnGluAlaProGl 115
              |||:::|||      ||| :::      |||   ::::::   :::
       432 ACTTTTGGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCAGCCAAAACAACAGC 491

       115 nAlaThrValPheProLysSerProVal---------LeuLeuGlyGlnProAsnThrLe 132
              :::|||:::|||   :::||||||              |||          |||||
       492 CCCATCGGTCTATCCACTGGCCCCTGTGTGTGGAGATACAACTGGCTCCTCGGTGACTCT 551

       132 uIleCysPheValAspAsnIlePheProProValIleAsnIleThrTrpLeuArgAsnSe 152
           |   |||   |||        ||||||      :::   :::||||||      |||||
       552 AGGATGCCTGGTCAAGGGTTATTTCCCTGAGCCAGTGACCTTGACCTGG------AACTC 605

       152 rLysSerValThrAspGlyValTyrGluThrSerPheLeuValAsnArgAspHisSerPh 172
           |   |||::::::   ||||||:::            ::::::      |||
       606 TGGATCCCTGTCCAGTGGTGTGCACACCTTCCCAGCTGTCCTGCAGTCTGAC------CT 659

       172 eHisLysLeuSerTyrLeuThrPheIleProSerAspAspAspIleTyrAspCysLysVa 192
            :::   ||||||   |||:::                          ||||||   ::
       660 CTACACCCTCAGCAG-CTCAGT-------------------------GACTGTAACCT 691

       192 lGluHis-TrpGlyLeuGluGluProValLeuLysHisTrpGluProGluIleProAlaP 212
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       692 CGAGCACCTGG-------------------------------------------------C 703

       212 roMetSerGluLeuThrGluThrGlyGlyGlyGlySerThrThrAlaProSerAlaGlnL 232
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       704 CCAGCCAGTCCATCACC---------TGCAATGTGGCCCACCCGGCAAGCAGCACCAAGG 754

       232 euGluLysGluLeuGlnAlaLeuGluLysGluAsnAlaGlnLeuGluTrpGluLeuGlnA 252
           :::::|||::::::
       755 TGGACAAGAAAATT-------------------------------------------- 768

       252 laLeuGluLysGluLeuAlaGlnAlaAlaSerGluProArgGlyProThrIleLysProC 272
                                              ||||||||||||||||||||||||||
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Qy        292 roProLysIleLysAspValLeuMetIleSerLeuSerProIleValThrCysValValV 312
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Qy        312 alAspValSerGluAspAspProAspValGlnIleSerTrpPheValAsnAsnValGluV 332
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Db        917 TGGATGTGAGCGAGGATGACCCAGATGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAG 976

Qy        332 alHisThrAlaGlnThrGlnThrHisArgGluAspTyrAsnSerThrLeuArgValValS 352
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        977 TACACACAGCTCAGACACAAACCCATAGAGAGGATTACAACAGTACTCTCCGGGTGGTCA 1036

Qy        352 erAlaLeuProIleGlnHisGlnAspTrpMetSerGlyLysGluPheLysCysLysValA 372
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Db       1037 GTGCCCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCA 1096

Qy        372 snAsnLysAspLeuProAlaProIleGluArgThrIleSerLysProLysGlySerValA 392
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1097 ACAACAAAGACCTGCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGGTCAGTAA 1156

Qy        392 rgAlaProGlnValTyrValLeuProProProGluGluGluMetThrLysLysGlnValT 412
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Db       1157 GAGCTCCACAGGTATATGTCTTGCCTCCACCAGAAGAAGAGATGACTAAGAAACAGGTCA 1216

Qy        412 hrLeuThrCysMetValThrAspPheMetProGluAspIleTyrValGluTrpThrAsnA 432
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Db       1217 CTCTGACCTGCATGGTCACAGACTTCATGCCTGAAGACATTTACGTGGAGTGGACCAACA 1276

Qy        432 snGlyLysThrGluLeuAsnTyrLysAsnThrGluProValLeuAspSerAspGlySerT 452
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1277 ACGGGAAAACAGAGCTAAACTACAAGAACACTGAACCAGTCCTGGACTCTGATGGTTCTT 1336

Qy        452 yrPheMetTyrSerLysLeuArgValGluLysLysAsnTrpValGluArgAsnSerTyrS 472
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1337 ACTTCATGTACAGCAAGCTGAGAGTGGAAAAGAAGAACTGGGTGGAAAGAAATAGCTACT 1396

Qy        472 erCysSerValValHisGluGlyLeuHisAsnHisHisThrThrLysSerPheSerArgT 492
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1397 CCTGTTCAGTGGTCCACGAGGGTCTGCACAATCACCACACGACTAAGAGCTTCTCCCGGA 1456

Qy        492 hrProGlyLys 495
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Db       1457 CTCCGGGTAAA 1467
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RESULT 6
MMIGHC2AA
LOCUS       MMIGHC2AA               1581 bp    mRNA    linear   ROD 30-SEP-1993
DEFINITION  M.musculus mRNA for monoclonal antibody heavy chain gamma 2a.
ACCESSION   X70423
VERSION     X70423.1  GI:406252
KEYWORDS    immunoglobulin; immunoglobulin gamma-2a; immunoglobulin heavy
            chain.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Ducancel,F.F.D.
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1581)
  AUTHORS   Ducancel,F.F.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-FEB-1993) F.F.D. Ducancel, C E A, Diep Bat 152, CEN
            de Saclay, 91191 Gif Yvette, Cedex, FRANCE
FEATURES             Location/Qualifiers
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                WMSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVT
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IGIN

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st Local Similarity: 59.0%         Mismatches:    81
ery Match:          49.8%          Indels:        89
:                   6              Gaps:          11

-10-048-116B-2 (1-495) x MMIGHC2AA (1-1581)

        34 PheTyrGlyThrThrValTyrGlnSerProGlyAsp----------IleGly------ 47
           :::|||          |||   |||   ||||||                ||||||
       211 TACTATATAAACTGGGTGAAGCAGAAGCCTGGACAGGGACTTAAATGGATTGGATGGATT 270

        48 --------------------GlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr 60
                             :::|||          |||   |||
       271 TATCCTGCAAGCGGTAATACTAAGTACAATGAGAACTTCAAGGGCAAGGCCACATTGACT 330

        61 ValAspLeuAspLysLysLysThrValTrpArgLeu--------------ProGluPhe 75
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       331 GTAGACACATCCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACACT 390

        76 GlyGlnLeuIleLeuPheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHis 95
                 |||   |||   :::      ||||||                          :::
       391 GCTGT-CTATTTCTGTGCAAGAGCTATGGGGGCTAC-----------------GGCTAC 431

        96 AsnLeuGlyIleLeuThrLysArg-SerAsnPheThrProAlaThrAsnGluAlaProGl 115
                 |||:::|||     ||| :::      |||   ::::::   :::
       432 ACTTTTGGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCAGCCAAAACAACAGC 491

       115 nAlaThrValPheProLysSerProVal---------LeuLeuGlyGlnProAsnThrLe 132
               :::|||:::|||   :::||||||              |||          |||||
       492 CCCATCGGTCTATCCACTGGCCCCTGTGTGTGGAGATACAACTGGCTCCTCGGTGACTCT 551

       132 uIleCysPheValAspAsnIlePheProProValIleAsnIleThrTrpLeuArgAsnSe 152
           |   |||   |||          ||||||      :::   :::||||||      |||||
       552 AGGATGCCTGGTCAAGGGTTATTTCCCTGAGCCAGTGACCTTGACCTGG------AACTC 605

       152 rLysSerValThrAspGlyValTyrGluThrSerPheLeuValAsnArgAspHisSerPh 172
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Qy      172 eHisLysLeuSerTyrLeuThrPheIleProSerAspAspAspIleTyrAspCysLysVa 192
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Qy      192 lGluHis-TrpGlyLeuGluGluProValLeuLysHisTrpGluProGluIleProAlaP 212
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Db      692 CGAGCACCTGG-------------------------------------------------C 703

Qy      212 roMetSerGluLeuThrGluThrGlyGlyGlyGlySerThrThrAlaProSerAlaGlnL 232
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Db      704 CCAGCCAGTCCATCACC---------TGCAATGTGGCCCACCCGGCAAGCAGCACCAAGG 754

Qy      232 euGluLysGluLeuGlnAlaLeuGluLysGluAsnAlaGlnLeuGluTrpGluLeuGlnA 252
             :::::|||::::::
Db      755 TGGACAAGAAAAATT---------------------------------------------- 768

Qy      252 laLeuGluLysGluLeuAlaGlnAlaAlaSerGluProArgGlyProThrIleLysProC 272
                                       ||||||||||||||||||||||||||||||
Db      769 ------------------------------GAGCCCAGAGGGCCCACAATCAAGCCCT 796

Qy      272 ysProProCysLysCysProAlaProAsnLeuLeuGlyGlyProSerValPheIlePheP 292
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      797 GTCCTCCATGCAAATGCCCAGCACCTAACCTCTTGGGTGGACCATCCGTCTTCATCTTCC 856

Qy      292 roProLysIleLysAspValLeuMetIleSerLeuSerProIleValThrCysValValV 312
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Db      857 CTCCAAAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCATAGTCACATGTGTGGTGG 916

Qy      312 alAspValSerGluAspAspProAspValGlnIleSerTrpPheValAsnAsnValGluV 332
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Db      917 TGGATGTGAGCGAGGATGACCCAGATGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAG 976

Qy      332 alHisThrAlaGlnThrGlnThrHisArgGluAspTyrAsnSerThrLeuArgValValS 352
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Db      977 TACACACAGCTCAGACACAAACCCATAGAGAGGATTACAACAGTACTCTCCGGGTGGTCA 1036

Qy      352 erAlaLeuProIleGlnHisGlnAspTrpMetSerGlyLysGluPheLysCysLysValA 372
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1037 GTGCCCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCA 1096

Qy      372 snAsnLysAspLeuProAlaProIleGluArgThrIleSerLysProLysGlySerValA 392
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1097 ACAACAAAGACCTGCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGGTCAGTAA 1156

Qy      392 rgAlaProGlnValTyrValLeuProProProGluGluGluMetThrLysLysGlnValT 412
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      412 hrLeuThrCysMetValThrAspPheMetProGluAspIleTyrValGluTrpThrAsnA 432
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Db      1217 CTCTGACCTGCATGGTCACAGACTTCATGCCTGAAGACATTTACGTGGAGTGGACCAACA 1276

Qy      432 snGlyLysThrGluLeuAsnTyrLysAsnThrGluProValLeuAspSerAspGlySerT 452
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Db      1277 ACGGGAAAACAGAGCTAAACTACAAGAACACTGAACCAGTCCTGGACTCTGATGGTTCTT 1336

Qy      452 yrPheMetTyrSerLysLeuArgValGluLysLysAsnTrpValGluArgAsnSerTyrS 472
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Db      1337 ACTTCATGTACAGCAAGCTGAGAGTGGAAAAGAAGAACTGGGTGGAAAGAAATAGCTACT 1396

Qy      472 erCysSerValValHisGluGlyLeuHisAsnHisHisThrThrLysSerPheSerArgT 492
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1397 CCTGTTCAGTGGTCCACGAGGGTCTGCACAATCACCACACGACTAAGAGCTTCTCCCGGA 1456

Qy      492 hrProGlyLys 495
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Db      1457 CTCCGGGTAAA 1467

RESULT 7
I07390
LOCUS       I07390                1341 bp    DNA     linear   PAT 02-DEC-1994
DEFINITION  Sequence 4 from Patent EP 0338767.
ACCESSION   I07390
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SION      I07390.1  GI:589918
WORDS     .
RCE       Unknown.
RGANISM   Unknown.
          Unclassified.
ERENCE    1  (bases 1 to 1341)
UTHORS    Beavers,L.S., Bumol,T.F., Gadski,R.A. and Weigel,B.J.
ITLE      Novel recombinant and chimeric antibodies directed against a human
          adenocarcinoma antigen
OURNAL    Patent: EP 0338767-A2 4 25-OCT-1989;
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d. No.:               5.05e-123      Length:         1341
re:                   1320.50        Matches:        269
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t Local Similarity:   66.7%          Mismatches:     45
ry Match:             49.6%          Indels:         64
                      2              Gaps:           7

10-048-116B-2 (1-495) x I07390 (1-1341)

        98 GlyIleLeuThrLysArg-SerAsnPheThrProAlaThrAsnGluAlaProGlnAlaTh 117
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       312 GGACTACTGGGGTCAAGGAACGTCAGTCACCGTCTCCTCAGCCAAAACAACAGCCCCATC 371

       117 rValPheProLysSerProVal---------LeuLeuGlyGlnProAsnThrLeuIleCy 134
           :|||:::|||   :::||||||                |||          ||||||   ||
       372 GGTCTATCCACTGGCCCCTGTGTGTGGAGATACAACTGGCTCCTCGGTGACTCTAGGATG 431

       134 sPheValAspAsnIlePheProProValIleAsnIleThrTrpLeuArgAsnSerLysSe 154
           |   |||     ||||||     :::   :::||||||      ||||||   ||
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           |::::::   ||||||:::            ::::::      |||         :::
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       174 sLeuSerTyrLeuThrPheIleProSerAspAspAspIleTyrAspCysLysValGluHi 194
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       540 CCTCAGCAG-CTCAGT--------------------------GACTGTAACCTCGAGCA 571

       194 s-TrpGlyLeuGluGluProValLeuLysHisTrpGluProGluIleProAlaProMetS 214
           | |||                                                  |||
       572 CCTGG-------------------------------------------------CCCAGCC 583

       214 erGluLeuThrGluThrGlyGlyGlyGlySerThrThrAlaProSerAlaGlnLeuGluL 234
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       584 AGTCCATCACC---------TGCAATGTGGCCCACCCGGCAAGCAGCACCAAGGTGGACA 634

       234 ysGluLeuGlnAlaLeuGluLysGluAsnAlaGlnLeuGluTrpGluLeuGlnAlaLeuG 254
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       635 AGAAAATT------------------------------------------------------ 642

       254 luLysGluLeuAlaGlnAlaAlaSerGluProArgGlyProThrIleLysProCysProP 274
                                        ||||||||||||||||||||||||||||||||
       643 -------------------------GAGCCCAGAGGGCCCACAATCAAGCCCTGTCCTC 676

       274 roCysLysCysProAlaProAsnLeuLeuGlyGlyProSerValPheIlePheProProL 294
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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       294 ysIleLysAspValLeuMetIleSerLeuSerProIleValThrCysValValValAspV 314
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Qy        334 hrAlaGlnThrGlnThrHisArgGluAspTyrAsnSerThrLeuArgValValSerAlaL 354
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Qy        354 euProIleGlnHisGlnAspTrpMetSerGlyLysGluPheLysCysLysValAsnAsnL 374
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Qy        434 ysThrGluLeuAsnTyrLysAsnThrGluProValLeuAspSerAspGlySerTyrPheM 454
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Qy        454 etTyrSerLysLeuArgValGluLysLysAsnTrpValGluArgAsnSerTyrSerCysS 474
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Qy        494 lyLys 495
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RESULT 8
BD057272
LOCUS       BD057272                1570 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Gene encoding antimalathion monoclonal antibody.
ACCESSION   BD057272
VERSION     BD057272.1  GI:22602878
KEYWORDS    JP 2001275682-A/9.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 1570)
  AUTHORS   Okawa,H., Nakata,M. and Yuasa,Y.
  TITLE     Gene encoding antimalathion monoclonal antibody
  JOURNAL   Patent: JP 2001275682-A 9 09-OCT-2001;
            KANKYO MENEKI GIJUTSU KENKYUSYO KK
COMMENT     PN   JP 2001275682-A/9
            PD   09-OCT-2001
            PF   31-MAR-2000 JP 2000098323
            PI   HIDEO OKAWA,MASANOBU NAKATA,YOJIRO YUASA
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            PC   C12P21/08//(C12N1/21,C12R1:19),(C12P21/02,C12R1:19),C12N15/00,
            PC   C12N5/00
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ORIGIN

Alignment Scores:
Pred. No.:              6.32e-123      Length:         1570
Score:                  1320.50        Matches:        272
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st Local Similarity:  65.4%          Mismatches:     42
ery Match:            49.6%          Indels:         81
:                     2              Gaps:           9

-10-048-116B-2 (1-495) x BD057272 (1-1570)

 84 GlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeuThrLysArg 103
423 CAAGGGACTCTGGTCACTGTCTCTGCAGCCAAA---------------------------- 455

104 SerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPheProLysSerPro 123
456 ---------------------ACAACAGCCCCA------TCGGTCTATCCACTGGCCCCT 488

124 Val---------LeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhe 140
489 GTGTGTGGAGATACAACTGGCTCCTCGGTGACTCTAGGATGCCTGGTCAAGGGTTATTTC 548

141 ProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyr 160
549 CCTGAGCCAGTGACCTTGACCTGG------AACTCTGGATCCCTGTCCAGTGGTGTGCAC 602

161 GluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPhe 180
603 ACCTTCCCAGCTGTCCTGCAGTCTGAC------CTCTACACCCTCAGCAG-CTCAGT--- 652

181 IleProSerAspAspAspIleTyrAspCysLysValGluHis-TrpGlyLeuGluGluPr 200
653 ----------------------GACTGTAACCTCGAGCACCTGG-------------- 674

200 oValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThrGl 220
675 --------------------------------CCCAGCCAGTCCATCACC-------- 692

220 yGlyGlyGlySerThrThrAlaProSerAlaGlnLeuGluLysGluLeuGlnAlaLeuGl 240
693 -TGCAATGTGGCCCACCCGGCAAGCAGCACCAAGGTGGACAAGAAAATT---------- 740

240 uLysGluAsnAlaGlnLeuGluTrpGluLeuGlnAlaLeuGluLysGluLeuAlaGlnAl 260
740 ------------------------------------------------------------ 740

260 aAlaSerGluProArgGlyProThrIleLysProCysProProCysLysCysProAlaPr 280
741 -------GAGCCCAGAGGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCAGCACC 793

280 oAsnLeuLeuGlyGlyProSerValPheIlePheProProLysIleLysAspValLeuMe 300
794 TAACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCAT 853

300 tIleSerLeuSerProIleValThrCysValValValAspValSerGluAspAspProAs 320
854 GATCTCCCTGAGCCCCATAGTCACATGTGTGGTGGTGGATGTGAGCGAGGATGACCCAGA 913

320 pValGlnIleSerTrpPheValAsnAsnValGluValHisThrAlaGlnThrGlnThrHi 340
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340 sArgGluAspTyrAsnSerThrLeuArgValValSerAlaLeuProIleGlnHisGlnAs 360
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380 eGluArgThrIleSerLysProLysGlySerValArgAlaProGlnValTyrValLeuPr 400
1094 CGAGAGAACCATCTCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTTGCC 1153

400 oProProGluGluGluMetThrLysLysGlnValThrLeuThrCysMetValThrAspPh 420

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Db       1214 CATGCCTGAAGACATTTACGTGGAGTGGACCAACAACGGGAAAACAGAGCTAAACTACAA 1273

Qy        440 sAsnThrGluProValLeuAspSerAspGlySerTyrPheMetTyrSerLysLeuArgVa 460

Db       1274 GAACACTGAACCAGTCCTGGACTCTGATGGTTCTTACTTCATGTACAGCAAGCTGAGAGT 1333

Qy        460 lGluLysLysAsnTrpValGluArgAsnSerTyrSerCysSerValValHisGluGlyLe 480

Db       1334 GGAAAAGAAGAACTGGGTGGAAAGAAATAGCTACTCCTGTTCAGTGGTCCACGAGGGTCT 1393

Qy        480 uHisAsnHisHisThrThrLysSerPheSerArgThrProGlyLys 495

Db       1394 GCACAATCACCACACGACTAAGAGCTTCTCCCGGACTCCGGGTAAA 1439
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RESULT 9
AB097847

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LOCUS       AB097847               1570 bp    mRNA    linear   ROD 08-APR-2003
DEFINITION  Mus musculus mRNA for immunoglobulin gamma-2a heavy chain, complete
            cds, anti-malathion monoclonal antibody MLT2-23.
ACCESSION   AB097847
VERSION     AB097847.1  GI:26665399
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Nishi,K., Imajuku,Y., Nakata,M., Ohde,K., Miyake,S., Morimune,K.,
            Kawata,M. and Ohkawa,H.
  TITLE     Molecular characteristics of the monoclonal and recombinant
            antibodies specific to the insecticide malathion
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1570)
  AUTHORS   Nishi,K., Imajuku,Y., Nakata,M., Ohde,K., Miyake,S., Morimune,K.,
            Kawata,M. and Ohkawa,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-DEC-2002) Kosuke Nishi, Kobe University, Research
            Center for Environmental Genomics; 1-1 Rokkodai-cho, Nada-ku, Kobe,
            Hyogo 657-8501, Japan (E-mail:nishikosuke@yahoo.co.jp,
            Tel:81-78-803-5863, Fax:81-78-871-3617)
FEATURES             Location/Qualifiers
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                     NVAHPASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMISLSP
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                     GKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFM
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GIN

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t. Local Similarity: 65.4%         Mismatches:    42
ry Match:           49.6%          Indels:        81
                    6              Gaps:          9

10-048-116B-2 (1-495) x AB097847 (1-1570)

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       423 CAAGGGACTCTGGTCACTGTCTCTGCAGCCAAA-------------------------- 455

       104 SerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPheProLysSerPro 123
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       456 --------------------ACAACAGCCCCA------TCGGTCTATCCACTGGCCCCT 488

       124 Val---------LeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhe 140
           |||         |||      ||||||   |||   |||          |||
       489 GTGTGTGGAGATACAACTGGCTCCTCGGTGACTCTAGGATGCCTGGTCAAGGGTTATTTC 548

       141 ProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyr 160
           |||      :::   :::||||||      ||||||   |||::::::   ||||||:::
       549 CCTGAGCCAGTGACCTTGACCTGG------AACTCTGGATCCCTGTCCAGTGGTGTGCAC 602

       161 GluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPhe 180
                   ::::::      |||          :::   ||||||   |||:::
       603 ACCTTCCCAGCTGTCCTGCAGTCTGAC------CTCTACACCCTCAGCAG-CTCAGT--- 652

       181 IleProSerAspAspAspIleTyrAspCysLysValGluHis-TrpGlyLeuGluGluPr 200
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       653 -----------------------GACTGTAACCTCGAGCACCTGG-------------- 674

       200 oValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThrGl 220
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       675 ---------------------------------CCCAGCCAGTCCATCACC-------- 692

       220 yGlyGlyGlySerThrThrAlaProSerAlaGlnLeuGluLysGluLeuGlnAlaLeuGl 240
                  :::      |||   |||   ::::::::::|||::::::
       693 -TGCAATGTGGCCCACCCGGCAAGCAGCACCAAGGTGGACAAGAAAATT----------- 740

       240 uLysGluAsnAlaGlnLeuGluTrpGluLeuGlnAlaLeuGluLysGluLeuAlaGlnAl 260

Db      740 ------------------------------------------------------------ 740

Qy      260 aAlaSerGluProArgGlyProThrIleLysProCysProProCysLysCysProAlaPr 280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      741 -------GAGCCCAGAGGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCAGCACC 793

Qy      280 oAsnLeuLeuGlyGlyProSerValPheIlePheProProLysIleLysAspValLeuMe 300
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Db      794 TAACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCAT 853

Qy      300 tIleSerLeuSerProIleValThrCysValValValAspValSerGluAspAspProAs 320
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Db      854 GATCTCCCTGAGCCCCATAGTCACATGTGTGGTGGTGGATGTGAGCGAGGATGACCCAGA 913

Qy      320 pValGlnIleSerTrpPheValAsnAsnValGluValHisThrAlaGlnThrGlnThrHi 340
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Db      914 TGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAAACCCA 973

Qy      340 sArgGluAspTyrAsnSerThrLeuArgValValSerAlaLeuProIleGlnHisGlnAs 360
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Qy      360 pTrpMetSerGlyLysGluPheLysCysLysValAsnAsnLysAspLeuProAlaProIl 380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1034 CTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAAGACCTCCCAGCGCCCAT 1093

Qy      380 eGluArgThrIleSerLysProLysGlySerValArgAlaProGlnValTyrValLeuPr 400
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Db     1094 CGAGAGAACCATCTCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTTGCC 1153

Qy      400 oProProGluGluGluMetThrLysLysGlnValThrLeuThrCysMetValThrAspPh 420
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Db     1154 TCCACCAGAAGAAGAGATGACTAAGAAACAGGTCACTCTGACCTGCATGGTCACAGACTT 1213

Qy      420 eMetProGluAspIleTyrValGluTrpThrAsnAsnGlyLysThrGluLeuAsnTyrLy 440
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Db     1214 CATGCCTGAAGACATTTACGTGGAGTGGACCAACAACGGGAAAACAGAGCTAAACTACAA 1273

Qy      440 sAsnThrGluProValLeuAspSerAspGlySerTyrPheMetTyrSerLysLeuArgVa 460
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1274 GAACACTGAACCAGTCCTGGACTCTGATGGTTCTTACTTCATGTACAGCAAGCTGAGAGT 1333

Qy      460 lGluLysLysAsnTrpValGluArgAsnSerTyrSerCysSerValValHisGluGlyLe 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1334 GGAAAAGAAGAACTGGGTGGAAAGAAATAGCTACTCCTGTTCAGTGGTCCACGAGGGTCT 1393

Qy      480 uHisAsnHisHisThrThrLysSerPheSerArgThrProGlyLys 495
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Db     1394 GCACAATCACCACACGACTAAGAGCTTCTCCCGGACTCCGGGTAAA 1439

RESULT 10
CS125905
LOCUS       CS125905               1407 bp    DNA     linear   PAT 21-JUL-2005
DEFINITION  Sequence 49 from Patent WO2005061545.
ACCESSION   CS125905
VERSION     CS125905.1  GI:71058939
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Hussain,I.
  TITLE     Nogoa antibodies for the treatment of alzheimer disease
  JOURNAL   Patent: WO 2005061545-A 49 07-JUL-2005;
            Glaxo Group Limited (GB)
FEATURES             Location/Qualifiers
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st Local Similarity:  58.6%          Mismatches:      68
ery Match:            49.6%          Indels:          108
:                     2              Gaps:            13

-10-048-116B-2 (1-495) x CS125905 (1-1407)

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        48 ------GlnTyrThrHisGluPheAspGlyAspGluLeuPheTyrValAspLeuAspLys 65
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       238 GGTACTAACTACAATGAGAAGTTCAAGAGCAAGGCCACACTGACTGTAGACAAATCCTCC 297

        66 LysLysThrValTrpArgLeuPro---------------------------------- 73
                    :::|||
       298 AGCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTATTGT 357

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           |||   ||||||         :::      ||||||   |||      :::::::::
       358 GAACTGGGACAG------GGCTACTGGGGCCAAGGCACACTAGTCACCGTCTCCTCAGCC 411

        94 LysHisAsnLeuGlyIleLeuThrLysArgSerAsnPheThrProAlaThrAsnGluAla 113
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       424 CCA------TCGGTCTATCCACTGGCCCCTGTGTGTGGAGATACAACTGGCTCCTCGGTG 477

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       478 ACTCTAGGATGCCTGGTCAAGGGTTATTTCCCTGAGCCAGTGACCTTGACCTGG------ 531

       151 AsnSerLysSerValThrAspGlyValTyrGluThrSerPheLeuValAsnArgAspHis 170
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       618 AACCTCGAGCACCTGG---------------------------------------- 633

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       634 ----CCCAGCCAGTCCATCACC---------TGCAATGTGGCCCACCCGGCAAGCAGCAC 680

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       290 ePheProProLysIleLysAspValLeuMetIleSerLeuSerProIleValThrCysVa 310
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       310 lValValAspValSerGluAspAspProAspValGlnIleSerTrpPheValAsnAsnVa 330
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Qy        330 lGluValHisThrAlaGlnThrGlnThrHisArgGluAspTyrAsnSerThrLeuArgVa 350
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Qy        350 lValSerAlaLeuProIleGlnHisGlnAspTrpMetSerGlyLysGluPheLysCysLy 370
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Qy        370 sValAsnAsnLysAspLeuProAlaProIleGluArgThrIleSerLysProLysGlySe 390
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Qy        390 rValArgAlaProGlnValTyrValLeuProProProGluGluGluMetThrLysLysGl 410
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Qy        410 nValThrLeuThrCysMetValThrAspPheMetProGluAspIleTyrValGluTrpTh 430
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Qy        490 rArgThrProGlyLys 495
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RESULT 11
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LOCUS       CS126190                1407 bp    DNA     linear   PAT 21-JUL-2005
DEFINITION  Sequence 49 from Patent WO2005061544.
ACCESSION   CS126190
VERSION     CS126190.1  GI:71059163
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Ellis,J.H.
  TITLE     Nogo-a neutralising immunoglobulins for treatment of neurological
            diseases
  JOURNAL   Patent: WO 2005061544-A 49 07-JUL-2005;
            Glaxo Group Limited (GB)
FEATURES             Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.:              6.08e-123      Length:          1407
Score:                  1320.00        Matches:         285
Percent Similarity:     64.0%          Conservative:    26
Best Local Similarity:  58.6%          Mismatches:      68
Query Match:            49.6%          Indels:          108
DB:                     2              Gaps:            13

US-10-048-116B-2 (1-495) x CS126190 (1-1407)
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238 GGTACTAACTACAATGAGAAGTTCAAGAGCAAGGCCACACTGACTGTAGACAAATCCTCC 297

 66 LysLysThrValTrpArgLeuPro---------------------------------- 73
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298 AGCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTATTGT 357

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358 GAACTGGGACAG------GGCTACTGGGGCCAAGGCACACTAGTCACCGTCTCCTCAGCC 411

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114 ProGlnAlaThrValPheProLysSerProVal---------LeuLeuGlyGlnProAsn 130
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424 CCA------TCGGTCTATCCACTGGCCCCTGTGTGTGGAGATACAACTGGCTCCTCGGTG 477

131 ThrLeuIleCysPheValAspAsnIleProProValIleAsnIleThrTrpLeuArg 150
    ||||||  |||  |||        ||||||     :::  :::||||||
478 ACTCTAGGATGCCTGGTCAAGGGTTATTTCCCTGAGCCAGTGACCTTGACCTGG------ 531

151 AsnSerLysSerValThrAspGlyValTyrGluThrSerPheLeuValAsnArgAspHis 170
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532 AACTCTGGATCCCTGTCCAGTGGTGTGCACACCTTCCCAGCTGTCCTGCAGTCTGAC--- 588

171 SerPheHisLysLeuSerTyrLeuThrPheIleProSerAspAspAspIleTyrAspCys 190
        :::  ||||||  |||:::                              ||||||
589 ---CTCTACACCCTCAGCAG-CTCAGT-------------------------GACTGT 617

191 LysValGluHis-TrpGlyLeuGluGluProValLeuLysHisTrpGluProGluIlePr 210
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618 AACCTCGAGCACCTGG---------------------------------------- 633

210 oAlaProMetSerGluLeuThrGluThrGlyGlyGlyGlySerThrThrAlaProSerAl 230
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634 ----CCCAGCCAGTCCATCACC---------TGCAATGTGGCCCACCCGGCAAGCAGCAC 680

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     :::::::::|||::::::
681 CAAGGTGGACAAGAAAATT---------------------------------------- 699

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700 ----------------------------------GAGCCCAGAGGGCCCACAATCAA 722

270 sProCysProProCysLysCysProAlaProAsnLeuLeuGlyGlyProSerValPheIl 290
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310 lValValAspValSerGluAspAspProAspValGlnIleSerTrpPheValAsnAsnVa 330
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330 lGluValHisThrAlaGlnThrGlnThrHisArgGluAspTyrAsnSerThrLeuArgVa 350
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903 GGAAGTACACACAGCTCAGACACAAACCCATAGAGAGGATTACAACAGTACTCTCCGGGT 962

350 lValSerAlaLeuProIleGlnHisGlnAspTrpMetSerGlyLysGluPheLysCysLy 370
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963 GGTCAGTGCCCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAA 1022

370 sValAsnAsnLysAspLeuProAlaProIleGluArgThrIleSerLysProLysGlySe 390
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Db       1023 GGTCAACAACAAAGACCTCCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGGTC 1082

Qy        390 rValArgAlaProGlnValTyrValLeuProProProGluGluGluMetThrLysLysGl 410
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Db       1083 AGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACCAGAAGAAGAGATGACTAAGAAACA 1142

Qy        410 nValThrLeuThrCysMetValThrAspPheMetProGluAspIleTyrValGluTrpTh 430
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Db       1143 GGTCACTCTGACCTGCATGGTCACAGACTTCATGCCTGAAGACATTTACGTGGAGTGGAC 1202

Qy        430 rAsnAsnGlyLysThrGluLeuAsnTyrLysAsnThrGluProValLeuAspSerAspGl 450
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1203 CAACAACGGGAAAACAGAGCTAAACTACAAGAACACTGAACCAGTCCTGGACTCTGATGG 1262

Qy        450 ySerTyrPheMetTyrSerLysLeuArgValGluLysLysAsnTrpValGluArgAsnSe 470
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Db       1263 TTCTTACTTCATGTACAGCAAGCTGAGAGTGGAAAAGAAGAACTGGGTGGAAAGAAATAG 1322

Qy        470 rTyrSerCysSerValValHisGluGlyLeuHisAsnHisHisThrThrLysSerPheSe 490
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Db       1323 CTACTCCTGTTCAGTGGTCCACGAGGGTCTGCACAATCACCACACGACTAAGAGCTTCTC 1382

Qy        490 rArgThrProGlyLys 495
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Db       1383 CCGGACTCCGGGTAAA 1398

RESULT 12
CS138860
LOCUS       CS138860                1401 bp    DNA     linear   PAT 17-AUG-2005
DEFINITION  Sequence 1 from Patent WO2005068503.
ACCESSION   CS138860
VERSION     CS138860.1  GI:73530223
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Liu,C.
  TITLE     M-csf-specific monoclonal antibody and uses thereof
  JOURNAL   Patent: WO 2005068503-A 1 28-JUL-2005;
            CHIRON CORPORATION (US); Liu, Cheng (US)
FEATURES             Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.:                6.79e-123      Length:          1401
Score:                    1319.50        Matches:         267
Percent Similarity:       72.6%          Conservative:    27
Best Local Similarity:    65.9%          Mismatches:      49
Query Match:              49.6%          Indels:          63
DB:                       2              Gaps:            7

US-10-048-116B-2 (1-495) x CS138860 (1-1401)

Qy         95 HisAsnLeuGlyIleLeuThrLysArgSerAsnPheThrProAlaThrAsnGluAlaPro 114
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Db        364 CACGCCATGGATTACTGGGGCCAAGGGACTTCGGTCACTGTCTCTTCCGCCAAAACAACA 423

Qy        115 GlnAlaThrValPheProLysSerProVal---------LeuLeuGlyGlnProAsnThr 131
              :::|||:::|||   :::||||||                 |||          |||
Db        424 GCCCCATCGGTCTATCCACTGGCCCCTGTGTGTGGAGATACAACTGGCTCCTCGGTGACT 483

Qy        132 LeuIleCysPheValAspAsnIlePheProProValIleAsnIleThrTrpLeuArgAsn 151
              |||   |||   |||        ||||||     :::   :::||||||      |||
Db        484 CTAGGATGCCTGGTCAAGGGTTATTTCCCTGAGCCAGTGACCTTGACCTGG------AAC 537
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 152 SerLysSerValThrAspGlyValTyrGluThrSerPheLeuValAsnArgAspHisSer 171
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 538 TCTGGATCCCTGTCCAGTGGTGTGCACACCTTCCCAGCTGTCCTGCAGTCTGAC------ 591

 172 PheHisLysLeuSerTyrLeuThrPheIleProSerAspAspAspIleTyrAspCysLys 191
        :::   ||||||   |||:::                                ||||||
 592 CTCTACACCCTCAGCAG-CTCAGT-------------------------GACTGTAAC 623

 192 ValGluHis-TrpGlyLeuGluGluProValLeuLysHisTrpGluProGluIleProAl 211
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 624 CTCGAGCACCTGG---------------------------------------------- 636

 211 aProMetSerGluLeuThrGluThrGlyGlyGlyGlySerThrThrAlaProSerAlaGl 231
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 637 -CCCAGCCAGTCCATCACC---------TGCAATGTGGCCCACCCGGCAAGCAGCACCAA 686

 231 nLeuGluLysGluLeuGlnAlaLeuGluLysGluAsnAlaGlnLeuGluTrpGluLeuGl 251
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 687 GGTGGACAAGAAAATT------------------------------------------- 702

 251 nAlaLeuGluLysGluLeuAlaGlnAlaAlaSerGluProArgGlyProThrIleLysPr 271
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 271 oCysProProCysLysCysProAlaProAsnLeuLeuGlyGlyProSerValPheIlePh 291
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 729 CTGTCCTCCATGCAAATGCCCAGCACCTAACCTCTTGGGTGGACCATCCGTCTTCATCTT 788

 291 eProProLysIleLysAspValLeuMetIleSerLeuSerProIleValThrCysValVa 311
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 311 lValAspValSerGluAspAspProAspValGlnIleSerTrpPheValAsnAsnValGl 331
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 849 GGTGGATGTGAGCGAGGATGACCCAGATGTCCAGATCAGCTGGTTTGTGAACAACGTGGA 908

 331 uValHisThrAlaGlnThrGlnThrHisArgGluAspTyrAsnSerThrLeuArgValVa 351
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 351 lSerAlaLeuProIleGlnHisGlnAspTrpMetSerGlyLysGluPheLysCysLysVa 371
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1029 CAACAACAAAGACCTCCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGGTCAGT 1088

 391 lArgAlaProGlnValTyrValLeuProProProGluGluGluMetThrLysLysGlnVa 411
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1089 AAGAGCTCCACAGGTATATGTCTTGCCTCCACCAGAAGAAGAGATGACTAAGAAACAGGT 1148

 411 lThrLeuThrCysMetValThrAspPheMetProGluAspIleTyrValGluTrpThrAs 431
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1149 CACTCTGACCTGCATGGTCACAGACTTCATGCCTGAAGACATTTACGTGGAGTGGACCAA 1208

 431 nAsnGlyLysThrGluLeuAsnTyrLysAsnThrGluProValLeuAspSerAspGlySe 451
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1209 CAACGGGAAAACAGAGCTAAACTACAAGAACACTGAACCAGTCCTGGACTCTGATGGTTC 1268

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1269 TTACTTCATGTACAGCAAGCTGAGAGTGGAAAAGAAGAACTGGGTGGAAAGAAATAGCTA 1328

 471 rSerCysSerValValHisGluGlyLeuHisAsnHisHisThrThrLysSerPheSerAr 491
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1329 CTCCTGTTCAGTGGTCCACGAGGGTCTGCACAATCACCACACGACTAAGAGCTTCTCCCG 1388

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1389 GACTCCGGGTAAA 1401
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MMU294738
LOCUS       MMU294738               990 bp    mRNA    linear   ROD 09-FEB-2001
DEFINITION  Mus musculus partial mRNA for immunoglobulin heavy chain constant
            region gamma2a (IGHG2A gene).
ACCESSION   AJ294738
VERSION     AJ294738.1  GI:12055401
KEYWORDS    constant region; gamma 2a; IGHG2A gene; immunoglobulin heavy chain.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   McLean,G.R., Nakouzi,A., Casadevall,A. and Green,N.S.
  TITLE     Human and murine immunoglobulin expression vector cassettes
  JOURNAL   Mol. Immunol. 37 (14), 837-845 (2000)
   PUBMED   11257305
REFERENCE   2  (bases 1 to 990)
  AUTHORS   McLean,G.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-SEP-2000) McLean G.R., Cell Biology, Albert Einstein
            College of Medicine, 1300 Morris Park Avenue, Bronx, New York
            10461, USA
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ORIGIN

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Percent Similarity:     73.7%           Conservative:   20
Best Local Similarity:  68.5%           Mismatches:     39
Query Match:            49.6%           Indels:         65
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US-10-048-116B-2 (1-495) x MMU294738 (1-990)

Qy        109 AlaThrAsnGluAlaProGlnAlaThrValPheProLysSerProVal---------Leu 125
                 |||         ||||||       :::|||:::|||   :::|||||
Db          1 GCCAAAACAACAGCCCCA------TCGGTCTATCCACTGGCCCCTGTGTGTGGAGATACA 54

Qy        126 LeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePheProProValIleAsn 145
                 |||         ||||||   |||   |||         ||||||      :::
Db         55 ACTGGCTCCTCGGTGACTCTAGGATGCCTGGTCAAGGGTTATTTCCCTGAGCCAGTGACC 114

Qy        146 IleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyrGluThrSerPheLeu 165
                 :::||||||       ||||||   |||::::::   ||||||:::           :::
Db        115 TTGACCTGG------AACTCTGGATCCCTGTCCAGTGGTGTGCACACCTTCCCAGCTGTC 168

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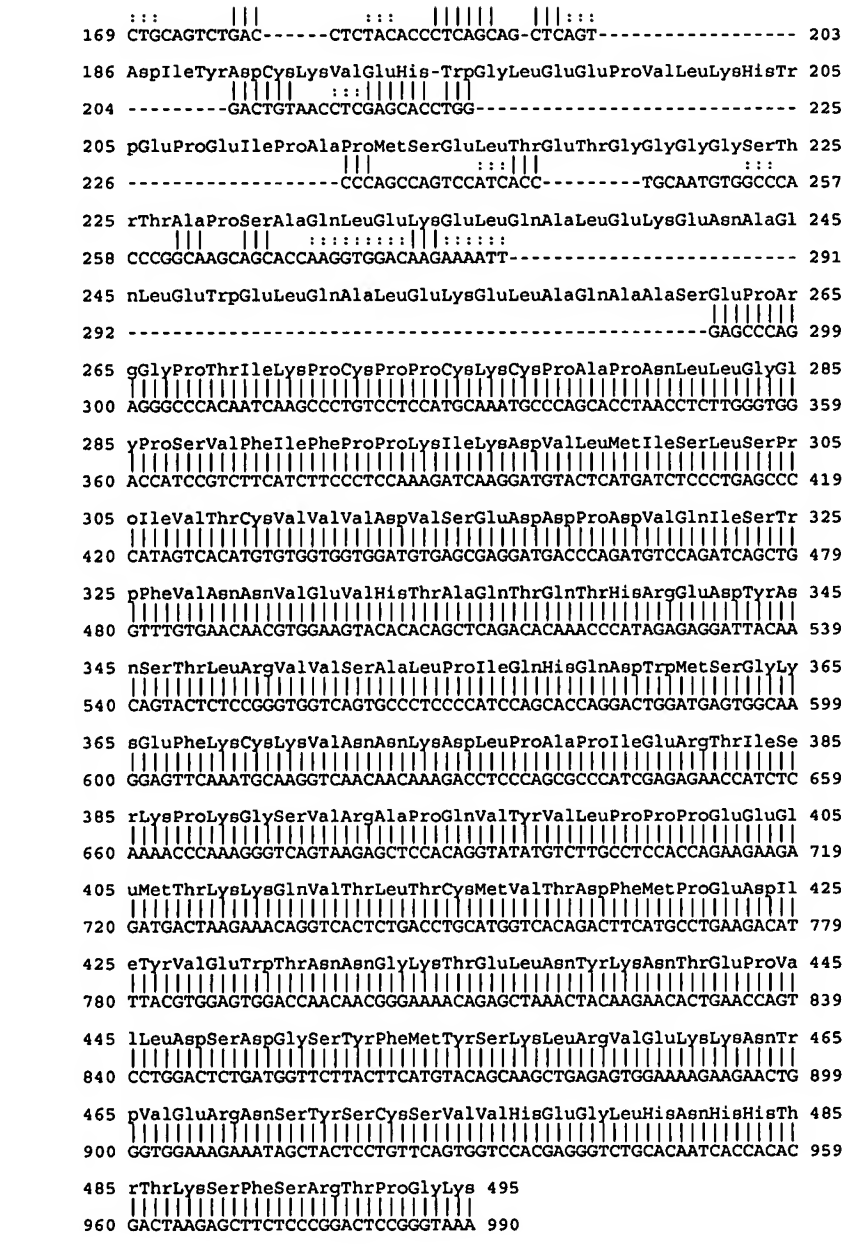

ULT 14
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'US MMIGG6 1095 bp mRNA linear ROD 17-NOV-2004
'INITION Mouse mRNA for gamma-2a-immunoglobulin heavy-chain.
'SSION V00798
SION V00798.1 GI:51835

KEYWORDS complementary DNA; gamma-immunoglobulin; immunoglobulin.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1095)
AUTHORS Sikorav,J.L., Auffray,C. and Rougeon,F.
TITLE Structure of the constant and 3' untranslated regions of the murine Balb/c gamma 2a heavy chain messenger RNA
JOURNAL Nucleic Acids Res. 8 (14), 3143-3155 (1980)
PUBMED 6777755
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ISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKN
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ORIGIN

Alignment Scores:

Pred. No.:	6.03e-123	Length:	1095
Score:	1318.50	Matches:	268
Percent Similarity:	73.7%	Conservative:	20
Best Local Similarity:	68.5%	Mismatches:	39
Query Match:	49.6%	Indels:	65
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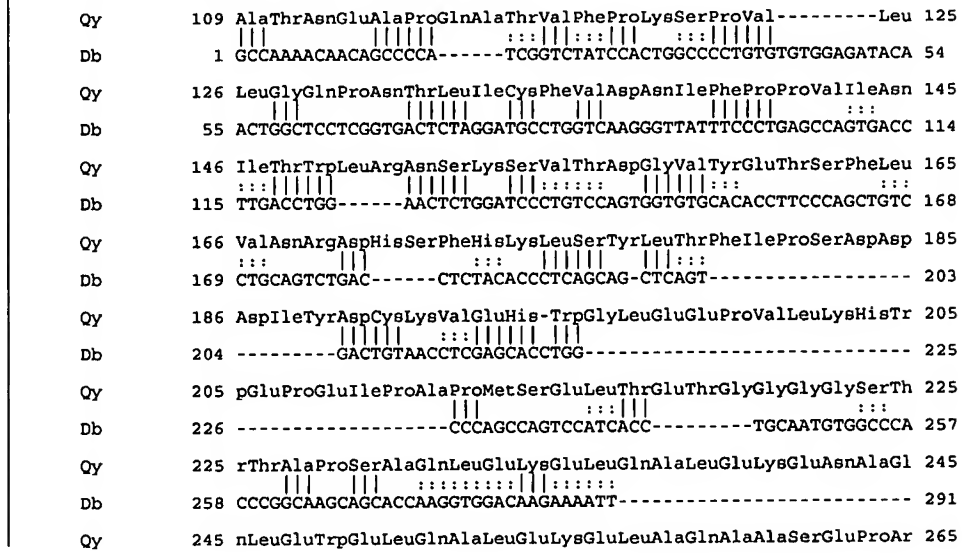
US-10-048-116B-2 (1-495) x MMIGG6 (1-1095)



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305 oIleValThrCysValValValAspValSerGluAspAspProAspValGlnIleSerTr 325
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325 pPheValAsnAsnValGluValHisThrAlaGlnThrGlnThrHisArgGluAspTyrAs 345
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540 CAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAA 599

365 sGluPheLysCysLysValAsnAsnLysAspLeuProAlaProIleGluArgThrIleSe 385
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600 GGAGTTCAAATGCAAGGTCAACAACAAAGACCTCCCAGCGCCCATCGAGAGAACCATCTC 659

385 rLysProLysGlySerValArgAlaProGlnValTyrValLeuProProProGluGluGl 405
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900 GGTGGAAAGAAATAGCTACTCCTGTTCAGTGGTCCACGAGGGTCTGCACAATCACCACAC 959

485 rThrLysSerPheSerArgThrProGlyLys 495
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SULT 15
166698
CUS         AF466698            1407 bp    mRNA    linear   ROD 17-DEC-2002
FINITION    Mus musculus strain BALB/c immunoglobulin heavy chain mRNA, partial
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CESSION     AF466698
RSION       AF466698.1  GI:27127159
YWORDS      .
URCE        Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
FERENCE     1  (bases 1 to 1407)
AUTHORS     Lai,Y.S., John,J.A.C., Guo,I.C., Chen,S.C., Fang,K. and Chang,C.Y.
TITLE       In vitro efficiency of intra- and extracellular immunization with
            mouse anti-YGNNV antibody against yellow grouper nervous necrosis
            virus
JOURNAL     Vaccine 20 (25-26), 3221-3229 (2002)
 PUBMED     12163274
FERENCE     2  (bases 1 to 1407)
AUTHORS     Lai,Y.-S., John,C., Guo,I.-C., Chen,S.-C., Fang,K. and Chang,C.-Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-JAN-2002) Institute of Zoology, Academia Sinica, 128
            Academia Road, NanKang, Taipei 11529, Taiwan, ROC
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ORIGIN

Alignment Scores:
Pred. No.:              8.61e-123      Length:        1407
Score:                  1318.50        Matches:       266
Percent Similarity:     73.2%          Conservative:  24
Best Local Similarity:  67.2%          Mismatches:    44
Query Match:            49.6%          Indels:        63
DB:                     6              Gaps:          7

US-10-048-116B-2 (1-495) x AF466698 (1-1407)

Qy        104 SerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPheProLysSerPro 123
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Qy        124 Val---------LeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhe 140
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Qy        141 ProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyr 160
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Qy        161 GluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPhe 180
                       ::::::      |||         :::   ||||||   |||:::
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Qy        200 oValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThrGl 220
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Qy        220 yGlyGlyGlySerThrThrAlaProSerAlaGlnLeuGluLysGluLeuGlnAlaLeuGl 240
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Db        661 -TGCAATGTGGCCCACCCGGCAAGCAGCACCAAGGTGGACAAGAAAATT----------- 708

Qy        240 uLysGluAsnAlaGlnLeuGluTrpGluLeuGlnAlaLeuGluLysGluLeuAlaGlnAl 260

Db        708 ------------------------------------------------------------ 708

Qy        260 aAlaSerGluProArgGlyProThrIleLysProCysProProCysLysCysProAlaPr 280
                     |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        709 -------GAGCCCAGAGGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCAGCACC 761

Qy        280 oAsnLeuLeuGlyGlyProSerValPheIlePheProProLysIleLysAspValLeuMe 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
       762 TAACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCAT 821

       300 tIleSerLeuSerProIleValThrCysValValValAspValSerGluAspAspProAs 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       822 GATCTCCCTGAGCCCCATAGTCACATGTGTGGTGGTGGATGTGAGCGAGGATGACCCAGA 881

       320 pValGlnIleSerTrpPheValAsnAsnValGluValHisThrAlaGlnThrGlnThrHi 340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       882 TGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAAACCCA 941

       340 sArgGluAspTyrAsnSerThrLeuArgValValSerAlaLeuProIleGlnHisGlnAs 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       942 TAGAGAGGATTACAACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGA 1001

       360 pTrpMetSerGlyLysGluPheLysCysLysValAsnAsnLysAspLeuProAlaProIl 380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1002 CTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAAGACCTCCCAGCGCCCAT 1061

       380 eGluArgThrIleSerLysProLysGlySerValArgAlaProGlnValTyrValLeuPr 400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1062 CGAGAGAACCATCTCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTTGCC 1121

       400 oProProGluGluGluMetThrLysLysGlnValThrLeuThrCysMetValThrAspPh 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1122 TCCACCAGAAGAAGAGATGACTAAGAAACAGGTCACTCTGACCTGCATGGTCACAGACTT 1181

       420 eMetProGluAspIleTyrValGluTrpThrAsnAsnGlyLysThrGluLeuAsnTyrLy 440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1182 CATGCCTGAAGACATTTACGTGGAGTGGACCAACAACGGGAAAACAGAGCTAAACTACAA 1241

       440 sAsnThrGluProValLeuAspSerAspGlySerTyrPheMetTyrSerLysLeuArgVa 460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1242 GAACACTGAACCAGTCCTGGACTCTGATGGTTCTTACTTCATGTACAGCAAGCTGAGAGT 1301

       460 lGluLysLysAsnTrpValGluArgAsnSerTyrSerCysSerValValHisGluGlyLe 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1302 GGAAAAGAAGAACTGGGTGGAAAGAAATAGCTACTCCTGTTCAGTGGTCCACGAGGGTCT 1361

       480 uHisAsnHisHisThrThrLysSerPheSerArgThrProGlyLys 495
           ||||||||||||||||||||||||||||||||||||||||||||||||
      1362 GCACAATCACCACACGACTAAGAGCTTCTCCCGGACTCCGGGTAAA 1407
```

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ch completed: June  1, 2006, 03:20:55
 time : 9336.63 secs
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GenCore version 5.1.8

protein - nucleic search, using frame_plus_p2n model

n on: May 31, 2006, 22:51:28 ; Search time 992.561 Seconds
(without alignments)
5215.692 Million cell updates/sec

tle: US-10-048-116B-2
rfect score: 2660
quence: 1 MPCSRALILGVLALNTMLSL.....VHEGLHNHHTTKSFSRTPGK 495

oring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

arched: 5244920 seqs, 3486124231 residues

tal number of hits satisfying chosen parameters: 10489840

nimum DB seq length: 0
ximum DB seq length: 2000000000

st-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

mmand line parameters:
)DEL=frame+_p2n.model -DEV=xlh
=/abss/ABSSWEB_spool/US10048116/runat_31052006_110043_25584/app_query.fasta_1
3=N_Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
NITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
)CALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
JTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss04
3ER=US10048116_@CGN_1_1_942_@runat_31052006_110043_25584 -NCPU=6 -ICPU=3
) MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
ARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
3APOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

tabase : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	Query Match	Length	DB	ID	Description
1	2655	99.8	1484	5	AAF55098	Aaf55098 DNA encod
2	2247	84.5	1676	4	ABI99041	Abi99041 Murine pC
3	1924.5	72.3	1446	2	AAT99707	Aat99707 DR2-IgG f
4	1924.5	72.3	1446	2	AAX87813	Aax87813 HLA-DR2 a
5	1924.5	72.3	1446	14	ADW44282	Adw44282 DR2-IgG f
6	1738	65.3	2346	4	ABI99027	Abi99027 IAS MBP 1
7	1737.5	65.3	2343	4	ABI99033	Abi99033 MBP 90-10
8	1521	57.2	2053	4	ABI99029	Abi99029 IAS MBP 9
9	1521	57.2	2059	4	ABI99032	Abi99032 MBP 1-14
10	1332	50.1	7528	4	AAF30316	Aaf30316 Bicistron
11	1328.5	49.9	3973	13	ADT77690	Adt77690 Monoclona
12	1324.5	49.8	1581	2	AAQ48037	Aaq48037 Monoclona
13	1321.5	49.7	1560	14	AED19725	Aed19725 Anti-PrP
14	1320	49.6	1407	14	AEB21727	Aeb21727 Anti-Nogo
15	1320	49.6	1407	14	AEB08761	Aeb08761 antibody
16	1319.5	49.6	1401	14	AEC20762	Aec20762 M-CSF spe
17	1318.5	49.6	990	12	ADL15694	Adl15694 Murine im
18	1318.5	49.6	1569	14	ADV26108	Adv26108 Mouse OKT
19	1318.5	49.6	1569	14	ADW71834	Adw71834 Murine OK
20	1318.5	49.6	1570	2	AAQ12637	Aaq12637 Monoclona
21	1318.5	49.6	1570	12	ADQ91058	Adq91058 Murine OK
22	1317.5	49.5	6729	4	AAF30341	Aaf30341 Bicistron
23	1315.5	49.5	1645	2	AAQ54652	Aaq54652 T84.12 He
24	1312.5	49.3	1341	1	AAN91659	Aan91659 Chimeric
25	1309.5	49.2	1356	12	ADN97544	Adn97544 Artificia
26	1300.5	48.9	1389	14	AEA27480	Aea27480 Monoclona
27	1285.5	48.3	1140	10	ADE85817	Ade85817 Murine in
28	1284	48.3	1194	2	AAV55415	Aav55415 Chimeric
29	1281.5	48.2	1524	14	AEE21946	Aee21946 Single ch
30	1280.5	48.1	1473	13	ADS31748	Ads31748 DNA encod
31	1280.5	48.1	1473	13	ADS92750	Ads92750 DNA encod
32	1280	48.1	1045	12	ADO07566	Ado07566 Fusion pr
33	1280	48.1	1509	14	AEE21942	Aee21942 Single ch
34	1279.5	48.1	1140	10	ADE85819	Ade85819 Murine mu
35	1278	48.0	1131	2	AAV55416	Aav55416 Chimeric
36	1275	47.9	1108	12	ADO07578	Ado07578 Fusion pr
37	1275	47.9	1108	12	ADO07577	Ado07577 Fusion pr
38	1275	47.9	1461	6	AAD22972	Aad22972 Mouse Zal
39	1272	47.8	729	3	AAZ35704	Aaz35704 Human gly
40	1270	47.7	1707	3	AAZ35706	Aaz35706 Human gly
41	1269.5	47.7	1431	14	AEB12362	Aeb12362 Fusion pr
42	1269.5	47.7	1431	14	AED64242	Aed64242 hOGH-mFC-
43	1269	47.7	1188	2	AAT59349	Aat59349 1-153 c-m
44	1269	47.7	1275	2	AAT62850	Aat62850 Mouse sol
45	1268	47.7	699	3	AAZ51300	Aaz51300 Murine im

ALIGNMENTS

RESULT 1
AAF55098
ID AAF55098 standard; DNA; 1484 BP.
XX
AC AAF55098;
XX
DT 15-MAY-2001 (first entry)
XX
DE DNA encoding a fusion protein comprising an alpha chain of MHC.
XX
KW Recombinant protein; alpha chain; beta chain; MHC; immunoglobulin;
KW major histocompatibility complex; Fc region; antigen; T lymphocyte;
KW immunostimulant; vaccine; infection; tumour; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1. .1482
FT /*tag= a
XX
PN WO200109194-A1.
XX
PD 08-FEB-2001.
XX
PF 28-JUL-2000; 2000WO-FR002193.
XX
PR 29-JUL-1999; 99FR-00009862.

(CNRS) CNRS CENT NAT RECH SCI.

Glaichenhaus N, Malherbe L;

WPI; 2001-182944/18.
P-PSDB; AAB67480.

New soluble recombinant protein, useful e.g. as immunostimulant, comprises dimeric major histocompatibility complex molecule fused to immunoglobulin Fc region.

Example 1; Page 31-33; 43pp; French.

The specification describes soluble recombinant proteins that comprise at least a dimer formed from the alpha and beta-chains of MHC (major histocompatibility complex) Class I and II molecules in which at least one chain has, attached to its C-terminus, at least part of the Fc region of an immunoglobulin. The recombinant proteins, when linked to an antigenic peptide, are used to count and/or purify antigen-reactive T lymphocytes and to characterize their phenotype, e.g. in preclinical evaluation of vaccines. They are also used as immunostimulants, particularly for vaccine development (against infections and tumours), to count and determine phenotype of autoreactive T cells in subjects with, or at risk of developing, autoimmune diseases, e.g. for staging or evaluating treatments, and (to purify and/or enrich Ag-reactive T cells from cell cultures or patient samples, for use in subsequent curative or preventative cellular therapy. The present sequence encodes a recombinant protein of the invention, comprising an alpha chain of MHC molecules

Sequence 1484 BP; 414 A; 394 C; 362 G; 314 T; 0 U; 0 Other;

gnment Scores:

d. No.:	1.06e-218	Length:	1484
re:	2655.00	Matches:	494
cent Similarity:	100.0%	Conservative:	0
t Local Similarity:	100.0%	Mismatches:	0
ry Match:	99.8%	Indels:	0
	5	Gaps:	0

10-048-116B-2 (1-495) x AAF55098 (1-1484)

```
          1 MetProCysSerArgAlaLeuIleLeuGlyValLeuAlaLeuAsnThrMetLeuSerLeu 20
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          1 ATGCCGTGCAGCAGAGCTCTGATTCTGGGGGTCCTCGCCCTGAACACCATGCTCAGCCTC 60

         21 CysGlyGlyGluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrThrValTyr 40
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         61 TGCGGAGGTGAAGACGACATTGAGGCCGACCACGTAGGCTTCTATGGTACAACTGTTTAT 120

         41 GlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        121 CAGTCTCCTGGAGACATTGGCCAGTACACACATGAATTTGATGGTGATGAGTTGTTCTAT 180

         61 ValAspLeuAspLysLysLysThrValTrpArgLeuProGluPheGlyGlnLeuIleLeu 80
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        181 GTGGACTTGGATAAGAAGAAAACTGTCTGGAGGCTTCCTGAGTTTGGCCAATTGATACTC 240

         81 PheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeu 100
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        241 TTTGAGCCCCAAGGTGGACTGCAAAACATAGCTGCAGAAAAACACAACTTGGGAATCTTG 300

        101 ThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPhePro 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        301 ACTAAGAGGTCAAATTTCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGTTCCCC 360

        121 LysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhe 140
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        361 AAGTCCCCTGTGCTGCTGGGTCAGCCCAACACCCTTATCTGCTTTGTGGACAACATCTTC 420

        141 ProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyr 160
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        421 CCACCTGTGATCAACATCACATGGCTCAGAAATAGCAAGTCAGTCACAGACGGCGTTTAT 480

Qy      161 GluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPhe 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 GAGACCAGCTTCCTCGTCAACCGTGACCATTCCTTCCACAAGCTGTCTTATCTCACCTTC 540

Qy      181 IleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluPro 200
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 ATCCCTTCTGATGATGACATTTATGACTGCAAGGTGGAGCACTGGGGCCTGGAGGAGCCG 600

Qy      201 ValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThrGly 220
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 GTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAAACTGGA 660

Qy      221 GlyGlyGlySerThrThrAlaProSerAlaGlnLeuGluLysGluLeuGlnAlaLeuGlu 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 GGTGGAGGATCCACTACAGCTCCATCAGCTCAGCTCGAAAAAGAGCTCCAGGCCCTGGAG 720

Qy      241 LysGluAsnAlaGlnLeuGluTrpGluLeuGlnAlaLeuGluLysGluLeuAlaGlnAla 260
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 AAGGAAAATGCACAGCTGGAATGGGAGTTGCAAGCACTGGAAAAGGAACTGGCTCAGGCA 780

Qy      261 AlaSerGluProArgGlyProThrIleLysProCysProProCysLysCysProAlaPro 280
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 GCATCTGAGCCCAGAGGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCAGCACCT 840

Qy      281 AsnLeuLeuGlyGlyProSerValPheIlePheProProLysIleLysAspValLeuMet 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 AACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATG 900

Qy      301 IleSerLeuSerProIleValThrCysValValValAspValSerGluAspAspProAsp 320
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 ATCTCCCTGAGCCCCATAGTCACATGTGTGGTGGTGGATGTGAGCGAGGATGACCCAGAT 960

Qy      321 ValGlnIleSerTrpPheValAsnAsnValGluValHisThrAlaGlnThrGlnThrHis 340
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 GTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAAACCCAT 1020

Qy      341 ArgGluAspTyrAsnSerThrLeuArgValValSerAlaLeuProIleGlnHisGlnAsp 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 AGAGAGGATTACAACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGAC 1080

Qy      361 TrpMetSerGlyLysGluPheLysCysLysValAsnAsnLysAspLeuProAlaProIle 380
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081 TGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAAGACCTCCCAGCGCCCATC 1140

Qy      381 GluArgThrIleSerLysProLysGlySerValArgAlaProGlnValTyrValLeuPro 400
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1141 GAGAGAACCATCTCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTTGCCT 1200

Qy      401 ProProGluGluGluMetThrLysLysGlnValThrLeuThrCysMetValThrAspPhe 420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1201 CCACCAGAAGAAGAGATGACTAAGAAACAGGTCACTCTGACCTGCATGGTCACAGACTTC 1260

Qy      421 MetProGluAspIleTyrValGluTrpThrAsnAsnGlyLysThrGluLeuAsnTyrLys 440
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1261 ATGCCTGAAGACATTTACGTGGAGTGGACCAACAACGGGAAAACAGAGCTAAACTACAAG 1320

Qy      441 AsnThrGluProValLeuAspSerAspGlySerTyrPheMetTyrSerLysLeuArgVal 460
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1321 AACACTGAACCAGTCCTGGACTCTGATGGTTCTTACTTCATGTACAGCAAGCTGAGAGTG 1380

Qy      461 GluLysLysAsnTrpValGluArgAsnSerTyrSerCysSerValValHisGluGlyLeu 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1381 GAAAAGAAGAACTGGGTGGAAAGAAATAGCTACTCCTGTTCAGTGGTCCACGAGGGTCTG 1440

Qy      481 HisAsnHisHisThrThrLysSerPheSerArgThrProGly 494
            |||||||||||||||||||||||||||||||||||||||||||
Db     1441 CACAATCACCACACGACTAAGAGCTTCTCCCGGACTCCGGGT 1482
```

RESULT 2
ABI99041
ID ABI99041 standard; cDNA; 1676 BP.
XX

ABI99041;

25-FEB-2002 (first entry)

Murine pCB223 coding sequence.

Mouse; MHC; major histocompatibility complex; MHC class II; multimer; single chain; immunosuppressive; antidiabetic; antiinflammatory; antianaemic; antirheumatoid; antiarthritic; neuroprotective; vaccine; autoimmune disease; insulin dependent diabetes; multiple sclerosis; myasthenia gravis; pernicious anaemia; autoimmune encephalomyelitis; rheumatoid arthritis; systemic lupus erythematosus; ss.

Mus sp.
Synthetic.

WO200170245-A1.

27-SEP-2001.

22-MAR-2001; 2001WO-US009616.

22-MAR-2000; 2000US-0191274P.
15-MAY-2000; 2000US-0204249P.
23-JAN-2001; 2001US-0264003P.

(CORI-) CORIXA CORP.

Carter D, Zhu S, Arimilli S, Wang A;

WPI; 2001-616371/71.
P-PSDB; ABB56471.

Multimeric complex for treating autoimmune diseases, comprises first and second single chain MHC class II molecules, each comprising alpha1 and beta1 domain linked through amino acid linker and multimerization domain.

Disclosure; Page 115; 147pp; English.

The invention relates to a multimeric complex comprising a first recombinant single chain major histocompatibility complex (MHC) class II molecule and a second recombinant single chain MHC class II molecule, each comprising an alpha1 domain and a beta1 domain linked through an amino acid linker and a multimerisation domain. The first and the second molecule are linked through the multimerisation domain to form a multimeric complex,. The complex is useful for treating autoimmune diseases. It is useful for treating insulin dependent diabetes, multiple sclerosis, myasthenia gravis, pernicious anaemia, autoimmune encephalomyelitis (EAE), rheumatoid arthritis and systemic lupus erythematosus. The present sequence encodes a single chain MHC class II molecule of the invention

Sequence 1676 BP; 438 A; 470 C; 407 G; 361 T; 0 U; 0 Other;

ignment Scores:

ed. No.:	1.68e-183	Length:	1676
ore:	2247.00	Matches:	432
rcent Similarity:	81.2%	Conservative:	13
st Local Similarity:	78.8%	Mismatches:	39
ery Match:	84.5%	Indels:	64
:	4	Gaps:	5

-10-048-116B-2 (1-495) x ABI99041 (1-1676)

```
          7 LeuIleLeuGlyValLeuAlaLeuAsnThrMetLeuSerLeuCysGly------GlyGlu 24
            |||:::        :::   :::      :::||||||     |||      ||||||
         37 CTCCTCTCGGCTGCTGTGGTGGTGCTGATGGTGCTGAGCAGCCCAGGGACTGAGGGCGAA 96

         25 AspAspIleGluAlaAspHisValGlyPheTyrGlyThrThrValTyrGlnSerProGly 44
            ||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
         97 GACGACATTGAGGCCGACCACGTAGGCGTCTATGGTACAACTGTATATCAGTCTCCTGGA 156

         45 AspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyrValAspLeuAsp 64
```

```
            ||||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db     157 GACATTGGCCAGTACACACATGAATTTGATGGTGATGAGTGGTTCTATGTGGACTTGGAT 216

Qy      65 LysLysLysThrValTrpArgLeuProGluPheGlyGlnLeuIleLeuPheGluProGln 84
           ||||||:::|||:::|||   |||||||||||||||||||||       |||:::||||||
Db     217 AAGAAGGAGACTATCTGGATGCTTCCTGAGTTTGGCCAATTGACAAGCTTTGACCCCCAA 276

Qy      85 GlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeuThrLysArgSer 104
           ||||||||||||||||||||      |||:::   ||||||||||||||||||||||||||
Db     277 GGTGGACTGCAAAACATAGCTACAGGAAAATACACCTTGGGAATCTTGACTAAGAGGTCA 336

Qy     105 AsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPheProLysSerProVal 124
           |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     337 AATTCCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGTTCCCCAAGTCCCCTGTG 396

Qy     125 LeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePheProProValIle 144
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     397 CTGCTGGGTCAGCCCAACACCCTCATCTGCTTTGTGGACAACATCTTCCCTCCTGTGATC 456

Qy     145 AsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyrGluThrSerPhe 164
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     457 AACATCACATGGCTCAGAAATAGTAAGTCAGTCACAGACGGCGTTTATGAGACCAGCTTC 516

Qy     165 LeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPheIleProSerAsp 184
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     517 CTTGTCAACCGTGACCATTCCTTCCACAAGCTGTCTTATCTCACCTTCATCCCTTCTGAC 576

Qy     185 AspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluProValLeuLysHis 204
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     577 GATGATATTTATGACTGCAAGGTGGAGCACTGGGGCCTGGAGGAGCCGGTTCTGAAACAC 636

Qy     205 TrpGluProGluIleProAlaProMetSerGluLeuThrGluThrGlyGlyGlyGlySer 224
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     637 TGGGAACCTGAGATTCCAGCCCCCATGTCAGAA--------------GGATCTGCCAAA 681

Qy     225 ThrThrAlaProSer---------------------------------------------- 229
           |||||||||||||||
Db     682 ACAACAGCCCCATCGGTCTATCCACTGGCCCCTGTGTGTGGAGATACAACTGGCTCCTCG 741

Qy     229 ------------------------------------------------------------ 229

Db     742 GTGACTCTAGGATGCCTGGTCAAGGGTTATTTCCCTGAGCCAGTGACCTTGACCTGGAAC 801

Qy     230 ----------------------------------AlaGlnLeuGluLysGluLeuGln 237
                                               |||   |||:::   :::|||
Db     802 TCTGGATCCCTGTCCAGTGGTGTGCACACCTTCCCAGCTGTCCTGCAGTCTGACCTCTAC 861

Qy     238 AlaLeuGluLysGlu------AsnAlaGlnLeuGluTrpGluLeuGlnAlaLeuGluLys 255
           |||                  |||       |||::::::
Db     862 ACCCTCAGCAGCTCAGTGACTGTAACCTCGAGCACCTGGCCCAGCCAGTCCATCACCTGC 921

Qy     256 GluLeuAlaGlnAlaAlaSer----------------------GluProArgGlyPro 267
              :::|||      ||||||                     ||||||||||||||||
Db     922 AATGTGGCCCACCCGGCAAGCAGCACCAAGGTGGACAAGAAAATTGAGCCCAGAGGGCCC 981

Qy     268 ThrIleLysProCysProProCysLysCysProAlaProAsnLeuLeuGlyGlyProSer 287
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     982 ACAATCAAGCCCTGTCCTCCATGCAAATGCCCAGCACCTAACCTCTTGGGTGGACCATCC 1041

Qy     288 ValPheIlePheProProLysIleLysAspValLeuMetIleSerLeuSerProIleVal 307
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1042 GTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCATAGTC 1101

Qy     308 ThrCysValValValAspValSerGluAspAspProAspValGlnIleSerTrpPheVal 327
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1102 ACATGTGTGGTGGTGGATGTGAGCGAGGATGACCCAGATGTCCAGATCAGCTGGTTTGTG 1161

Qy     328 AsnAsnValGluValHisThrAlaGlnThrGlnThrHisArgGluAspTyrAsnSerThr 347
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1162 AACAACGTGGAAGTACACACAGCTCAGACACAAACCCATAGAGAGGATTACAACAGTACT 1221

Qy     348 LeuArgValValSerAlaLeuProIleGlnHisGlnAspTrpMetSerGlyLysGluPhe 367
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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      1222 CTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTC 1281

       368 LysCysLysValAsnAsnLysAspLeuProAlaProIleGluArgThrIleSerLysPro 387
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1282 AAATGCAAGGTCAACAACAAAGACCTCCCAGCGCCCATCGAGAGAACCATCTCAAAACCC 1341

       388 LysGlySerValArgAlaProGlnValTyrValLeuProProProGluGluGluMetThr 407
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1342 AAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACCAGAAGAAGAGATGACT 1401

       408 LysLysGlnValThrLeuThrCysMetValThrAspPheMetProGluAspIleTyrVal 427
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1402 AAGAAACAGGTCACTCTGACCTGCATGGTCACAGACTTCATGCCTGAAGACATTTACGTG 1461

       428 GluTrpThrAsnAsnGlyLysThrGluLeuAsnTyrLysAsnThrGluProValLeuAsp 447
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1462 GAGTGGACCAACAACGGGAAAACAGAGCTAAACTACAAGAACACTGAACCAGTCCTGGAC 1521

       448 SerAspGlySerTyrPheMetTyrSerLysLeuArgValGluLysLysAsnTrpValGlu 467
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1522 TCTGATGGTTCTTACTTCATGTACAGCAAGCTGAGAGTGGAAAAGAAGAACTGGGTGGAA 1581

       468 ArgAsnSerTyrSerCysSerValValHisGluGlyLeuHisAsnHisHisThrThrLys 487
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1582 AGAAATAGCTACTCCTGTTCAGTGGTCCACGAGGGTCTGCACAATCACCACACGACTAAG 1641

       488 SerPheSerArgThrProGlyLys 495
           |||||||||||||||||||||||||
      1642 AGCTTCTCCCGGACTCCGGGTAAA 1665

ULT 3
99707
  AAT99707 standard; cDNA; 1446 BP.

  AAT99707;

  17-OCT-2003  (revised)
  17-AUG-1998  (first entry)

  DR2-IgG fusion construct.

  Major histocompatibility complex class II; MHC class II; human; mouse;
  fusion protein; HLA-DR2; DRA*0101; binding domain; Fos;
  dimerisation domain; IgG; allergy; autoimmune disease; vaccine;
  multiple sclerosis; therapy; ss.

  Homo sapiens.
  Mus musculus.
  Chimeric.

  WO9806749-A2.

  19-FEB-1998.

  15-AUG-1997;   97WO-US014503.

  16-AUG-1996;   96US-0024077P.

  (HARD ) HARVARD COLLEGE.

  Wucherpfennig KW,  Strominger JL;

  WPI; 1998-159459/14.

  New Class II MHC fusion proteins - comprising a MHC Class II binding
  domain and a dimerisation domain or an immunoglobulin region used for
  modulating immune responses.

  Example; Page 49; 76pp; English.

  This nucleotide sequences codes for a bivalent DR2 fusion protein
  obtained by fusion of the Fc portion of IgG2a to the 3' end of a DR-alpha
  -Fos cDNA construct (see AAV16866). The Fc portion was amplified by RT-
CC   PCR from mouse hybridoma L243. The PCR product was then fused in frame
CC   with the DR-alpha-Fos construct by overlapping PCR. The DR2-IgG fusion
CC   was expressed in the Drosophila Schneider cell system. The invention
CC   relates to new soluble monovalent and multivalent Class II MHC fusion
CC   proteins comprising a MHC Class II binding domain and a dimerisation
CC   domain or an immunoglobulin region that can be used for the treatment of
CC   allergic and autoimmune diseases (e.g. multiple sclerosis), for
CC   tolerising a subject to foreign tissue before or after organ or tissue
CC   transplantation, or for vaccination against pathogens. (Updated on 17-OCT
CC   -2003 to standardise OS field)
XX
SQ   Sequence 1446 BP; 414 A; 375 C; 356 G; 301 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                8.16e-156      Length:          1446
Score:                    1924.50        Matches:         364
Percent Similarity:       83.2%          Conservative:    32
Best Local Similarity:    76.5%          Mismatches:      73
Query Match:              72.3%          Indels:          7
DB:                       2              Gaps:            4

US-10-048-116B-2 (1-495) x AAT99707 (1-1446)

Qy         26 AspIleGluAlaAspHisValGlyPheTyrGlyThrThrValTyrGlnSerProGlyAsp 45
              :::|||:::   :::||||||                 |||   :::|||
Db         13 GAGATCAAAGAAGAACATGTG---ATCATCCAGGCCGAGTTCTATCTGAATCCTGACCAA 69

Qy         46 IleGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyrValAspLeuAspLys 65
                 ||:::::      :::|||||||||||||||:::|||:::|||||||:::   |||
Db         70 TCAGGCGAGTTTATGTTTGACTTTGATGGTGATGAGATTTTCCATGTGGATATGGCAAAG 129

Qy         66 LysLysThrValTrpArgLeuProGluPheGlyGlnLeuIleLeuPheGluProGlnGly 85
              |||:::|||||||||||||||    |||||||||:::          ||||||   ||||||
Db        130 AAGGAGACGGTCTGGCGGCTTGAAGAATTTGGACGATTTGCCAGCTTTGAGGCTCAAGGT 189

Qy         86 GlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeuThrLysArgSerAsn 105
              |||   |||||||||  :::|||   ||||||   |||:::|||||||||||||||||
Db        190 GCATTGGCCAACATAGCTGTGGACAAAGCCAACTTGGAAATCATGACAAAGCGCTCCAAC 249

Qy        106 PheThrProAlaThrAsnGluAlaProGlnAlaThrValPheProLysSerProValLeu 125
              :::||||||   ||||||      |||:::   ||||||        |||||||||
Db        250 TATACTCCGATCACCAATGTACCTCCAGAGGTAACTGTGCTCACGAACAGCCCTGTGGAA 309

Qy        126 LeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePheProProValIleAsn 145
              |||   :::||||||    ||||||||||||:::|||          |||||||||:::|||
Db        310 CTGAGAGAGCCCAACGTCCTCATCTGTTTCATAGACAAGTTCACCCCACCAGTGGTCAAT 369

Qy        146 IleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyrGluThrSerPheLeu 165
              :::||||||||||||||    |||   ||||||   ||||||   ||||||   ||||||
Db        370 GTCACGTGGCTTCGAAATGGAAAACCTGTCACCACAGGAGTGTCAGAGACAGTCTTCCTG 429

Qy        166 ValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPheIleProSerAspAsp 185
                    ||||||   |||   |||        ||||||   |||:::||||||   :::
Db        430 CCCAGGGAAGACCACCTTTTCCGCAAGTTCCACTATCTCCCCTTCCTGCCCTCAACTGAG 489

Qy        186 AspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluProValLeuLysHisTrp 205
              |||:::|||||||:::|||||||||||||||||:::||||||::|||||||||||||
Db        490 GACGTTTACGACTGCAGGGTGGAGCACTGGGGCTTGGATGAGCCTCTTCTCAAGCACTGG 549

Qy        206 GluProGluIleProAlaProMetSerGluLeuThrGluThr---GlyGlyGlyGlySer 224
              |||   :::   |||:::|||:::   |||   ||||||      ||||||||||
Db        550 GAGTTTGATGCTCCAAGCCCTCTCCCAGAGACTACAGAGGTCGACGGAGGTGGCGGCGGT 609

Qy        225 ThrThr------------AlaProSerAlaGlnLeuGluLysGluLeuGlnAlaLeuGlu 240
                 |||             |||   :::   |||||||||   |||      ||||||:::
Db        610 TTAACTGATACACTCCAAGCGGAGACAGATCAACTTGAAGACGAGAAGTCTGCGTTGCAG 669

Qy        241 LysGluAsnAlaGlnLeuGluTrpGluLeuGlnAlaLeuGluLysGluLeu---AlaGln 259
              |||   |||   |||      |||   :::   ||||||      |||   |||
Db        670 ACCGAGATTGCCAATCTACTGAAAGAGAAGGAAAAACTGGAGTTCATCCTGGCCGCCCAT 729

Qy        260 AlaAlaSerGluProArgGlyProThrIleLysProCysProProCysLysCysProAla 279
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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 730 GCAGCATCTGAGCCCAGAGGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCAGCA 789

 280 ProAsnLeuLeuGlyGlyProSerValPheIlePheProProLysIleLysAspValLeu 299
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 790 CCTAACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTC 849

 300 MetIleSerLeuSerProIleValThrCysValValValAspValSerGluAspAspPro 319
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 850 ATGATCTCCCTGAGCCCCATAGTCACATGTGTGGTGGTGGATGTGAGCGAGGATGACCCA 909

 320 AspValGlnIleSerTrpPheValAsnAsnValGluValHisThrAlaGlnThrGlnThr 339
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 910 GATGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAAACC 969

 340 HisArgGluAspTyrAsnSerThrLeuArgValValSerAlaLeuProIleGlnHisGln 359
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 970 CATAGAGAGGATTACAACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAG 1029

 360 AspTrpMetSerGlyLysGluPheLysCysLysValAsnAsnLysAspLeuProAlaPro 379
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1030 GACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAAGACCTCCCAGCGCCC 1089

 380 IleGluArgThrIleSerLysProLysGlySerValArgAlaProGlnValTyrValLeu 399
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1090 ATCGAGAGAACCATCTCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTTG 1149

 400 ProProProGluGluGluMetThrLysLysGlnValThrLeuThrCysMetValThrAsp 419
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1150 CCTCCACCAGAAGAAGAGATGACTAAGAAACAGGTCACTCTGACCTGCATGGTCACAGAC 1209

 420 PheMetProGluAspIleTyrValGluTrpThrAsnAsnGlyLysThrGluLeuAsnTyr 439
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1210 TTCATGCCTGAAGACATTTACGTGGAGTGGACCAACAACGGGAAAACAGAGCTAAACTAC 1269

 440 LysAsnThrGluProValLeuAspSerAspGlySerTyrPheMetTyrSerLysLeuArg 459
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1270 AAGAACACTGAACCAGTCCTGGACTCTGATGGTTCTTACTTCATGTACAGCAAGCTGAGA 1329

 460 ValGluLysLysAsnTrpValGluArgAsnSerTyrSerCysSerValValHisGluGly 479
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1330 GTGGAAAAGAAGAACTGGGTGGAAAGAAATAGCTACTCCTGTTCAGTGGTCCACGAGGGT 1389

 480 LeuHisAsnHisHisThrThrLysSerPheSerArgThrProGlyLys 495
     ||||||||||||||||||||||||||||||||||||||||||||||||
1390 CTGCACAATCACCACACGACTAAGAGCTTCTCCCGGACTCCGGGTAAA 1437
```

SULT 4
X87813
AAX87813 standard; DNA; 1446 BP.

AAX87813;

09-NOV-1999 (first entry)

HLA-DR2 alpha-Fos-IgG fusion construct.

Major histocompatability complex Class II; MHC; binding domain; HLA-DR2; leucine zipper; Fos; IgG; Fc; immunoglobulin; antibody; fusion protein; multiple sclerosis; rheumatoid arthritis; graft rejection; allergy; autoimmune disease; pemphigus vulgaris; systemic lupus erythematosus; T lymphocyte; T cell; diagnosis; therapy; adoptive immunotherapy; ss.

Homo sapiens.
Saccharomyces cerevisiae.
Synthetic.
Chimeric.

Key	Location/Qualifiers
CDS	1. .1440
	/*tag= a
sig_peptide	1. .15
	/*tag= b
	/note= "alpha-mating factor secretion signal"
mat_peptide	16. .1437
	/*tag= c
	/product= "DR2-Fos-Fc"

XX
PN WO9942597-A1.
XX
PD 26-AUG-1999.
XX
PF 19-FEB-1999; 99WO-US003603.
XX
PR 19-FEB-1998; 98US-0075351P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Wucherpfennig KW, Strominger JL;
XX
DR WPI; 1999-527481/44.
DR P-PSDB; AAY31654.
XX
PT New HMC Class II binding domain fusion proteins and conjugates - used
PT for, e.g. treating allergic and autoimmune diseases or detecting,
PT isolating, activating or killing specific T cells.
XX
PS Example 7; Page 100-102; 113pp; English.
XX
CC This nucleotide sequence codes for a divalent HLA-DR2 MHC binding domain
CC fusion protein (see AAY31654) comprising an alpha-mating factor secretion
CC signal, the extracellular domain of the HLA-DR2 alpha chain (residues 1-
CC 191 of DRA*0101), a 7-amino acid linker, the 40-amino acid leucine zipper
CC dimerization domain of Fos, and the Fc portion of IgG2a. The DR-alpha-Fc
CC chain corresponds to an antibody heavy chain. The invention provides new
CC monovalent, multivalent and multimeric MHC Class II binding domain fusion
CC proteins and conjugates comprising at least a binding domain of an MHC
CC Class II alpha or beta chain and a dimerization domain, especially a Fos
CC or Jun leucine zipper domain. The MHC fusion proteins and conjugates can
CC be used: for detecting and isolating T cells having a defined MHC/peptide
CC complex specificity (claimed); to confer to a subject adoptive immunity
CC to a defined MHC/peptide complex (claimed); to stimulate or activate T
CC cells reactive to a defined MHC/peptide complex (claimed); for selective
CC killing of T cells reactive to a defined MHC complex (claimed); to
CC tolerize a subject to a defined MHC/peptide complex (claimed); to treat
CC allergic and autoimmune diseases, e.g. multiple sclerosis, rheumatoid
CC arthritis, pemphigus vulgaris, and systemic lupus erythematosus; and to
CC prevent organ or tissue transplant rejection. The DR2-IgG design was
CC chosen to increase the affinity for the T cell receptor by increasing
CC valency, and to attach an effector domain, the Fc region of IgG2a.
CC Complement fixation may result in the lysis of target T cells following
CC binding of DR2-IgG molecules to the T cell receptor. DR2-IgG molecules
CC may therefore be useful for the selective depletion of autoaggressive T
CC cells
XX
SQ Sequence 1446 BP; 414 A; 375 C; 356 G; 301 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	8.16e-156	Length:	1446
Score:	1924.50	Matches:	364
Percent Similarity:	83.2%	Conservative:	32
Best Local Similarity:	76.5%	Mismatches:	73
Query Match:	72.3%	Indels:	7
DB:	2	Gaps:	4

US-10-048-116B-2 (1-495) x AAX87813 (1-1446)

```
Qy         26 AspIleGluAlaAspHisValGlyPheTyrGlyThrThrValTyrGlnSerProGlyAsp 45
              :::|||:::   :::||||||                  |||   :::|||
Db         13 GAGATCAAAGAAGAACATGTG---ATCATCCAGGCCGAGTTCTATCTGAATCCTGACCAA 69

Qy         46 IleGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyrValAspLeuAspLys 65
                 |||::::::      :::|||||||||||||||:::|||:::||||||:::   |||
Db         70 TCAGGCGAGTTTATGTTTGACTTTGATGGTGATGAGATTTTCCATGTGGATATGGCAAAG 129

Qy         66 LysLysThrValTrpArgLeuProGluPheGlyGlnLeuIleLeuPheGluProGlnGly 85
              |||:::|||||||||||||||   |||||||||:::         ||||||   ||||||
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130 AAGGAGACGGTCTGGCGGCTTGAAGAATTTGGACGATTTGCCAGCTTTGAGGCTCAAGGT 189

 86 GlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeuThrLysArgSerAsn 105

190 GCATTGGCCAACATAGCTGTGGACAAAGCCAACTTGGAAATCATGACAAAGCGCTCCAAC 249

106 PheThrProAlaThrAsnGluAlaProGlnAlaThrValProLysSerProValLeu 125

250 TATACTCCGATCACCAATGTACCTCCAGAGGTAACTGTGCTCACGAACAGCCCTGTGGAA 309

126 LeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIleProProValIleAsn 145

310 CTGAGAGAGCCCAACGTCCTCATCTGTTTCATAGACAAGTTCACCCCACCAGTGGTCAAT 369

146 IleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyrGluThrSerPheLeu 165

370 GTCACGTGGCTTCGAAATGGAAAACCTGTCACCACAGGAGTGTCAGAGACAGTCTTCCTG 429

166 ValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPheIleProSerAspAsp 185

430 CCCAGGGAAGACCACCTTTTCCGCAAGTTCCACTATCTCCCCTTCCTGCCCTCAACTGAG 489

186 AspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluProValLeuLysHisTrp 205

490 GACGTTTACGACTGCAGGGTGGAGCACTGGGGCTTGGATGAGCCTCTTCTCAAGCACTGG 549

206 GluProGluIleProAlaProMetSerGluLeuThrGluThr---GlyGlyGlyGlySer 224

550 GAGTTTGATGCTCCAAGCCCTCTCCCAGAGACTACAGAGGTCGACGGAGGTGGCGGCGGT 609

225 ThrThr----------AlaProSerAlaGlnLeuGluLysGluLeuGlnAlaLeuGlu 240

610 TTAACTGATACACTCCAAGCGGAGACAGATCAACTTGAAGACGAGAAGTCTGCGTTGCAG 669

241 LysGluAsnAlaGlnLeuGluTrpGluLeuGlnAlaLeuGluLysGluLeu---AlaGln 259

670 ACCGAGATTGCCAATCTACTGAAAGAGAAGGAAAAACTGGAGTTCATCCTGGCCGCCCAT 729

260 AlaAlaSerGluProArgGlyProThrIleLysProCysProProCysLysCysProAla 279

730 GCAGCATCTGAGCCCAGAGGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCAGCA 789

280 ProAsnLeuLeuGlyGlyProSerValPheIlePheProProLysIleLysAspValLeu 299

790 CCTAACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTC 849

300 MetIleSerLeuSerProIleValThrCysValValValAspValSerGluAspAspPro 319

850 ATGATCTCCCTGAGCCCCATAGTCACATGTGTGGTGGTGGATGTGAGCGAGGATGACCCA 909

320 AspValGlnIleSerTrpPheValAsnAsnValGluValHisThrAlaGlnThrGlnThr 339

910 GATGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAAACC 969

340 HisArgGluAspTyrAsnSerThrLeuArgValValSerAlaLeuProIleGlnHisGln 359

970 CATAGAGAGGATTACAACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAG 1029

360 AspTrpMetSerGlyLysGluPheLysCysLysValAsnAsnLysAspLeuProAlaPro 379

1030 GACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAAGACCTCCCAGCGCCC 1089

380 IleGluArgThrIleSerLysProLysGlySerValArgAlaProGlnValTyrValLeu 399

1090 ATCGAGAGAACCATCTCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTTG 1149

400 ProProProGluGluGluMetThrLysLysGlnValThrLeuThrCysMetValThrAsp 419

1150 CCTCCACCAGAAGAAGAGATGACTAAGAAACAGGTCACTCTGACCTGCATGGTCACAGAC 1209

420 PheMetProGluAspIleTyrValGluTrpThrAsnAsnGlyLysThrGluLeuAsnTyr 439

1210 TTCATGCCTGAAGACATTTACGTGGAGTGGACCAACAACGGGAAAACAGAGCTAAACTAC 1269
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Qy        440 LysAsnThrGluProValLeuAspSerAspGlySerTyrPheMetTyrSerLysLeuArg 459

Db       1270 AAGAACACTGAACCAGTCCTGGACTCTGATGGTTCTTACTTCATGTACAGCAAGCTGAGA 1329

Qy        460 ValGluLysLysAsnTrpValGluArgAsnSerTyrSerCysSerValValHisGluGly 479

Db       1330 GTGGAAAAGAAGAACTGGGTGGAAAGAAATAGCTACTCCTGTTCAGTGGTCCACGAGGGT 1389

Qy        480 LeuHisAsnHisHisThrThrLysSerPheSerArgThrProGlyLys 495

Db       1390 CTGCACAATCACCACACGACTAAGAGCTTCTCCCGGACTCCGGGTAAA 1437
```

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RESULT 5
ADW44282
ID   ADW44282 standard; DNA; 1446 BP.
XX
AC   ADW44282;
XX
DT   24-MAR-2005  (first entry)
XX
DE   DR2-IgG fusion protein encoding DNA.
XX
KW   Major histocompatibility complex; fusion protein; immunoconjugate;
KW   adoptive immunotherapy; dermatological; immunosuppressive; antirheumatic;
KW   antiarthritic; neuroprotective; antiinflammatory; autoimmune diseases;
KW   pemphigus vulgaris; rheumatoid arthritis; multiple sclerosis;
KW   systemic lupus erythematosus; immune disorder; DR2-IgG protein; gene; ds.
XX
OS   Homo sapiens.
OS   Chimeric.
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
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FT                   /product= "DR2-IgG fusion protein"
FT                   /partial
FT                   /note= "No start codon"
FT   misc_feature    1. .15
FT                   /*tag=  a
FT                   /note= "3' end of secretory signal"
FT   misc_feature    16. .588
FT                   /*tag=  c
FT                   /note= "DRA*0101extracellular domain"
FT   misc_feature    589. .609
FT                   /*tag=  d
FT                   /note= "Linker sequence"
FT   misc_feature    610. .729
FT                   /*tag=  e
FT                   /note= "Fos Leucine zipper domain"
FT   misc_feature    730. .1437
FT                   /*tag=  f
FT                   /note= "IgG domain"
XX
PN   US2005003431-A1.
XX
PD   06-JAN-2005.
XX
PF   21-JUL-2004; 2004US-00895543.
XX
PR   16-AUG-1996;   96US-0024077P.
PR   15-AUG-1997;   97WO-US014503.
PR   19-FEB-1998;   98US-0075351P.
PR   12-FEB-1999;   99US-00248964.
XX
PA   (WUCH/) WUCHERPFENNIG K W.
PA   (STRO/) STROMINGER J L.
XX
PI   Wucherpfennig KW,  Strominger JL;
XX
DR   WPI; 2005-089945/10.
DR   P-PSDB; ADW44283.
```

Novel class II major histocompatibility complex (MHC) fusion protein having MHC class II binding domain of MHC class II alpha chain, and dimerization domain, useful for treating pemphigus vulgaris, rheumatoid arthritis.

Example; SEQ ID NO 11; 55pp; English.

The present invention relates to the class II major histocompatibility complex (MHC) fusion protein having MHC class II binding domain of MHC class II alpha chain and a dimerization domain. The invention is useful in adoptive immunotherapy and tolerizing against foreign tissue. The invention is also useful for treating autoimmune diseases such as pemphigus vulgaris, rheumatoid arthritis, multiple sclerosis and systemic lupus erythematosus. The present sequence is the DR2-IgG fusion protein encoding DNA.

Sequence 1446 BP; 414 A; 375 C; 356 G; 301 T; 0 U; 0 Other;

ignment Scores:

ed. No.:	8.16e-156	Length:	1446
ore:	1924.50	Matches:	364
rcent Similarity:	83.2%	Conservative:	32
st Local Similarity:	76.5%	Mismatches:	73
ery Match:	72.3%	Indels:	7
:	14	Gaps:	4

-10-048-116B-2 (1-495) x ADW44282 (1-1446)

```
Qy         26 AspIleGluAlaAspHisValGlyPheTyrGlyThrThrValTyrGlnSerProGlyAsp 45
              :::|||:::   :::||||||                        |||   :::|||
Db         13 GAGATCAAAGAAGAACATGTG---ATCATCCAGGCCGAGTTCTATCTGAATCCTGACCAA 69

Qy         46 IleGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyrValAspLeuAspLys 65
                 |||::::::      :::||||||||||||||||:::|||:::||||||:::   |||
Db         70 TCAGGCGAGTTTATGTTTGACTTTGATGGTGATGAGATTTTCCATGTGGATATGGCAAAG 129

Qy         66 LysLysThrValTrpArgLeuProGluPheGlyGlnLeuIleLeuPheGluProGlnGly 85
              |||:::|||||||||||||||   |||||||||:::          ||||||   ||||||
Db        130 AAGGAGACGGTCTGGCGGCTTGAAGAATTTGGACGATTTGCCAGCTTTGAGGCTCAAGGT 189

Qy         86 GlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeuThrLysArgSerAsn 105
                 |||   |||||||||   :::|||   ||||||   |||:::||||||||||||||||
Db        190 GCATTGGCCAACATAGCTGTGGACAAAGCCAACTTGGAAATCATGACAAAGCGCTCCAAC 249

Qy        106 PheThrProAlaThrAsnGluAlaProGlnAlaThrValPheProLysSerProValLeu 125
              :::||||||   ||||||       |||:::   ||||||          |||||||||
Db        250 TATACTCCGATCACCAATGTACCTCCAGAGGTAACTGTGCTCACGAACAGCCCTGTGGAA 309

Qy        126 LeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePheProProValIleAsn 145
              |||   :::||||||   |||||||||||||:::|||          ||||||||||:::|||
Db        310 CTGAGAGAGCCCAACGTCCTCATCTGTTTCATAGACAAGTTCACCCCACCAGTGGTCAAT 369

Qy        146 IleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyrGluThrSerPheLeu 165
              :::|||||||||||||||   |||   ||||||   ||||||   ||||||   ||||||
Db        370 GTCACGTGGCTTCGAAATGGAAAACCTGTCACCACAGGAGTGTCAGAGACAGTCTTCCTG 429

Qy        166 ValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPheIleProSerAspAsp 185
                    ||||||   |||   |||       ||||||   |||:::||||||   :::
Db        430 CCCAGGGAAGACCACCTTTTCCGCAAGTTCCACTATCTCCCCTTCCTGCCCTCAACTGAG 489

Qy        186 AspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluProValLeuLysHisTrp 205
              |||:::|||||||||:::|||||||||||||||||||:::|||||||:::||||||||||||
Db        490 GACGTTTACGACTGCAGGGTGGAGCACTGGGGCTTGGATGAGCCTCTTCTCAAGCACTGG 549

Qy        206 GluProGluIleProAlaProMetSerGluLeuThrGluThr---GlyGlyGlyGlySer 224
              |||   :::   |||:::|||:::   |||   ||||||       ||||||||||||
Db        550 GAGTTTGATGCTCCAAGCCCTCTCCCAGAGACTACAGAGGTCGACGGAGGTGGCGGCGGT 609

Qy        225 ThrThr----------AlaProSerAlaGlnLeuGluLysGluLeuGlnAlaLeuGlu 240
                 |||           |||   :::   ||||||||   |||       ||||||:::
Db        610 TTAACTGATACACTCCAAGCGGAGACAGATCAACTTGAAGACGAGAAGTCTGCGTTGCAG 669

Qy        241 LysGluAsnAlaGlnLeuGluTrpGluLeuGlnAlaLeuGluLysGluLeu---AlaGln 259
                 |||   |||   |||       |||   :::   ||||||       |||   |||
Db        670 ACCGAGATTGCCAATCTACTGAAAGAGAAGGAAAAACTGGAGTTCATCCTGGCCGCCCAT 729

Qy        260 AlaAlaSerGluProArgGlyProThrIleLysProCysProProCysLysCysProAla 279
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 GCAGCATCTGAGCCCAGAGGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCAGCA 789

Qy        280 ProAsnLeuLeuGlyGlyProSerValPheIlePheProProLysIleLysAspValLeu 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 CCTAACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTC 849

Qy        300 MetIleSerLeuSerProIleValThrCysValValValAspValSerGluAspAspPro 319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 ATGATCTCCCTGAGCCCCATAGTCACATGTGTGGTGGTGGATGTGAGCGAGGATGACCCA 909

Qy        320 AspValGlnIleSerTrpPheValAsnAsnValGluValHisThrAlaGlnThrGlnThr 339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 GATGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAAACC 969

Qy        340 HisArgGluAspTyrAsnSerThrLeuArgValValSerAlaLeuProIleGlnHisGln 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 CATAGAGAGGATTACAACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAG 1029

Qy        360 AspTrpMetSerGlyLysGluPheLysCysLysValAsnAsnLysAspLeuProAlaPro 379
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1030 GACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAAGACCTCCCAGCGCCC 1089

Qy        380 IleGluArgThrIleSerLysProLysGlySerValArgAlaProGlnValTyrValLeu 399
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1090 ATCGAGAGAACCATCTCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTTG 1149

Qy        400 ProProProGluGluGluMetThrLysLysGlnValThrLeuThrCysMetValThrAsp 419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1150 CCTCCACCAGAAGAAGAGATGACTAAGAAACAGGTCACTCTGACCTGCATGGTCACAGAC 1209

Qy        420 PheMetProGluAspIleTyrValGluTrpThrAsnAsnGlyLysThrGluLeuAsnTyr 439
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1210 TTCATGCCTGAAGACATTTACGTGGAGTGGACCAACAACGGGAAAACAGAGCTAAACTAC 1269

Qy        440 LysAsnThrGluProValLeuAspSerAspGlySerTyrPheMetTyrSerLysLeuArg 459
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1270 AAGAACACTGAACCAGTCCTGGACTCTGATGGTTCTTACTTCATGTACAGCAAGCTGAGA 1329

Qy        460 ValGluLysLysAsnTrpValGluArgAsnSerTyrSerCysSerValValHisGluGly 479
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1330 GTGGAAAAGAAGAACTGGGTGGAAAGAAATAGCTACTCCTGTTCAGTGGTCCACGAGGGT 1389

Qy        480 LeuHisAsnHisHisThrThrLysSerPheSerArgThrProGlyLys 495
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1390 CTGCACAATCACCACACGACTAAGAGCTTCTCCCGGACTCCGGGTAAA 1437
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RESULT 6
ABI99027
ID ABI99027 standard; cDNA; 2346 BP.
XX
AC ABI99027;
XX
DT 25-FEB-2002 (first entry)
XX
DE IAS MBP 1-14 CH1.CH2.CH3 coding sequence.
XX
KW Mouse; MHC; major histocompatibility complex; MHC class II; multimer;
KW single chain; immunosuppressive; antidiabetic; antiinflammatory;
KW antianaemic; antirheumatoid; antiarthritic; neuroprotective; vaccine;
KW autoimmune disease; insulin dependent diabetes; multiple sclerosis;
KW myasthenia gravis; pernicious anaemia; autoimmune encephalomyelitis;
KW rheumatoid arthritis; systemic lupus erythematosus; ss.
XX
OS Mus sp.
OS Synthetic.
XX
PN WO200170245-A1.

27-SEP-2001.

22-MAR-2001; 2001WO-US009616.

22-MAR-2000; 2000US-0191274P.
15-MAY-2000; 2000US-0204249P.
23-JAN-2001; 2001US-0264003P.

(CORI-) CORIXA CORP.

Carter D, Zhu S, Arimilli S, Wang A;

WPI; 2001-616371/71.
P-PSDB; ABB56457.

Multimeric complex for treating autoimmune diseases, comprises first and second single chain MHC class II molecules, each comprising alpha1 and beta1 domain linked through amino acid linker and multimerization domain.

Disclosure; Page 91-92; 147pp; English.

The invention relates to a multimeric complex comprising a first recombinant single chain major histocompatibility complex (MHC) class II molecule and a second recombinant single chain MHC class II molecule, each comprising an alpha1 domain and a beta1 domain linked through an amino acid linker and a multimerisation domain. The first and the second molecule are linked through the multimerisation domain to form a multimeric complex,. The complex is useful for treating autoimmune diseases. It is useful for treating insulin dependent diabetes, multiple sclerosis, myasthenia gravis, pernicious anaemia, autoimmune encephalomyelitis (EAE), rheumatoid arthritis and systemic lupus erythematosus. The present sequence encodes a single chain MHC class II molecule of the invention

Sequence 2346 BP; 560 A; 663 C; 646 G; 477 T; 0 U; 0 Other;

ginment Scores:

d. No.:	1.77e-139	Length:	2346
:e:	1738.00	Matches:	336
ent Similarity:	70.8%	Conservative:	44
t Local Similarity:	62.6%	Mismatches:	79
y Match:	65.3%	Indels:	78
	4	Gaps:	8

:0-048-116B-2 (1-495) x ABI99027 (1-2346)

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Qy      22 GlyGly---------GluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrThr 38
Db     766 GGCGGTTCCTCGAGTGAAGACGACATTGAGGCCGACCACGTAGGCGTCTATGGTACAACT 825

Qy      39 ValTyrGlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeu 58
Db     826 GTATATCAGTCTCCTGGAGACATTGGCCAGTACACACATGAATTTGATGGTGATGAGTGG 885

Qy      59 PheTyrValAspLeuAspLysLysLysThrValTrpArgLeuProGluPheGlyGlnLeu 78
Db     886 TTCTATGTGGACTTGGATAAGAAGGAGACTATCTGGATGCTTCCTGAGTTTGGCCAATTG 945

Qy      79 IleLeuPheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGly 98
Db     946 ACAAGCTTTGACCCCCAAGGTGGACTGCAAAACATAGCTACAGGAAAATACACCTTGGGA 1005

Qy      99 IleLeuThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrVal 118
Db    1006 ATCTTGACTAAGAGGTCAAATTCCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTG 1065

Qy     119 PheProLysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsn 138
Db    1066 TTCCCCAAGTCCCCTGTGCTGCTGGGTCAGCCCAACACCCTCATCTGCTTTGTGGACAAC 1125

Qy     139 IlePheProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGly 158
Db    1126 ATCTTCCCTCCTGTGATCAACATCACATGGCTCAGAAATAGTAAGTCAGTCACAGACGGC 1185

Qy     159 ValTyrGluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeu 178
Db    1186 GTTTATGAGACCAGCTTCCTTGTCAACCGTGACCATTCCTTCCACAAGCTGTCTTATCTC 1245

Qy     179 ThrPheIleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGlu 198
Db    1246 ACCTTCATCCCTTCTGACGATGATATTTATGACTGCAAGGTGGAGCACTGGGGCCTGGAG 1305

Qy     199 GluProValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGlu 218
Db    1306 GAGCCGGTTCTGAAACACTGG----------------------------------GCT 1329

Qy     219 ThrGlyGlyGlyGlySer----------------ThrThrAlaProSer--------- 229
Db    1330 AGCGGAGGGGGCGGAAGCGGCGGAGGGGGAGCCAAAACGACACCCCCATCTGTCTATCCA 1389

Qy     229 ------------------------------------------------------------ 229
Db    1390 CTGGCCCCTGGATCTGCTGCCCAAACTAACTCCATGGTGACCCTGGGATGCCTGGTCAAG 1449

Qy     229 ------------------------------------------------------------ 229
Db    1450 GGCTATTTCCCTGAGCCAGTGACAGTGACCTGGAACTCTGGATCCCTGTCCAGCGGTGTG 1509

Qy     230 ----------AlaGlnLeuGluLysGluLeuGlnAlaLeuGluLysGluAsnAla--- 244
Db    1510 CACACCTTCCCAGCTGTCCTGCAGTCTGACCTCTACACTCTGAGCAGCTCAGTGACTGTC 1569

Qy     245 ---GlnLeuGluTrpGluLeuGlnAlaLeuGluLysGluLeuAlaGlnAlaAlaSerGlu 263
Db    1570 CCCTCCAGCACCTGGCCCAGCGAGACCGTCACCTGCAACGTTGCCCACCCGGCCAGCAGC 1629

Qy     264 ProArg---GlyProThrIleLysPro-----------CysProProCysLysCysPro 278
Db    1630 ACCAAGGTGGACAAGAAAATTGTGCCCAGGGATTGTGGTTGTAAGCCTTGCATATGTACA 1689

Qy     279 AlaProAsnLeuLeuGlyGlyProSerValPheIlePheProProLysIleLysAspVal 298
Db    1690 GTCCCAGAAGTA---------TCATCTGTCTTCATCTTCCCCCCAAAGCCCAAGGATGTG 1740

Qy     299 LeuMetIleSerLeuSerProIleValThrCysValValValAspValSerGluAspAsp 318
Db    1741 CTCACCATTACTCTGACTCCTAAGGTCACGTGTGTTGTGGTAGACATCAGCAAGGATGAT 1800

Qy     319 ProAspValGlnIleSerTrpPheValAsnAsnValGluValHisThrAlaGlnThrGln 338
Db    1801 CCCGAGGTCCAGTTCAGCTGGTTTGTAGATGATGTGGAGGTGCACACAGCTCAGACGCAA 1860

Qy     339 ThrHisArgGluAspTyrAsnSerThrLeuArgValValSerAlaLeuProIleGlnHis 358
Db    1861 CCCCGGGAGGAGCAGTTCAACAGCACTTTCCGCTCAGTCAGTGAACTTCCCATCATGCAC 1920

Qy     359 GlnAspTrpMetSerGlyLysGluPheLysCysLysValAsnAsnLysAspLeuProAla 378
Db    1921 CAGGACTGGCTCAATGGCAAGGAGTTCAAATGCAGGGTCAACAGTGCAGCTTTCCCTGCC 1980

Qy     379 ProIleGluArgThrIleSerLysProLysGlySerValArgAlaProGlnValTyrVal 398
Db    1981 CCCATCGAGAAAACCATCTCCAAAACCAAAGGCAGACCGAAGGCTCCACAGGTGTACACC 2040

Qy     399 LeuProProProGluGluGluMetThrLysLysGlnValThrLeuThrCysMetValThr 418
Db    2041 ATTCCACCTCCCAAGGAGCAGATGGCCAAGGATAAAGTCAGTCTGACCTGCATGATAACA 2100

Qy     419 AspPheMetProGluAspIleTyrValGluTrpThrAsnAsnGlyLysThrGluLeuAsn 438
Db    2101 GACTTCTTCCCTGAAGACATTACTGTGGAGTGGCAGTGGAATGGGCAGCCAGCGGAGAAC 2160

Qy     439 TyrLysAsnThrGluProValLeuAspSerAspGlySerTyrPheMetTyrSerLysLeu 458
Db    2161 TACAAGAACACTCAGCCCATCATGGACACAGATGGCTCTTACTTCGTCTACAGCAAGCTC 2220
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 459 ArgValGluLysLysAsnTrpValGluArgAsnSerTyrSerCysSerValValHisGlu 478
2221 AATGTGCAGAAGAGCAACTGGGAGGCAGGAAATACTTTCACCTGCTCTGTGTTACATGAG 2280

 479 GlyLeuHisAsnHisHisThrThrLysSerPheSerArgThrProGlyLys 495
2281 GGCCTGCACAACCACCATACTGAGAAGAGCCTCTCCCACTCTCCTGGTAAA 2331
```

SULT 7
I99033
ABI99033 standard; cDNA; 2343 BP.

ABI99033;

25-FEB-2002 (first entry)

MBP 90-101 CH1.H.CH2.CH3 coding sequence.

Mouse; MHC; major histocompatibility complex; MHC class II; multimer; single chain; immunosuppressive; antidiabetic; antiinflammatory; antianaemic; antirheumatoid; antiarthritic; neuroprotective; vaccine; autoimmune disease; insulin dependent diabetes; multiple sclerosis; myasthenia gravis; pernicious anaemia; autoimmune encephalomyelitis; rheumatoid arthritis; systemic lupus erythematosus; ss.

Mus sp.
Synthetic.

WO200170245-A1.

27-SEP-2001.

22-MAR-2001; 2001WO-US009616.

22-MAR-2000; 2000US-0191274P.
15-MAY-2000; 2000US-0204249P.
23-JAN-2001; 2001US-0264003P.

(CORI-) CORIXA CORP.

Carter D, Zhu S, Arimilli S, Wang A;

WPI; 2001-616371/71.
P-PSDB; ABB56463.

Multimeric complex for treating autoimmune diseases, comprises first and second single chain MHC class II molecules, each comprising alpha1 and beta1 domain linked through amino acid linker and multimerization domain.

Disclosure; Page 96; 147pp; English.

The invention relates to a multimeric complex comprising a first recombinant single chain major histocompatibility complex (MHC) class II molecule and a second recombinant single chain MHC class II molecule, each comprising an alpha1 domain and a beta1 domain linked through an amino acid linker and a multimerisation domain. The first and the second molecule are linked through the multimerisation domain to form a multimeric complex,. The complex is useful for treating autoimmune diseases. It is useful for treating insulin dependent diabetes, multiple sclerosis, myasthenia gravis, pernicious anaemia, autoimmune encephalomyelitis (EAE), rheumatoid arthritis and systemic lupus erythematosus. The present sequence encodes a single chain MHC class II molecule of the invention

Sequence 2343 BP; 562 A; 665 C; 635 G; 481 T; 0 U; 0 Other;

ignment Scores:			
ed. No.:	1.95e-139	Length:	2343
ore:	1737.50	Matches:	336
rcent Similarity:	70.6%	Conservative:	44
st Local Similarity:	62.5%	Mismatches:	79
ery Match:	65.3%	Indels:	79

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DB:                    4              Gaps:          8

US-10-048-116B-2 (1-495) x ABI99033 (1-2343)

Qy        22 GlyGly---------GluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrThr 38
Db       760 GGCGGTTCCTCGAGTGAAGACGACATTGAGGCCGACCACGTAGGCGTCTATGGTACAACT 819

Qy        39 ValTyrGlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeu 58
Db       820 GTATATCAGTCTCCTGGAGACATTGGCCAGTACACACATGAATTTGATGGTGATGAGTGG 879

Qy        59 PheTyrValAspLeuAspLysLysLysThrValTrpArgLeuProGluPheGlyGlnLeu 78
Db       880 TTCTATGTGGACTTGGATAAGAAGGAGACTATCTGGATGCTTCCTGAGTTTGGCCAATTG 939

Qy        79 IleLeuPheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGly 98
Db       940 ACAAGCTTTGACCCCCAAGGTGGACTGCAAAACATAGCTACAGGAAAATACACCTTGGGA 999

Qy        99 IleLeuThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrVal 118
Db      1000 ATCTTGACTAAGAGGTCAAATTCCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTG 1059

Qy       119 PheProLysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsn 138
Db      1060 TTCCCCAAGTCCCCTGTGCTGCTGGGTCAGCCCAACACCCTCATCTGCTTTGTGGACAAC 1119

Qy       139 IlePheProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGly 158
Db      1120 ATCTTCCCTCCTGTGATCAACATCACATGGCTCAGAAATAGTAAGTCAGTCACAGACGGC 1179

Qy       159 ValTyrGluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeu 178
Db      1180 GTTTATGAGACCAGCTTCCTTGTCAACCGTGACCATTCCTTCCACAAGCTGTCTTATCTC 1239

Qy       179 ThrPheIleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGlu 198
Db      1240 ACCTTCATCCCTTCTGACGATGATATTTATGACTGCAAGGTGGAGCACTGGGGCCTGGAG 1299

Qy       199 GluProValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGlu 218
Db      1300 GAGCCGGTTCTGAAACACTGG----------------------------------GCT 1323

Qy       219 ThrGlyGlyGlyGlySer--------------------ThrThrAlaProSer------ 229
Db      1324 AGCGGAGGGGGCGGAAGCGGCGGAGGAAGCTTAGCCAAAACGACACCCCCATCTGTCTAT 1383

Qy       229 ------------------------------------------------------------ 229
Db      1384 CCACTGGCCCCTGGATCTGCTGCCCAAACTAACTCCATGGTGACCCTGGGATGCCTGGTC 1443

Qy       229 ------------------------------------------------------------ 229
Db      1444 AAGGGCTATTTCCCTGAGCCAGTGACAGTGACCTGGAACTCTGGATCCCTGTCCAGCGGT 1503

Qy       230 --------------AlaGlnLeuGluLysGluLeuGlnAlaLeuGluLysGluAsnAla 244
Db      1504 GTGCACACCTTCCCAGCTGTCCTGCAGTCTGACCTCTACACTCTGAGCAGCTCAGTGACT 1563

Qy       245 ------GlnLeuGluTrpGluLeuGlnAlaLeuGluLysGluLeuAlaGlnAlaAlaSer 262
Db      1564 GTCCCCTCCAGCACCTGGCCCAGCGAGACCGTCACCTGCAACGTTGCCCACCCGGCCAGC 1623

Qy       263 GluProArg---GlyProThrIleLysPro------------CysProProCysLysCys 277
Db      1624 AGCACCAAGGTGGACAAGAAAATTGTGCCCAGGGATTGTGGTTGTAAGCCTTGCATATGT 1683

Qy       278 ProAlaProAsnLeuLeuGlyGlyProSerValPheIlePheProProLysIleLysAsp 297
Db      1684 ACAGTCCCAGAAGTA---------TCATCTGTCTTCATCTTCCCCCCAAAGCCCAAGGAT 1734

Qy       298 ValLeuMetIleSerLeuSerProIleValThrCysValValValAspValSerGluAsp 317
```

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      1735 GTGCTCACCATTACTCTGACTCCTAAGGTCACGTGTGTTGTGGTAGACATCAGCAAGGAT 1794

       318 AspProAspValGlnIleSerTrpPheValAsnAsnValGluValHisThrAlaGlnThr 337
      1795 GATCCCGAGGTCCAGTTCAGCTGGTTTGTAGATGATGTGGAGGTGCACACAGCTCAGACG 1854

       338 GlnThrHisArgGluAspTyrAsnSerThrLeuArgValValSerAlaLeuProIleGln 357
      1855 CAACCCCGGGAGGAGCAGTTCAACAGCACTTTCCGCTCAGTCAGTGAACTTCCCATCATG 1914

       358 HisGlnAspTrpMetSerGlyLysGluPheLysCysLysValAsnAsnLysAspLeuPro 377
      1915 CACCAGGACTGGCTCAATGGCAAGGAGTTCAAATGCAGGGTCAACAGTGCAGCTTTCCCT 1974

       378 AlaProIleGluArgThrIleSerLysProLysGlySerValArgAlaProGlnValTyr 397
      1975 GCCCCCATCGAGAAAACCATCTCCAAAACCAAAGGCAGACCGAAGGCTCCACAGGTGTAC 2034

       398 ValLeuProProProGluGluGluMetThrLysLysGlnValThrLeuThrCysMetVal 417
      2035 ACCATTCCACCTCCCAAGGAGCAGATGGCCAAGGATAAAGTCAGTCTGACCTGCATGATA 2094

       418 ThrAspPheMetProGluAspIleTyrValGluTrpThrAsnAsnGlyLysThrGluLeu 437
      2095 ACAGACTTCTTCCCTGAAGACATTACTGTGGAGTGGCAGTGGAATGGGCAGCCAGCGGAG 2154

       438 AsnTyrLysAsnThrGluProValLeuAspSerAspGlySerTyrPheMetTyrSerLys 457
      2155 AACTACAAGAACACTCAGCCCATCATGGACACAGATGGCTCTTACTTCGTCTACAGCAAG 2214

       458 LeuArgValGluLysLysAsnTrpValGluArgAsnSerTyrSerCysSerValValHis 477
      2215 CTCAATGTGCAGAAGAGCAACTGGGAGGCAGGAAATACTTTCACCTGCTCTGTGTTACAT 2274

       478 GluGlyLeuHisAsnHisHisThrThrLysSerPheSerArgThrProGlyLys 495
      2275 GAGGGCCTGCACAACCACCATACTGAGAAGAGCCTCTCCCACTCTCCTGGTAAA 2328
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ULT 8
99029
ABI99029 standard; cDNA; 2053 BP.

ABI99029;

25-FEB-2002 (first entry)

IAS MBP 90-101 CH1.H.CH2 coding sequence.

Mouse; MHC; major histocompatibility complex; MHC class II; multimer; single chain; immunosuppressive; antidiabetic; antiinflammatory; antianaemic; antirheumatoid; antiarthritic; neuroprotective; vaccine; autoimmune disease; insulin dependent diabetes; multiple sclerosis; myasthenia gravis; pernicious anaemia; autoimmune encephalomyelitis; rheumatoid arthritis; systemic lupus erythematosus; ss.

Mus sp.
Synthetic.

WO200170245-A1.

27-SEP-2001.

22-MAR-2001; 2001WO-US009616.

22-MAR-2000; 2000US-0191274P.
15-MAY-2000; 2000US-0204249P.
23-JAN-2001; 2001US-0264003P.

(CORI-) CORIXA CORP.

Carter D, Zhu S, Arimilli S, Wang A;

DR WPI; 2001-616371/71.
DR P-PSDB; ABB56459.
XX
PT Multimeric complex for treating autoimmune diseases, comprises first and
PT second single chain MHC class II molecules, each comprising alpha1 and
PT beta1 domain linked through amino acid linker and multimerization domain.
XX
PS Disclosure; Page 93; 147pp; English.
XX
CC The invention relates to a multimeric complex comprising a first
CC recombinant single chain major histocompatibility complex (MHC) class II
CC molecule and a second recombinant single chain MHC class II molecule,
CC each comprising an alpha1 domain and a beta1 domain linked through an
CC amino acid linker and a multimerisation domain. The first and the second
CC molecule are linked through the multimerisation domain to form a
CC multimeric complex,. The complex is useful for treating autoimmune
CC diseases. It is useful for treating insulin dependent diabetes, multiple
CC sclerosis, myasthenia gravis, pernicious anaemia, autoimmune
CC encephalomyelitis (EAE), rheumatoid arthritis and systemic lupus
CC erythematosus. The present sequence encodes a single chain MHC class II
CC molecule of the invention
XX
SQ Sequence 2053 BP; 492 A; 585 C; 563 G; 413 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	7.19e-121	Length:	2053
Score:	1521.00	Matches:	304
Percent Similarity:	72.0%	Conservative:	12
Best Local Similarity:	69.2%	Mismatches:	39
Query Match:	57.2%	Indels:	84
DB:	4	Gaps:	8

US-10-048-116B-2 (1-495) x ABI99029 (1-2053)

```
Qy         22 GlyGly---------GluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrThr 38
Db        760 GGCGGTTCCTCGAGTGAAGACGACATTGAGGCCGACCACGTAGGCGTCTATGGTACAACT 819

Qy         39 ValTyrGlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeu 58
Db        820 GTATATCAGTCTCCTGGAGACATTGGCCAGTACACACATGAATTTGATGGTGATGAGTGG 879

Qy         59 PheTyrValAspLeuAspLysLysLysThrValTrpArgLeuProGluPheGlyGlnLeu 78
Db        880 TTCTATGTGGACTTGGATAAGAAGGAGACTATCTGGATGCTTCCTGAGTTTGGCCAATTG 939

Qy         79 IleLeuPheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGly 98
Db        940 ACAAGCTTTGACCCCCAAGGTGGACTGCAAAACATAGCTACAGGAAAATACACCTTGGGA 999

Qy         99 IleLeuThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrVal 118
Db       1000 ATCTTGACTAAGAGGTCAAATTCCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTG 1059

Qy        119 PheProLysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsn 138
Db       1060 TTCCCCAAGTCCCCTGTGCTGCTGGGTCAGCCCAACACCCTCATCTGCTTTGTGGACAAC 1119

Qy        139 IleProProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGly 158
Db       1120 ATCTTCCCTCCTGTGATCAACATCACATGGCTCAGAAATAGTAAGTCAGTCACAGACGGC 1179

Qy        159 ValTyrGluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeu 178
Db       1180 GTTTATGAGACCAGCTTCCTTGTCAACCGTGACCATTCCTTCCACAAGCTGTCTTATCTC 1239

Qy        179 ThrPheIleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGlu 198
Db       1240 ACCTTCATCCCTTCTGACGATGATATTTATGACTGCAAGGTGGAGCACTGGGGCCTGGAG 1299

Qy        199 GluProValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGlu 218
Db       1300 GAGCCGGTTCTGAAACACTGG----------------------------------GCT 1323
```

```
 219 ThrGlyGlyGlyGlySer-----------------ThrThrAlaProSer--------- 229
     :::|||||||||||||||||                 ||||||  ||||||
1324 AGCGGAGGGGGCGGAAGCGGCGGAGGGGGAGCCAAAACAACACCCCCATCAGTCTATCCA 1383

 229 ------------------------------------------------------------ 229

1384 CTGGCCCCTGGGTGTGGAGATACAACTGGTTCCTCCGTGACTCTGGGATGCCTGGTCAAG 1443

 229 ------------------------------------------------------------ 229

1444 GGCTACTTCCCTGAGTCAGTGACTGTGACTTGGAACTCTGGCTCCCTGTCCAGCAGTGTG 1503

 230 ------------AlaGlnLeuGluLysGluLeuGlnAlaLeuGluLysGluAsnAla--- 244
                 |||  |||:::     |||     :::
1504 CACACCTTCCCAGCTCTCCTGCAGTCTGGACTCTACACTATGAGCAGCTCAGTGACTGTC 1563

 245 ---GlnLeuGluTrpGluLeuGlnAlaLeuGluLysGluLeuAlaGlnAlaAlaSer--- 262
                |||      |||   :::         :::|||      ||||||
1564 CCCTCCAGCACCTGGCCAAGTCAGACCGTCACCTGCAGCGTTGCTCACCCAGCCAGCAGC 1623

 263 --------------------GluProArgGlyPro------ThrIleLysProCysPro 273
                          ||||||  ||||||      ||||||  |||||||||
1624 ACCACGGTGGACAAAAAACTTGAGCCCAGCGGGCCCATTTCAACAATCAACCCCTGTCCT 1683

 274 ProCys------------LysCysProAlaProAsnLeuLeuGlyGlyProSerValPhe 289
     ||||||            ||||||||||||||||||||  ||||||||||||||||||
1684 CCATGCAAGGAGTGTCACAAATGCCCAGCTCCTAACCTGGAGGGTGGACCATCCGTCTTC 1743

 290 IleProProLysIleLysAspValLeuMetIleSerLeuSerProIleValThrCys 309
     ||||||||||||  ||||||||||||||||||||||||||:::|||  |||||||||
1744 ATCTTCCCTCCAAATATCAAGGATGTACTCATGATCTCCCTGACACCCAAGGTCACGTGT 1803

 310 ValValValAspValSerGluAspAspProAspValGlnIleSerTrpPheValAsnAsn 329
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1804 GTGGTGGTGGATGTGAGCGAGGATGACCCAGACGTCCAGATCAGCTGGTTTGTGAACAAC 1863

 330 ValGluValHisThrAlaGlnThrGlnThrHisArgGluAspTyrAsnSerThrLeuArg 349
     |||||||||||||||||||||||||||||||||||||||||||||||||||||:::|||
1864 GTGGAAGTACACACAGCTCAGACACAAACCCATAGAGAGGATTACAACAGTACTATCCGG 1923

 350 ValValSerAlaLeuProIleGlnHisGlnAspTrpMetSerGlyLysGluPheLysCys 369
     |||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
1924 GTGGTCAGCACCCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGC 1983

 370 LysValAsnAsnLysAspLeuProAlaProIleGluArgThrIleSerLysProLys 388
     ||||||||||||||||||||||:::|||||||||||||||||||||||||    |||
1984 AAGGTCAACAACAAAGACCTCCCATCACCCATCGAGAGAACCATCTCAAAAATTAAA 2040
```

SULT 9
I99032
ABI99032 standard; cDNA; 2059 BP.

ABI99032;

25-FEB-2002 (first entry)

MBP 1-14 CH1.H.CH2 coding sequence.

Mouse; MHC; major histocompatibility complex; MHC class II; multimer; single chain; immunosuppressive; antidiabetic; antiinflammatory; antianaemic; antirheumatoid; antiarthritic; neuroprotective; vaccine; autoimmune disease; insulin dependent diabetes; multiple sclerosis; myasthenia gravis; pernicious anaemia; autoimmune encephalomyelitis; rheumatoid arthritis; systemic lupus erythematosus; ss.

Mus sp.
Synthetic.

WO200170245-A1.

27-SEP-2001.

PF 22-MAR-2001; 2001WO-US009616.
XX
PR 22-MAR-2000; 2000US-0191274P.
PR 15-MAY-2000; 2000US-0204249P.
PR 23-JAN-2001; 2001US-0264003P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Carter D, Zhu S, Arimilli S, Wang A;
XX
DR WPI; 2001-616371/71.
DR P-PSDB; ABB56462.
XX
PT Multimeric complex for treating autoimmune diseases, comprises first and
PT second single chain MHC class II molecules, each comprising alpha1 and
PT beta1 domain linked through amino acid linker and multimerization domain.
XX
PS Disclosure; Page 95; 147pp; English.
XX
CC The invention relates to a multimeric complex comprising a first
CC recombinant single chain major histocompatibility complex (MHC) class II
CC molecule and a second recombinant single chain MHC class II molecule,
CC each comprising an alpha1 domain and a beta1 domain linked through an
CC amino acid linker and a multimerisation domain. The first and the second
CC molecule are linked through the multimerisation domain to form a
CC multimeric complex,. The complex is useful for treating autoimmune
CC diseases. It is useful for treating insulin dependent diabetes, multiple
CC sclerosis, myasthenia gravis, pernicious anaemia, autoimmune
CC encephalomyelitis (EAE), rheumatoid arthritis and systemic lupus
CC erythematosus. The present sequence encodes a single chain MHC class II
CC molecule of the invention
XX
SQ Sequence 2059 BP; 493 A; 585 C; 571 G; 410 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	7.22e-121	Length:	2059
Score:	1521.00	Matches:	304
Percent Similarity:	72.0%	Conservative:	12
Best Local Similarity:	69.2%	Mismatches:	39
Query Match:	57.2%	Indels:	84
DB:	4	Gaps:	8

US-10-048-116B-2 (1-495) x ABI99032 (1-2059)

```
Qy        22 GlyGly---------GluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrThr 38
             ||||||         ||||||||||||||||||||||||||||||  ||||||||||||
Db       766 GGCGGTTCCTCGAGTGAAGACGACATTGAGGCCGACCACGTAGGCGTCTATGGTACAACT 825

Qy        39 ValTyrGlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeu 58
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       826 GTATATCAGTCTCCTGGAGACATTGGCCAGTACACACATGAATTTGATGGTGATGAGTGG 885

Qy        59 PheTyrValAspLeuAspLysLysLysThrValTrpArgLeuProGluPheGlyGlnLeu 78
             ||||||||||||||||||||||:::|||:::|||   ||||||||||||||||||||
Db       886 TTCTATGTGGACTTGGATAAGAAGGAGACTATCTGGATGCTTCCTGAGTTTGGCCAATTG 945

Qy        79 IleLeuPheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGly 98
                ||:::|||||||||||||||||||||||||||||      |||:::   ||||||
Db       946 ACAAGCTTTGACCCCCAAGGTGGACTGCAAAACATAGCTACAGGAAAATACACCTTGGGA 1005

Qy        99 IleLeuThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrVal 118
             ||||||||||||||||||||    ||||||||||||||||||||||||||||||||||||
Db      1006 ATCTTGACTAAGAGGTCAAATTCCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTG 1065

Qy       119 ProLysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsn 138
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1066 TTCCCCAAGTCCCCTGTGCTGCTGGGTCAGCCCAACACCCTCATCTGCTTTGTGGACAAC 1125

Qy       139 IleProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGly 158
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1126 ATCTTCCCTCCTGTGATCAACATCACATGGCTCAGAAATAGTAAGTCAGTCACAGACGGC 1185

Qy       159 ValTyrGluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeu 178
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      1186 GTTTATGAGACCAGCTTCCTTGTCAACCGTGACCATTCCTTCCACAAGCTGTCTTATCTC 1245

       179 ThrPheIleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGlu 198
      1246 ACCTTCATCCCTTCTGACGATGATATTTATGACTGCAAGGTGGAGCACTGGGGCCTGGAG 1305

       199 GluProValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGlu 218
      1306 GAGCCGGTTCTGAAACACTGG----------------------------------GCT 1329

       219 ThrGlyGlyGlyGlySer-----------------ThrThrAlaProSer--------- 229
      1330 AGCGGAGGGGGCGGAAGCGGCGGAGGGGGAGCCAAAACAACACCCCCATCAGTCTATCCA 1389

       229 ------------------------------------------------------------ 229
      1390 CTGGCCCCTGGGTGTGGAGATACAACTGGTTCCTCCGTGACTCTGGGATGCCTGGTCAAG 1449

       229 ------------------------------------------------------------ 229
      1450 GGCTACTTCCCTGAGTCAGTGACTGTGACTTGGAACTCTGGCTCCCTGTCCAGCAGTGTG 1509

       230 -----------AlaGlnLeuGluLysGluLeuGlnAlaLeuGluLysGluAsnAla--- 244
      1510 CACACCTTCCCAGCTCTCCTGCAGTCTGGACTCTACACTATGAGCAGCTCAGTGACTGTC 1569

       245 ---GlnLeuGluTrpGluLeuGlnAlaLeuGluLysGluLeuAlaGlnAlaAlaSer--- 262
      1570 CCCTCCAGCACCTGGCCAAGTCAGACCGTCACCTGCAGCGTTGCTCACCCAGCCAGCAGC 1629

       263 --------------------GluProArgGlyPro------ThrIleLysProCysPro 273
      1630 ACCACGGTGGACAAAAAACTTGAGCCCAGCGGGCCCATTTCAACAATCAACCCCTGTCCT 1689

       274 ProCys------------LysCysProAlaProAsnLeuLeuGlyGlyProSerValPhe 289
      1690 CCATGCAAGGAGTGTCACAAATGCCCAGCTCCTAACCTGGAGGGTGGACCATCCGTCTTC 1749

       290 IlePheProProLysIleLysAspValLeuMetIleSerLeuSerProIleValThrCys 309
      1750 ATCTTCCCTCCAAATATCAAGGATGTACTCATGATCTCCCTGACACCCAAGGTCACGTGT 1809

       310 ValValValAspValSerGluAspAspProAspValGlnIleSerTrpPheValAsnAsn 329
      1810 GTGGTGGTGGATGTGAGCGAGGATGACCCAGACGTCCAGATCAGCTGGTTTGTGAACAAC 1869

       330 ValGluValHisThrAlaGlnThrGlnThrHisArgGluAspTyrAsnSerThrLeuArg 349
      1870 GTGGAAGTACACACAGCTCAGACACAAACCCATAGAGAGGATTACAACAGTACTATCCGG 1929

       350 ValValSerAlaLeuProIleGlnHisGlnAspTrpMetSerGlyLysGluPheLysCys 369
      1930 GTGGTCAGCACCCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGC 1989

       370 LysValAsnAsnLysAspLeuProAlaProIleGluArgThrIleSerLysProLys 388
      1990 AAGGTCAACAACAAAGACCTCCCATCACCCATCGAGAGAACCATCTCAAAAATTAAA 2046
```

```
ULT 10
:0316
  AAF30316 standard; cDNA; 7528 BP.

  AAF30316;

  11-SEP-2003  (revised)
  14-MAY-2001  (first entry)

  Bicistronic idiotype plasmid VR1642.

  Flt-3 ligand; Fms-like tyrosine kinase; mouse; human; vaccine;
  immunotherapy; therapy; tumour; lymphoma; gene therapy; VR1642;
  plasmid VAXID; antibody; idiotype; vector; ss.

XX
OS   Cytomegalovirus.
OS   Mus musculus.
OS   Homo sapiens.
OS   Bos taurus.
OS   Chimeric.
XX
PN   WO200109303-A2.
XX
PD   08-FEB-2001.
XX
PF   31-JUL-2000; 2000WO-US020679.
XX
PR   30-JUL-1999;   99US-0146170P.
XX
PA   (VICA-) VICAL INC.
XX
PI   Hermanson GG;
XX
DR   WPI; 2001-123319/13.
XX
PT   Immunogenic compositions comprising Flt-3 ligand encoding polynucleotide
PT   and one or more antigen, or cytokine encoding polynucleotides, useful for
PT   suppressing tumor growth and for treating autoimmune diseases (e.g.
PT   rheumatoid arthritis).
XX
PS   Example 2; Page 101-106; 149pp; English.
XX
CC   The present sequence is that of patient-specific bicistronic chimeric
CC   idiotype VR1642 (plasmid VAXID), which is used to treat B-cell lymphoma
CC   patients. The plasmid includes the cytomegalovirus immediate-early
CC   promoter, enhancer and 5' untranslated sequences, driving the expression
CC   of mouse-human chimeric immunoglobulin light and heavy chain sequences.
CC   The human light and heavy chain variable regions are derived from B-cell
CC   lymphoma cell line RAMOS. The transcriptional terminator region includes
CC   polyA and termination signals from the bovine growth hormone gene.
CC   According to the invention, co-administration of VR1642 with a plasmid
CC   (see AAF30314) encoding human Fms-like tyrosine kinase (Flt-3 ligand)
CC   provides a means of treating a patient with B-cell lymphoma. (Updated on
CC   11-SEP-2003 to standardise OS field)
XX
SQ   Sequence 7528 BP; 1896 A; 1980 C; 1847 G; 1805 T; 0 U; 0 Other;
```

Alignment Scores:			
Pred. No.:	7.53e-104	Length:	7528
Score:	1332.00	Matches:	290
Percent Similarity:	64.8%	Conservative:	42
Best Local Similarity:	56.6%	Mismatches:	89
Query Match:	50.1%	Indels:	92
DB:	4	Gaps:	15

US-10-048-116B-2 (1-495) x AAF30316 (1-7528)

```
Qy         10 GlyValLeuAlaLeuAsnThrMetLeuSerLeu---CysGlyGlyGluAspAspIleGlu 28
Db       1322 GGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCGGT---------GTTTATGGT 1372

Qy         29 AlaAspHisValGlyPheTyrGlyThrThrValTyrGlnSerProGlyAsp--------- 45
Db       1373 GGGTCCTTCAGTGGTTACTACTGGAGCTGGATCCGCCAGCCCCCAGGGAAGGGGCTGGAG 1432

Qy         46 ---IleGlyGlnTyrThrHis----------------------GluPheAspGlyAsp 56
Db       1433 TGGATTGGGGAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGA 1492

Qy         57 GluLeuPheTyrValAspLeuAspLysLysLysThrValTrpArgLeuProGlu------ 74
Db       1493 GTCACCATATCAGTAGACACGTCCAAGAAGCAGCTCTCCCTGAAGTTGAGCTCTGTGAAC 1552

Qy         75 --------------------PheGlyGlnLeuIleLeuPheGluProGlnGlyGlyLeu 87
Db       1553 GCCGCGGACACGGCTGTGTATTACTGTGCGAGAGTTATTACTAGGGCGAGTCCTGGCACA 1612
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  88 GlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeuThrLysArgSerAsnPheThr 107
                     ::::::   :::   :::      :::   :::       |||
1613 GACGGG-----------AGGTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACG 1660

 108 ProAlaThrAsnGluAlaProGlnAlaThrValPheProLysSerProVal--------- 124
      ::::::   :::             :::|||:::|||   :::||||||
1661 GTCTCCTCGGCCAAAACGGCCGCCCCATCGGTCTATCCACTGGCCCCTGTGTGTGGAGAT 1720

 125 LeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePheProProValIle 144
         |||         ||||||   |||   |||         ||||||      :::
1721 ACAAGTGGCTCCTCGGTGACTCTAGGATGCCTGGTCAAGGGTTATTTCCCTGAGCCAGTG 1780

 145 AsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyrGluThrSerPhe 164
      :::||||||      ||||||   |||:::::   ||||||:::
1781 ACCTTGACCTGG------AACTCTGGATCCCTGTCCAGTGGTGTGCACACCTTCCCAGCT 1834

 165 LeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPheIleProSerAsp 184
     ::::::      |||         :::   ||||||   |||:::
1835 GTCCTGCAGTCTGAC------CTCTACACCCTCAGCAG-CTCAGT--------------- 1872

 185 AspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluProValLeuLysHis 204
               ||||||   :::||||||       |||   :::||||||      |||
1873 -----------GACTGTAACCTCGAGCAC------CTGGCCCAGCCAGTC------CAT 1908

 205 TrpGluProGluIleProAlaProMetSerGluLeuThrGluThrGlyGlyGlyGly-Se 224
     :::                              :::   |||      ||| ||
1909 TAC------------------------------CTGCAATGTGGCCCACCCGGCAAG 1935

 224 rThrThrAlaProSerAlaGlnLeuGluLysGluLeuGlnAlaLeuGluLysGluAsnAl 244
     |:::|||           :::::::::|||::::::
1936 CAGCACC-----------AAGGTGGACAAGAAAATT---------------------- 1960

 244 aGlnLeuGluTrpGluLeuGlnAlaLeuGluLysGluLeuAlaGlnAlaAlaSerGluPr 264
                                                          |||||
1961 ----------------------------------------------------GAGCC 1965

 264 oArgGlyProThrIleLysProCysProProCysLysCysProAlaProAsnLeuLeuGl 284
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1966 CAGAGGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCAGCACCTAACCTCTTGGG 2025

 284 yGlyProSerValPheIlePheProProLysIleLysAspValLeuMetIleSerLeuSe 304
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2026 TGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTCCCTGAG 2085

 304 rProIleValThrCysValValValAspValSerGluAspAspProAspValGlnIleSe 324
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2086 CCCCATAGTCACATGTGTGGTGGTGGATGTGAGCGAGGATGACCCAGATGTCCAGATCAG 2145

 324 rTrpPheValAsnAsnValGluValHisThrAlaGlnThrGlnThrHisArgGluAspTy 344
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2146 CTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAAACCCATAGAGAGGATTA 2205

 344 rAsnSerThrLeuArgValValSerAlaLeuProIleGlnHisGlnAspTrpMetSerGl 364
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2206 CAACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGACTGGATGAGTGG 2265

 364 yLysGluPheLysCysLysValAsnAsnLysAspLeuProAlaProIleGluArgThrIl 384
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2266 CAAGGAGTTCAAATGCAAGGTCAACAACAAAGACCTCCCAGCGCCCATCGAGAGAACCAT 2325

 384 eSerLysProLysGlySerValArgAlaProGlnValTyrValLeuProProProGluGl 404
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2326 CTCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACCAGAAGA 2385

 404 uGluMetThrLysLysGlnValThrLeuThrCysMetValThrAspPheMetProGluAs 424
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2386 AGAGATGACTAAGAAACAGGTCACTCTGACCTGCATGGTCACAGACTTCATGCCTGAAGA 2445

 424 pIleTyrValGluTrpThrAsnAsnGlyLysThrGluLeuAsnTyrLysAsnThrGluPr 444
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2446 CATTTACGTGGAGTGGACCAACAACGGGAAAACAGAGCTAAACTACAAGAACACTGAACC 2505

 444 oValLeuAspSerAspGlySerTyrPheMetTyrSerLysLeuArgValGluLysLysAs 464
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                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2506 AGTCCTGGACTCTGATGGTTCTTACTTCATGTACAGCAAGCTGAGAGTGGAAAAGAAGAA 2565

Qy        464 nTrpValGluArgAsnSerTyrSerCysSerValValHisGluGlyLeuHisAsnHisHi 484
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2566 CTGGGTGGAAAGAAATAGCTACTCCTGTTCAGTGGTCCACGAGGGTCTGCACAATCACCA 2625

Qy        484 sThrThrLysSerPheSerArgThrProGlyLys 495
                     ||||||||||||||||||||||||||||||
Db       2626 CACGACTAAGAGCTTCTCCCGGACTCCGGGTAAA 2659

RESULT 11
ADT77690
ID   ADT77690 standard; DNA; 3973 BP.
XX
AC   ADT77690;
XX
DT   13-JAN-2005  (first entry)
XX
DE   Monoclonal antibody mAb17-1A expression construct.
XX
KW   Mouse; IgG2a; antibody; monoclonal antibody; mAb17-1A; cancer; vaccine;
KW   gene; ds.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             25. .756
FT                   /*tag=  a
FT                   /product= "mAb17-1A kappa chain"
FT   CDS             1357. .2754
FT                   /*tag=  b
FT                   /product= "mAb17-A gamma chain"
XX
PN   WO2004091655-A2.
XX
PD   28-OCT-2004.
XX
PF   16-APR-2004; 2004WO-EP004059.
XX
PR   17-APR-2003; 2003AT-00000599.
XX
PA   (IGEN-) IGENEON KREBS IMMUNTHERAPIE FORSCHUNGS.
XX
PI   Loibner H,  Himmler G,  Waxenecker G,  Schuster M,  Putz T;
XX
DR   WPI; 2004-758278/74.
DR   P-PSDB; ADT77691, ADT77692.
XX
PT   New immunogenic recombinant antibody comprising a part of a murine IgG2a
PT   subtype amino acid sequence and a mammalian glycosylation, useful in
PT   preparing a vaccine for immunizing primates against infectious or
PT   autoimmune disorders.
XX
PS   Disclosure; SEQ ID NO 1; 59pp; English.
XX
CC   The present sequence is that of the cloning cassette of a tri-cistronic
CC   mAb17-1A expression and dihydrofolate reductase selection construct for
CC   use in the production of recombinant IgG2a mAb17-1A antibody. In examples
CC   from the invention, comparison of the original, hybridoma-derived
CC   immunisation antigen 17-1A and recombinantly expressed mAb17-1A from CHO
CC   cells did not reveal any immunological differences in rhesus monkey
CC   trials. Both formulations showed identical kinetics building up the
CC   immunisation antigen and target antigen specific immune response, and
CC   raised IgG and IgM titres were similar. Recombinant mAb17-1A is an
CC   example of an immunogenic recombinant antibody of the invention designed
CC   for immunisation of primates and comprising at least a part of a murine
CC   IgG2a subtype amino acid sequence with mammalian glycosylation.
CC   Recombinant DNA methods are used to produce the immunogenic antibody in a
CC   standardised manner. The humoral immune response induced by the IgG2a
CC   immunogenic antibodies of the invention is significantly improved in
CC   terms of the quantity of specific antibody induced by the patients and
CC   the specificity against selected targets and epitopes. The improved
```

immune response is dependent on the glycosylation pattern of the antibody. Recombinant antibody expressed in hamster or human cells were shown to have a similar immunogenicity as antibody expressed by murine hybridoma cells. This is of particular relevance for antibodies that are to be used for immunisation purposes. The antibody may have a murine amino acid sequence or any other mammalian amino acid sequence that is combined with the murine IgG2a part. Preferably mammalian sequences are human, humanized, human/murine chimeric or murine sequences. The antibody may also be an anti-idiotypic antibody or a mimotopic Ab1 antibody. The IgG2a immunogenic recombinant antibody can be directed against a tumour associated antigen. The invention also provides vaccines comprising the IgG2a immunogenic antibody. The vaccines may be used for the prophylaxis and therapy of cancer associated diseases, e.g. metastatic disease in cancer patients. The vaccine specifically modulates antigen-presenting cells in vivo or ex vivo, thus generating an immune response to the epitope that is targeted by the IgG2a immunogenic antibody. The preferred method of producing the antibody comprises: transforming a CHO host cell with a multicistronic antibody-expression construct containing at least a nucleotide sequence encoding a kappa light chain and a nucleotide sequence encoding a gamma heavy chain, where at least one of these sequences comprises a nucleotide sequence encoding at least a part of a murine IgG2a subtype amino acid sequence, and at least 2 IRES elements; and expressing the sequences under the control of a single CMV promoter to produce an intact antibody. The kappa light chain and gamma heavy chain are expressed in about equimolar quantity, and antibody concentrations of 5-300 ug/ml are achieved.

Sequence 3973 BP; 1052 A; 1038 C; 993 G; 888 T; 0 U; 2 Other;

gnment Scores:

d. No.:	6.48e-104	Length:	3973
re:	1328.50	Matches:	281
cent Similarity:	65.0%	Conservative:	26
t Local Similarity:	59.5%	Mismatches:	71
ry Match:	49.9%	Indels:	95
	13	Gaps:	11

:0-048-116B-2 (1-495) x ADT77690 (1-3973)

```
      42 SerProGlyAspIleGly---GlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr 60
         :::||||||      |||      |||      :::|||   |||
    1567 AATCCTGGAAGTGGTGGTACTAACTACAATGAGAAGTTCAAGGGCAAGGCAACACTGACT 1626

      61 ValAspLeuAspLysLysLysThrValTrpArgLeuProGluPhe--------------- 75
         |||                      :::|||
    1627 GCAGACAAATCCTCCAGCACTGCCTACATGCAGCTCAGCAGCCTGACATCTGATGACTCT 1686

      76 ------------------------GlyGlnLeuIleLeuPheGluProGlnGlyGlyLeu 87
                                 |||          :::    ||||||   |||
    1687 GCGGTCTATTTCTGTGCAAGAGATGGTCCCTGGTTTGCTTACTGGGGCCAAGGGACTCTG 1746

      88 GlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeuThrLysArgSerAsnPheThr 107
            ::::::|||   |||
    1747 GTCACTGTCTCTGCAGCCAAA------------------------------------- 1767

     108 ProAlaThrAsnGluAlaProGlnAlaThrValPheProLysSerProVal--------- 124
                  ||||||      :::|||:::|||   :::||||||
    1768 ---------ACAACAGCCCCA------TCGGTCTATCCACTGGCCCCTGTGTGTGGAGAT 1812

     125 LeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIleProProProValIle 144
            |||         ||||||   |||   |||         ||||||      :::
    1813 ACAACTGGCTCCTCGGTGACTCTAGGATGCCTGGTCAAGGGTTATTTCCCTGAGCCAGTG 1872

     145 AsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyrGluThrSerPhe 164
            :::||||||      ||||||   |||:::::   ||||||:::
    1873 ACCTTGACCTGG------AACTCTGGATCCCTGTCCAGTGGTGTGCACACCTTCCCAGCT 1926

     165 LeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPheIleProSerAsp 184
         ::::::      |||          :::   ||||||   |||:::
    1927 GTCCTGCAGTCTGAC------CTCTACACCCTCAGCAG-CTCAGT--------------- 1964

     185 AspAspIleTyrAspCysLysValGluHis-TrpGlyLeuGluGluProValLeuLysHi 204
                    ||||||   :::|||||| |||
```

```
Db      1965 ----------GACTGTAACCTCGAGCACCTGG------------------------- 1986

Qy       204 sTrpGluProGluIleProAlaProMetSerGluLeuThrGluThrGlyGlyGlyGlySe 224
                                     |||        :::|||          ::
Db      1987 ---------------------CCCAGCCAGTCCATCACC---------TGCAATGTGGC 2015

Qy       224 rThrThrAlaProSerAlaGlnLeuGluLysGluLeuGlnAlaLeuGluLysGluAsnAl 244
             :      |||   |||   :::::::::|||::::::
Db      2016 CCACCCGGCAAGCAGCACCAAGGTGGACAAGAAAATT---------------------- 2052

Qy       244 aGlnLeuGluTrpGluLeuGlnAlaLeuGluLysGluLeuAlaGlnAlaAlaSerGluPr 264
                                                                  |||||
Db      2053 ------------------------------------------------------GAGCC 2057

Qy       264 oArgGlyProThrIleLysProCysProProCysLysCysProAlaProAsnLeuLeuGl 284
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2058 CAGAGGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCAGCACCTAACCTCTTGGG 2117

Qy       284 yGlyProSerValPheIlePheProProLysIleLysAspValLeuMetIleSerLeuSe 304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2118 TGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTCCCTGAG 2177

Qy       304 rProIleValThrCysValValValAspValSerGluAspAspProAspValGlnIleSe 324
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2178 CCCCATAGTCACATGTGTGGTGGTGGATGTGAGCGAGGATGACCCAGATGTCCAGATCAG 2237

Qy       324 rTrpPheValAsnAsnValGluValHisThrAlaGlnThrGlnThrHisArgGluAspTy 344
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2238 CTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAAACCCATAGAGAGGATTA 2297

Qy       344 rAsnSerThrLeuArgValValSerAlaLeuProIleGlnHisGlnAspTrpMetSerGl 364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2298 CAACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGACTGGATGAGTGG 2357

Qy       364 yLysGluPheLysCysLysValAsnAsnLysAspLeuProAlaProIleGluArgThrIl 384
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2358 CAAGGAGTTCAAATGCAAGGTCAACAACAAAGACCTCCCAGCGCCCATCGAGAGAACCAT 2417

Qy       384 eSerLysProLysGlySerValArgAlaProGlnValTyrValLeuProProProGluGl 404
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2418 CTCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACCAGAAGA 2477

Qy       404 uGluMetThrLysLysGlnValThrLeuThrCysMetValThrAspPheMetProGluAs 424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2478 AGAGATGACTAAGAAACAGGTCACTCTGACCTGCATGGTCACAGACTTCATGCCTGAAGA 2537

Qy       424 pIleTyrValGluTrpThrAsnAsnGlyLysThrGluLeuAsnTyrLysAsnThrGluPr 444
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2538 CATTTACGTGGAGTGGACCAACAACGGGAAAACAGAGCTAAACTACAAGAACACTGAACC 2597

Qy       444 oValLeuAspSerAspGlySerTyrPheMetTyrSerLysLeuArgValGluLysLysAs 464
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2598 AGTCCTGGACTCTGATGGTTCTTACTTCATGTACAGCAAGCTGAGAGTGGAAAAGAAGAA 2657

Qy       464 nTrpValGluArgAsnSerTyrSerCysSerValValHisGluGlyLeuHisAsnHisHi 484
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2658 CTGGGTGGAAAGAAATAGCTACTCCTGTTCAGTGGTCCACGAGGGTCTGCACAATCACCA 2717

Qy       484 sThrThrLysSerPheSerArgThrProGlyLys 495
             |||||||||||||||||||||||||||||||
Db      2718 CACGACTAAGAGCTTCTCCCGGACTCCGGGTAAA 2751
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RESULT 12
AAQ48037
ID AAQ48037 standard; cDNA to mRNA; 1581 BP.
XX
AC AAQ48037;
XX
DT 25-MAR-2003 (revised)
DT 10-MAR-2003 (revised)
DT 08-FEB-1994 (first entry)
XX
DE Monoclonal antibody M(alpha)2-3 H-chain coding sequence.

anti-snake small neurotoxin antibody; heavy chain; IgG2; immunoglobulin; bispecific bivalent antibody; cell-targetting; cytotoxic agent; ss.

Unidentified.

Key	Location/Qualifiers
CDS	61. .1470
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	/product= "Ig_heavy-chain"
sig_peptide	61. .117
	/*tag= a
mat_peptide	118. .477
	/*tag= c
	/product= "Ig_variable_region"
mat_peptide	478. .768
	/*tag= d
	/product= "Ig_constant_region"
mat_peptide	769. .816
	/*tag= e
	/product= "Ig_joining_region"
mat_peptide	817. .1146
	/*tag= f
	/product= "Ig_constant_region"
mat_peptide	1147. .1167
	/*tag= g
	/product= "Ig_constant_region"

EP556111-A1.

18-AUG-1993.

09-FEB-1993; 93EP-00400323.

11-FEB-1992; 92FR-00001505.

(COMS) COMMISSARIAT ENERGIE ATOMIQUE.

Boulain J, Ducancel F, Gillet D, Menez A;

WPI; 1993-260351/33.
P-PSDB; AAR40384.

New immunoglobulin hybrid proteins - with immunoglobulin fragments linked to dimeric protein, for diagnostic or therapeutic use.

Example 1; Fig 3A; 37pp; French.

A fragment of the heavy chain (VH + CH1) from the anti-snake small neurotoxin monoclonal antibody M(alpha)2-3 was PCR-amplified from hybridoma-derived cDNA using primers AAQ48039 and AAQ48040. A light chain fragment (VL + CL) was amplified from the same source using primers AAQ48041 and AAQ48042. The two amplified fragments were inserted into the same vector; the H-chain fragment was inserted (in-frame) between codons 6-7 of the phoA coding sequence and the L-chain fragment was inserted into a cassette which contained a phoA S-D sequence, a signal peptide and the first 6 codons of phoA. The cassette was positioned between the termination codon and the transcription termination sequence of phoA. The fusion construct is expected to to encode a hybrid protein comprising two identical Ab-derived units. The invention also covers hybrid proteins containing two different Ab-derived units (i.e. to produce bispecific antibodies). When a toxic protein is used in place of phoA, the hybrid molecules can be used as cell-targetting therapeutic agents. (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PN field.)

Sequence 1581 BP; 435 A; 448 C; 373 G; 325 T; 0 U; 0 Other;

ignment Scores:			
ed. No.:	4.24e-104	Length:	1581
ore:	1324.50	Matches:	286
rcent Similarity:	65.4%	Conservative:	31
st Local Similarity:	59.0%	Mismatches:	81
Query Match:	49.8%	Indels:	89
DB:	2	Gaps:	11

US-10-048-116B-2 (1-495) x AAQ48037 (1-1581)

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Qy        34 PheTyrGlyThrThrValTyrGlnSerProGlyAsp-----------IleGly------ 47
             :::|||          |||   |||   ||||||                |||||| 
Db       211 TACTATATAAACTGGGTGAAGCAGAAGCCTGGACAGGGACTTAAATGGATTGGATGGATT 270

Qy        48 --------------------GlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr 60
                                 :::|||          |||   |||              
Db       271 TATCCTGCAAGCGGTAATACTAAGTACAATGAGAACTTCAAGGGCAAGGCCACATTGACT 330

Qy        61 ValAspLeuAspLysLysLysThrValTrpArgLeu---------------ProGluPhe 75
             ||||||                  :::|||                    :::     
Db       331 GTAGACACATCCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACACT 390

Qy        76 GlyGlnLeuIleLeuPheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHis 95
                |||   |||   :::      ||||||                          :::  
Db       391 GCTGT-CTATTTCTGTGCAAGAGCTATGGGGGCTAC-----------------GGCTAC 431

Qy        96 AsnLeuGlyIleLeuThrLysArg-SerAsnPheThrProAlaThrAsnGluAlaProGl 115
                |||:::|||      ||| :::      |||   ::::::   :::           
Db       432 ACTTTTGGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCAGCCAAAACAACAGC 491

Qy       115 nAlaThrValPheProLysSerProVal---------LeuLeuGlyGlnProAsnThrLe 132
                :::|||:::|||   :::||||||          |||              |||||  
Db       492 CCCATCGGTCTATCCACTGGCCCCTGTGTGTGGAGATACAACTGGCTCCTCGGTGACTCT 551

Qy       132 uIleCysPheValAspAsnIleProProValIleAsnIleThrTrpLeuArgAsnSe 152
             |   |||   |||          ||||||      :::   :::||||||      |||||  
Db       552 AGGATGCCTGGTCAAGGGTTATTTCCCTGAGCCAGTGACCTTGACCTGG------AACTC 605

Qy       152 rLysSerValThrAspGlyValTyrGluThrSerPheLeuValAsnArgAspHisSerPh 172
             |   |||::::::   ||||||:::            ::::::      |||           
Db       606 TGGATCCCTGTCCAGTGGTGTGCACACCTTCCCAGCTGTCCTGCAGTCTGAC------CT 659

Qy       172 eHisLysLeuSerTyrLeuThrPheIleProSerAspAspAspIleTyrAspCysLysVa 192
              :::   ||||||   |||:::                          ||||||   ::  
Db       660 CTACACCCTCAGCAG-CTCAGT--------------------------GACTGTAACCT 691

Qy       192 lGluHis-TrpGlyLeuGluGluProValLeuLysHisTrpGluProGluIleProAlaP 212
             :|||||| |||                                                |  
Db       692 CGAGCACCTGG-----------------------------------------------C 703

Qy       212 roMetSerGluLeuThrGluThrGlyGlyGlyGlySerThrThrAlaProSerAlaGlnL 232
             ||          :::|||          :::       |||   |||   ::::       
Db       704 CCAGCCAGTCCATCACC---------TGCAATGTGGCCCACCCGGCAAGCAGCACCAAGG 754

Qy       232 euGluLysGluLeuGlnAlaLeuGluLysGluAsnAlaGlnLeuGluTrpGluLeuGlnA 252
             :::::|||::::::                                               
Db       755 TGGACAAGAAAATT---------------------------------------------- 768

Qy       252 laLeuGluLysGluLeuAlaGlnAlaAlaSerGluProArgGlyProThrIleLysProC 272
                                          ||||||||||||||||||||||||||||||  
Db       769 ------------------------------GAGCCCAGAGGGCCCACAATCAAGCCCT 796

Qy       272 ysProProCysLysCysProAlaProAsnLeuLeuGlyGlyProSerValPheIlePheP 292
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db       797 GTCCTCCATGCAAATGCCCAGCACCTAACCTCTTGGGTGGACCATCCGTCTTCATCTTCC 856

Qy       292 roProLysIleLysAspValLeuMetIleSerLeuSerProIleValThrCysValValV 312
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db       857 CTCCAAAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCATAGTCACATGTGTGGTGG 916

Qy       312 alAspValSerGluAspAspProAspValGlnIleSerTrpPheValAsnAsnValGluV 332
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db       917 TGGATGTGAGCGAGGATGACCCAGATGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAG 976

Qy       332 alHisThrAlaGlnThrGlnThrHisArgGluAspTyrAsnSerThrLeuArgValValS 352
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db       977 TACACACAGCTCAGACACAAACCCATAGAGAGGATTACAACAGTACTCTCCGGGTGGTCA 1036
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       352 erAlaLeuProIleGlnHisGlnAspTrpMetSerGlyLysGluPheLysCysLysValA 372
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1037 GTGCCCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCA 1096

       372 snAsnLysAspLeuProAlaProIleGluArgThrIleSerLysProLysGlySerValA 392
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1097 ACAACAAAGACCTGCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGGTCAGTAA 1156

       392 rgAlaProGlnValTyrValLeuProProProGluGluGluMetThrLysLysGlnValT 412
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1157 GAGCTCCACAGGTATATGTCTTGCCTCCACCAGAAGAAGAGATGACTAAGAAACAGGTCA 1216

       412 hrLeuThrCysMetValThrAspPheMetProGluAspIleTyrValGluTrpThrAsnA 432
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1217 CTCTGACCTGCATGGTCACAGACTTCATGCCTGAAGACATTTACGTGGAGTGGACCAACA 1276

       432 snGlyLysThrGluLeuAsnTyrLysAsnThrGluProValLeuAspSerAspGlySerT 452
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1277 ACGGGAAAACAGAGCTAAACTACAAGAACACTGAACCAGTCCTGGACTCTGATGGTTCTT 1336

       452 yrPheMetTyrSerLysLeuArgValGluLysLysAsnTrpValGluArgAsnSerTyrS 472
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1337 ACTTCATGTACAGCAAGCTGAGAGTGGAAAAGAAGAACTGGGTGGAAAGAAATAGCTACT 1396

       472 erCysSerValValHisGluGlyLeuHisAsnHisHisThrThrLysSerPheSerArgT 492
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1397 CCTGTTCAGTGGTCCACGAGGGTCTGCACAATCACCACACGACTAAGAGCTTCTCCCGGA 1456

       492 hrProGlyLys 495
           ||||||||||
      1457 CTCCGGGTAAA 1467
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ULT 13
: 9725
AED19725 standard; DNA; 1560 BP.

AED19725;

15-DEC-2005 (first entry)

Anti-PrP antibody heavy chain 44B1H DNA SEQ ID NO 5.

cerebroprotective; cell therapy; gene therapy; drug delivery; prion disease; 44B1H; ds; therapeutic; monoclonal antibody; heavy chain.

Unidentified.

WO2005094846-A1.

13-OCT-2005.

30-MAR-2005; 2005WO-JP006189.

30-MAR-2004; 2004JP-00100649.

(RENO-) RENOMEDIX INST INC.

Fujinaga K, Shinagawa M, Niitsu Y, Hamada H, Horiuchi M; Honmou O, Umetani A;

WPI; 2005-725409/74.

Agent useful for treating prion disease or delivering a substance to a lesioned region of prion disease, comprises a mesenchymal cell.

Claim 4; SEQ ID NO 5; 34pp; Japanese.

The invention describes an agent (I) for treating prion disease or delivering a substance to the lesioned region of prion disease, comprising a mesenchymal cell. Also described are: a nucleic acid (II) having an anti-prion antibody gene comprising: an antibody heavy chain gene having SEQ ID No: 1, 3, 5, 30, 32 and 34, a nucleotide sequence consisting of a degenerate genetic code, which encodes a polypeptide same as that of the above nucleotide sequence, a nucleotide sequence, which is a mutant of the above sequences, or a nucleotide sequence that is complementary to the above sequences and that hybridizes under stringent conditions with the above sequences; and an antibody light chain gene having SEQ ID No: 2, 4, 6, 31, 33 and 35, a nucleotide sequence consisting of degenerate genetic code, which encodes a polypeptide same as that of the above nucleotide sequence, a nucleotide sequence, which is a mutant of the above sequences, or a nucleotide sequence that is complementary to the above sequences and that hybridizes under stringent conditions with the above sequences; a vector (III) comprising (II); an anti-prion chimeric antibody (IV) comprising variable region of antibody encoded by (II) and constant region of antibody of animal other than mouse; a nucleic acid that encodes (IV); preparing (M1) a cell having abnormal prion proliferation inhibition activity, comprising transducing a gene that provides abnormal prion proliferation inhibition activity to the cell; a cell (V) having abnormal prion proliferation inhibition activity, being obtainable by (M1) or by utilizing (II) or (III); a sustainable formulation (VI) for discharge of an anti-prion antibody utilized for treating prion disease; use of a mesenchymal cell for producing an agent for delivering a substance to the lesioned region of prion disease; and delivering a substance to the lesioned region of a prion disease, comprising utilizing mesenchymal cell. (I) Is useful for treating prion disease or delivering a substance to the lesioned region of prion disease. (II), (III) Or (M1) is useful for preparing a cell having abnormal prion proliferation inhibition activity. (I), (II), (III), (IV) Or (VI) is useful for treating prion disease. (I) Enables improvement of the symptoms of prion disease. This sequence an anti-PrP monoclonal antibody heavy chain. Note: This sequence does not appear in the printed specification but has been obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_squences.

XX

SQ Sequence 1560 BP; 413 A; 424 C; 388 G; 335 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	7.55e-104	Length:	1560
Score:	1321.50	Matches:	269
Percent Similarity:	73.7%	Conservative:	19
Best Local Similarity:	68.8%	Mismatches:	39
Query Match:	49.7%	Indels:	65
DB:	14	Gaps:	8

US-10-048-116B-2 (1-495) x AED19725 (1-1560)

```
Qy        109 AlaThrAsnGluAlaProGlnAlaThrValProLysSerProVal---------Leu 125
              |||          ||||||      :::|||:::|||   :::||||||
Db        560 GCCAAAACAACAGCCCCA------TCGGTCTATCCACTGGCCCCTGTGTGTGGAGGTACA 613

Qy        126 LeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePheProProValIleAsn 145
                |||          ||||||   |||   |||          ||||||      :::
Db        614 ACTGGCTCCTCGGTGACTCTAGGATGCCTGGTCAAGGGTTATTTCCCTGAGCCAGTGACC 673

Qy        146 IleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyrGluThrSerPheLeu 165
              :::||||||      ||||||   |||::::::   ||||||:::           |||
Db        674 TTGACCTGG------AACTCTGGATCCCTGTCCAGTGGTGTGCACACCTTCCCAGCTCTC 727

Qy        166 ValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPheIleProSerAspAsp 185
              :::      |||          :::   ||||||   |||:::
Db        728 CTGCAGTCTGAC------CTCTACACCCTCAGCAG-CTCAGT----------------- 762

Qy        186 AspIleTyrAspCysLysValGluHis-TrpGlyLeuGluGluProValLeuLysHisTr 205
                      ||||||   :::|||||| |||
Db        763 ---------GACTGTAACCTCGAGCACCTGG---------------------------- 784

Qy        205 pGluProGluIleProAlaProMetSerGluLeuThrGluThrGlyGlyGlyGlySerTh 225
                                  |||         :::|||                 :::
Db        785 ------------------CCCAGCCAGTCCATCACC---------TGCAATGTGGCCCA 816

Qy        225 rThrAlaProSerAlaGlnLeuGluLysGluLeuGlnAlaLeuGluLysGluAsnAlaGl 245
                |||   |||   :::::::::|||::::::
Db        817 CCCGGCAAGCAGCACCAAGGTGGACAAGAAAATT------------------------- 850

Qy        245 nLeuGluTrpGluLeuGlnAlaLeuGluLysGluLeuAlaGlnAlaAlaSerGluProAr 265
                                                                ||||||||
```

```
 851 ----------------------------------------------------GAGCCCAG 858

 265 gGlyProThrIleLysProCysProProCysLysCysProAlaProAsnLeuLeuGlyGl 285
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 859 AGGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCAGCACCTAACCTCTTGGGTGG 918

 285 yProSerValPheIlePheProProLysIleLysAspValLeuMetIleSerLeuSerPr 305
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 919 ACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTCCCTGAGCCC 978

 305 oIleValThrCysValValValAspValSerGluAspAspProAspValGlnIleSerTr 325
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 979 CATAGTCACATGTGTGGTGGTGGATGTGAGCGAGGATGACCCAGATGTCCAGATCAGCTG 1038

 325 pPheValAsnAsnValGluValHisThrAlaGlnThrGlnThrHisArgGluAspTyrAs 345
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1039 GTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAAACCCATAGAGAGGATTACAA 1098

 345 nSerThrLeuArgValValSerAlaLeuProIleGlnHisGlnAspTrpMetSerGlyLy 365
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1099 CAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAA 1158

 365 sGluPheLysCysLysValAsnAsnLysAspLeuProAlaProIleGluArgThrIleSe 385
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1159 GGAGTTCAAATGCAAGGTCAACAACAAAGACCTCCCAGCGCCCATCGAGAGAACCATCTC 1218

 385 rLysProLysGlySerValArgAlaProGlnValTyrValLeuProProProGluGluGl 405
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1219 AAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACCAGAAGAAGA 1278

 405 uMetThrLysLysGlnValThrLeuThrCysMetValThrAspPheMetProGluAspIl 425
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1279 GATGACTAAGAAACAGGTCACTCTGACCTGCATGGTCACAGACTTCATGCCTGAAGACAT 1338

 425 eTyrValGluTrpThrAsnAsnGlyLysThrGluLeuAsnTyrLysAsnThrGluProVa 445
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1339 TTACGTGGAGTGGACCAACAACGGGAAAACAGAGCTAAACTACAAGAACACTGAACCAGT 1398

 445 lLeuAspSerAspGlySerTyrPheMetTyrSerLysLeuArgValGluLysLysAsnTr 465
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1399 CCTGGACTCTGATGGTTCTTACTTCATGTACAGCAAGCTGAGAGTGGAAAAGAAGAACTG 1458

 465 pValGluArgAsnSerTyrSerCysSerValValHisGluGlyLeuHisAsnHisHisTh 485
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1459 GGTGGAAAGAAATAGCTACTCCTGTTCAGTGGTCCACGAGGGTCTGCACAATCACCACAC 1518

 485 rThrLysSerPheSerArgThrProGlyLys 495
     ||||||||||||||||||||||||||||||
1519 GACTAAGAGCTTCTCCCGGACTCCGGGTAAA 1549
```

SULT 14
B21727

AEB21727 standard; DNA; 1407 BP.

AEB21727;

08-SEP-2005 (first entry)

Anti-Nogo-antibody 2A10 heavy chain polynucleotide.

neuroprotective; nootropic; cerebroprotective; vasotropic; antiparkinsonian; anticonvulsant; protein production; therapeutic; pharmaceutical; amyloidosis; metabolic disorder; cerebrovascular ischemia; cardiovascular disease; neurological disease; brain injury; injury; spinal cord injury; vulnerary; dementia; peripheral neuropathy; parkinsons disease; Huntingtons chorea; genetic disorder; Creutzfeldt Jakob disease; infection; motor neurone disease; cns-gen.; muscular-gen.; myositis; antiinflammatory; inflammation; musculoskeletal disease; Alzheimers disease; degeneration; antibody; heavy chain; ds.

Mus sp.

PN WO2005061545-A2.
XX
PD 07-JUL-2005.
XX
PF 20-DEC-2004; 2004WO-GB005343.
XX
PR 22-DEC-2003; 2003GB-00029684.
PR 22-DEC-2003; 2003GB-00029711.
XX
PA (GLAX) GLAXO GROUP LTD.
XX
PI Hussain I, Prinjha RK;
XX
DR WPI; 2005-522181/53.
XX
PT Modulating production of amyloidogenic peptide in, e.g. Alzheimer's
PT disease, by contacting cell and Nogo polypeptide with Nogo antagonist.
XX
PS Example 4; SEQ ID NO 49; 53pp; English.
XX
CC The invention describes a method of modulating production of an
CC amyloidogenic peptide comprising contacting a cell which is expressing
CC the precursor from which the amyloidogenic peptide is derived and a Nogo
CC polypeptide, with a Nogo antagonist. Also described are: use of a Nogo
CC antagonist in the manufacture of a medicament for the treatment or
CC prophylaxis of a disease involving amyloidosis; and a method of treatment
CC or prophylaxis of Alzheimer's disease comprising administering to the
CC human in need an anti-Nogo antibody. The invention is used for modulating
CC production of amyloidogenic peptide in, e.g. Alzheimer's disease, stroke,
CC traumatic brain injury and spinal cord injury, fronto-temporal dementias,
CC peripheral neuropathy, Parkinson's disease, Huntington's disease,
CC Creutzfeldt-Jakob disease, amyotropic lateral sclerosis, multiple
CC sclerosis, or inclusion body myositis. The invention provides an
CC unexpected route for therapeutic intervention in particularly Alzheimer's
CC disease. This sequence represents an anti-Nogo-antibody 2A10 heavy chain
CC polynucleotide.
XX
SQ Sequence 1407 BP; 378 A; 396 C; 346 G; 287 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	8.87e-104	Length:	1407
Score:	1320.00	Matches:	285
Percent Similarity:	64.0%	Conservative:	26
Best Local Similarity:	58.6%	Mismatches:	68
Query Match:	49.6%	Indels:	108
DB:	14	Gaps:	13

US-10-048-116B-2 (1-495) x AEB21727 (1-1407)

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Qy         39 ValTyrGlnSerProGlyAsp-----------IleGly---------------------- 47
              |||  |||  ||||||                 ||||||
Db        178 GTGAAGCAGAGGCCTGGACAAGGCCTTGAGTGGATTGGAAATATTAATCCTAGCAATGGT 237

Qy         48 ------GlnTyrThrHisGluPheAspGlyAspGluLeuPheTyrValAspLeuAspLys 65
                   |||     :::|||                          ||||||
Db        238 GGTACTAACTACAATGAGAAGTTCAAGAGCAAGGCCACACTGACTGTAGACAAATCCTCC 297

Qy         66 LysLysThrValTrpArgLeuPro---------------------------------- 73
                     :::|||
Db        298 AGCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTATTGT 357

Qy         74 GluPheGlyGlnLeuIleLeuPheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGlu 93
              |||  ||||||        :::     ||||||  |||     :::::::::
Db        358 GAACTGGGACAG------GGCTACTGGGGCCAAGGCACACTAGTCACCGTCTCCTCAGCC 411

Qy         94 LysHisAsnLeuGlyIleLeuThrLysArgSerAsnPheThrProAlaThrAsnGluAla 113
              |||                                                      |||
Db        412 AAA----------------------------------------------ACAACAGCC 423

Qy        114 ProGlnAlaThrValPheProLysSerProVal---------LeuLeuGlyGlnProAsn 130
              |||     :::|||:::|||   :::||||||           |||
Db        424 CCA------TCGGTCTATCCACTGGCCCCTGTGTGTGGAGATACAACTGGCTCCTCGGTG 477
```

```
131 ThrLeuIleCysPheValAspAsnIlePheProProValIleAsnIleThrTrpLeuArg 150
    ||||||   |||   |||          ||||||      :::   :::|||||||
478 ACTCTAGGATGCCTGGTCAAGGGTTATTTCCCTGAGCCAGTGACCTTGACCTGG------ 531

151 AsnSerLysSerValThrAspGlyValTyrGluThrSerPheLeuValAsnArgAspHis 170
    ||||||   |||:::::   ||||||:::              ::::::      |||
532 AACTCTGGATCCCTGTCCAGTGGTGTGCACACCTTCCCAGCTGTCCTGCAGTCTGAC--- 588

171 SerPheHisLysLeuSerTyrLeuThrPheIleProSerAspAspAspIleTyrAspCys 190
          :::   ||||||   |||:::                              ||||||
589 ---CTCTACACCCTCAGCAG-CTCAGT-------------------------GACTGT 617

191 LysValGluHis-TrpGlyLeuGluGluProValLeuLysHisTrpGluProGluIlePr 210
      :::|||||| |||
618 AACCTCGAGCACCTGG---------------------------------------- 633

210 oAlaProMetSerGluLeuThrGluThrGlyGlyGlyGlySerThrThrAlaProSerAl 230
      |||         :::|||                 :::       |||   |||
634 ----CCCAGCCAGTCCATCACC---------TGCAATGTGGCCCACCCGGCAAGCAGCAC 680

230 aGlnLeuGluLysGluLeuGlnAlaLeuGluLysGluAsnAlaGlnLeuGluTrpGluLe 250
    :::::::::|||:::::
681 CAAGGTGGACAAGAAAATT---------------------------------------- 699

250 uGlnAlaLeuGluLysGluLeuAlaGlnAlaAlaSerGluProArgGlyProThrIleLy 270
                                        ||||||||||||||||||||||
700 ------------------------------------GAGCCCAGAGGGCCCACAATCAA 722

270 sProCysProProCysLysCysProAlaProAsnLeuLeuGlyGlyProSerValPheIl 290
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
723 GCCCTGTCCTCCATGCAAATGCCCAGCACCTAACCTCCTGGGTGGCCCATCCGTCTTCAT 782

290 ePheProProLysIleLysAspValLeuMetIleSerLeuSerProIleValThrCysVa 310
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
783 CTTCCCTCCAAAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCATAGTCACATGTGT 842

310 lValValAspValSerGluAspAspProAspValGlnIleSerTrpPheValAsnAsnVa 330
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
843 GGTGGTGGATGTGAGCGAGGATGACCCAGATGTCCAGATCAGCTGGTTTGTGAACAACGT 902

330 lGluValHisThrAlaGlnThrGlnThrHisArgGluAspTyrAsnSerThrLeuArgVa 350
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
903 GGAAGTACACACAGCTCAGACACAAACCCATAGAGAGGATTACAACAGTACTCTCCGGGT 962

350 lValSerAlaLeuProIleGlnHisGlnAspTrpMetSerGlyLysGluPheLysCysLy 370
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
963 GGTCAGTGCCCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAA 1022

370 sValAsnAsnLysAspLeuProAlaProIleGluArgThrIleSerLysProLysGlySe 390
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1023 GGTCAACAACAAAGACCTCCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGGTC 1082

390 rValArgAlaProGlnValTyrValLeuProProProGluGluGluMetThrLysLysGl 410
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1083 AGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACCAGAAGAAGAGATGACTAAGAAACA 1142

410 nValThrLeuThrCysMetValThrAspPheMetProGluAspIleTyrValGluTrpTh 430
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1143 GGTCACTCTGACCTGCATGGTCACAGACTTCATGCCTGAAGACATTTACGTGGAGTGGAC 1202

430 rAsnAsnGlyLysThrGluLeuAsnTyrLysAsnThrGluProValLeuAspSerAspGl 450
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1203 CAACAACGGGAAAACAGAGCTAAACTACAAGAACACTGAACCAGTCCTGGACTCTGATGG 1262

450 ySerTyrPheMetTyrSerLysLeuArgValGluLysLysAsnTrpValGluArgAsnSe 470
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1263 TTCTTACTTCATGTACAGCAAGCTGAGAGTGGAAAAGAAGAACTGGGTGGAAAGAAATAG 1322

470 rTyrSerCysSerValValHisGluGlyLeuHisAsnHisHisThrThrLysSerPheSe 490
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1323 CTACTCCTGTTCAGTGGTCCACGAGGGTCTGCACAATCACCACACGACTAAGAGCTTCTC 1382

490 rArgThrProGlyLys 495
```

```
                ||||||||||||||||
Db       1383 CCGGACTCCGGGTAAA 1398
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RESULT 15
AEB08761
ID AEB08761 standard; DNA; 1407 BP.
XX
AC AEB08761;
XX
DT 08-SEP-2005 (first entry)
XX
DE antibody 2A10 heavy chain polynucleotide SEQ ID NO 49.
XX
KW cerebroprotective; vasotropic; neuroprotective; vulnerary; nootropic;
KW antiparkinsonian; anticonvulsant; neuroleptic; antibody engineering;
KW pharmaceutical; cerebrovascular ischemia; cardiovascular disease;
KW neurological disease; brain injury; injury; spinal cord injury;
KW Alzheimers disease; degeneration; dementia; neuropathy;
KW parkinsons disease; Huntingtons chorea; genetic disorder;
KW multiple sclerosis; immune disorder; Creutzfeldt Jakob disease;
KW infection; schizophrenia; psychiatric disorder; motor neurone disease;
KW cns-gen.; muscular-gen.; ds.
XX
OS Unidentified.
XX
PN WO2005061544-A2.
XX
PD 07-JUL-2005.
XX
PF 20-DEC-2004; 2004WO-GB005325.
XX
PR 22-DEC-2003; 2003GB-00029684.
PR 22-DEC-2003; 2003GB-00029711.
XX
PA (GLAX) GLAXO GROUP LTD.
XX
PI Ellis JH, Eon-Duval A, Grundy RI, Hussain F, Mcadam R;
PI Plumpton C, Prinjha RK, Wilson PA;
XX
DR WPI; 2005-479448/48.
XX
PT New antibody or its functional fragment that binds with and neutralizes
PT human neurite outgrowth useful for treating or prophylaxis of stroke and
PT other neurological disease e.g. traumatic brain injury, spinal cord
PT injury, Alzheimer's disease.
XX
PS Example 3; SEQ ID NO 49; 143pp; English.
XX
CC The invention describes an antibody (A1) or its functional fragment, that
CC binds with and neutralizes human neurite outgrowth (NOGO). Also described
CC are: providing a first vector encoding a heavy chain of the antibody;
CC providing a second vector encoding a light chain of the antibody; co-
CC transfecting a mammalian host cell with the first and second vectors;
CC culturing the host cell in culture media (preferably serum free) under
CC conditions permissive to the secretion of the antibody from the host cell
CC into the culture media; recovering (and optionally purifying) the
CC secreted antibody; and promoting axonal sprouting involving contacting a
CC human axon with an anti-NOGO antibody. The antibody is useful in the
CC preparation of a medicament for treating or prophylaxis of stroke and
CC other neurological disease/disorders (e.g. traumatic brain injury, spinal
CC cord injury, Alzheimer's disease, frontotemporal dementias (tauopathies),
CC peripheral neuropathy, Parkinson's disease, Huntington's disease and
CC multiple sclerosis); Creutzfeldt-jakob disease (CJD), Schizophrenia,
CC amyotrophic lateral sclerosis (ALS), inclusion body myositis. The
CC antibody inhibits neurodegeneration and/or promotes functional recovery
CC in a human patient suffering, or at risk of developing, stroke or other
CC neurological diseases/disorder. This sequence represents an antibody 2A10
CC heavy chain polynucleotide used in the creation of recombinant anti-NOGO
CC antibodies.
XX
SQ Sequence 1407 BP; 378 A; 396 C; 346 G; 287 T; 0 U; 0 Other;

Alignment Scores:

ed. No.:	8.87e-104	Length:	1407
ore:	1320.00	Matches:	285
rcent Similarity:	64.0%	Conservative:	26
st Local Similarity:	58.6%	Mismatches:	68
ery Match:	49.6%	Indels:	108
:	14	Gaps:	13

-10-048-116B-2 (1-495) x AEB08761 (1-1407)

```
         39 ValTyrGlnSerProGlyAsp-----------IleGly--------------------- 47
            |||   |||   ||||||             ||||||
        178 GTGAAGCAGAGGCCTGGACAAGGCCTTGAGTGGATTGGAAATATTAATCCTAGCAATGGT 237

         48 ------GlnTyrThrHisGluPheAspGlyAspGluLeuPheTyrValAspLeuAspLys 65
                  |||      :::|||                 ||||||
        238 GGTACTAACTACAATGAGAAGTTCAAGAGCAAGGCCACACTGACTGTAGACAAATCCTCC 297

         66 LysLysThrValTrpArgLeuPro----------------------------------- 73
                     :::|||
        298 AGCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTATTGT 357

         74 GluPheGlyGlnLeuIleLeuPheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGlu 93
            |||   ||||||         :::      ||||||   |||      :::::::::
        358 GAACTGGGACAG------GGCTACTGGGGCCAAGGCACACTAGTCACCGTCTCCTCAGCC 411

         94 LysHisAsnLeuGlyIleLeuThrLysArgSerAsnPheThrProAlaThrAsnGluAla 113
            |||                                                     |||
        412 AAA-----------------------------------------------ACAACAGCC 423

        114 ProGlnAlaThrValPheProLysSerProVal---------LeuLeuGlyGlnProAsn 130
            |||      :::|||:::|||   :::||||||               |||
        424 CCA------TCGGTCTATCCACTGGCCCCTGTGTGTGGAGATACAACTGGCTCCTCGGTG 477

        131 ThrLeuIleCysPheValAspAsnIlePheProProValIleAsnIleThrTrpLeuArg 150
            ||||||   |||   |||         ||||||     :::   :::||||||
        478 ACTCTAGGATGCCTGGTCAAGGGTTATTTCCCTGAGCCAGTGACCTTGACCTGG------ 531

        151 AsnSerLysSerValThrAspGlyValTyrGluThrSerPheLeuValAsnArgAspHis 170
            ||||||   |||::::::   ||||||:::             ::::::      |||
        532 AACTCTGGATCCCTGTCCAGTGGTGTGCACACCTTCCCAGCTGTCCTGCAGTCTGAC--- 588

        171 SerPheHisLysLeuSerTyrLeuThrPheIleProSerAspAspAspIleTyrAspCys 190
                :::   ||||||   |||:::                              ||||||
        589 ---CTCTACACCCTCAGCAG-CTCAGT-------------------------GACTGT 617

        191 LysValGluHis-TrpGlyLeuGluGluProValLeuLysHisTrpGluProGluIlePr 210
              :::|||||| |||
        618 AACCTCGAGCACCTGG------------------------------------------- 633

        210 oAlaProMetSerGluLeuThrGluThrGlyGlyGlyGlySerThrThrAlaProSerAl 230
                |||         :::|||                :::      |||   |||
        634 ----CCCAGCCAGTCCATCACC---------TGCAATGTGGCCCACCCGGCAAGCAGCAC 680

        230 aGlnLeuGluLysGluLeuGlnAlaLeuGluLysGluAsnAlaGlnLeuGluTrpGluLe 250
             ::::::::::|||::::::
        681 CAAGGTGGACAAGAAAATT---------------------------------------- 699

        250 uGlnAlaLeuGluLysGluLeuAlaGlnAlaAlaSerGluProArgGlyProThrIleLy 270
                                                  ||||||||||||||||||||
        700 ----------------------------------GAGCCCAGAGGGCCCACAATCAA 722

        270 sProCysProProCysLysCysProAlaProAsnLeuLeuGlyGlyProSerValPheIl 290
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        723 GCCCTGTCCTCCATGCAAATGCCCAGCACCTAACCTCCTGGGTGGCCCATCCGTCTTCAT 782

        290 ePheProProLysIleLysAspValLeuMetIleSerLeuSerProIleValThrCysVa 310
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        783 CTTCCCTCCAAAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCATAGTCACATGTGT 842

        310 lValValAspValSerGluAspAspProAspValGlnIleSerTrpPheValAsnAsnVa 330
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        843 GGTGGTGGATGTGAGCGAGGATGACCCAGATGTCCAGATCAGCTGGTTTGTGAACAACGT 902
```

```
Qy      330 lGluValHisThrAlaGlnThrGlnThrHisArgGluAspTyrAsnSerThrLeuArgVa 350
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      903 GGAAGTACACACAGCTCAGACACAAACCCATAGAGAGGATTACAACAGTACTCTCCGGGT 962

Qy      350 lValSerAlaLeuProIleGlnHisGlnAspTrpMetSerGlyLysGluPheLysCysLy 370
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      963 GGTCAGTGCCCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAA 1022

Qy      370 sValAsnAsnLysAspLeuProAlaProIleGluArgThrIleSerLysProLysGlySe 390
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1023 GGTCAACAACAAAGACCTCCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGGTC 1082

Qy      390 rValArgAlaProGlnValTyrValLeuProProProGluGluGluMetThrLysLysGl 410
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1083 AGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACCAGAAGAAGAGATGACTAAGAAACA 1142

Qy      410 nValThrLeuThrCysMetValThrAspPheMetProGluAspIleTyrValGluTrpTh 430
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1143 GGTCACTCTGACCTGCATGGTCACAGACTTCATGCCTGAAGACATTTACGTGGAGTGGAC 1202

Qy      430 rAsnAsnGlyLysThrGluLeuAsnTyrLysAsnThrGluProValLeuAspSerAspGl 450
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1203 CAACAACGGGAAAACAGAGCTAAACTACAAGAACACTGAACCAGTCCTGGACTCTGATGG 1262

Qy      450 ySerTyrPheMetTyrSerLysLeuArgValGluLysLysAsnTrpValGluArgAsnSe 470
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1263 TTCTTACTTCATGTACAGCAAGCTGAGAGTGGAAAAGAAGAACTGGGTGGAAAGAAATAG 1322

Qy      470 rTyrSerCysSerValValHisGluGlyLeuHisAsnHisHisThrThrLysSerPheSe 490
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1323 CTACTCCTGTTCAGTGGTCCACGAGGGTCTGCACAATCACCACACGACTAAGAGCTTCTC 1382

Qy      490 rArgThrProGlyLys 495
            |||||||||||||||
Db     1383 CCGGACTCCGGGTAAA 1398
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Search completed: May 31, 2006, 23:18:22
Job time : 1013.56 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.

protein - nucleic search, using frame_plus_p2n model

n on: May 31, 2006, 22:51:28 ; Search time 557.439 Seconds
(without alignments)
5215.692 Million cell updates/sec

:le: US-10-048-116B-2_COPY_1_278
rfect score: 1496
quence: 1 MPCSRALILGVLALNTMLSL.....QAASEPRGPTIKPCPPCKCP 278

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

rched: 5244920 seqs, 3486124231 residues

:al number of hits satisfying chosen parameters: 10489840

nimum DB seq length: 0
ximum DB seq length: 2000000000

st-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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B=N_Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
NITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
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) MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
ARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
GAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

:abase : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	% Query Match	Length	DB	ID	Description
1	1496	100.0	1484	5	AAF55098	Aaf55098 DNA encod
2	1214.5	81.2	777	12	ADQ31223	Adq31223 Class II
3	1182	79.0	4713	2	AAV12067	Aav12067 Murine IA
4	1105	73.9	1344	2	AAT60705	Aat60705 cDNA enco
5	1083	72.4	1676	4	ABI99041	Abi99041 Murine pC
6	1078	72.1	776	2	AAQ03169	Aaq03169 Sequence
7	1075	71.9	978	14	ADX26089	Adx26089 Novel cel
8	1072	71.7	776	2	AAT06285	Aat06285 I-Ab-alph
9	1072	71.7	776	2	AAQ56919	Aaq56919 Mouse I-A
10	1065.5	71.2	1508	2	AAT17587	Aat17587 Vector SC
11	1065.5	71.2	1508	2	AAT86988	Aat86988 SCT1 sing
12	1065.5	71.2	1508	2	AAX89069	Aax89069 Single ch
13	1065.5	71.2	1508	8	ACA60743	Aca60743 Mouse MHC
14	1065	71.2	588	2	AAT60698	Aat60698 Alphalalp
15	1052	70.3	776	2	AAQ35054	Aaq35054 IAB alpha
16	1039	69.5	1013	4	ABI99044	Abi99044 Murine pC
17	1036	69.3	1323	2	AAT60700	Aat60700 cDNA enco
18	1007.5	67.3	1382	2	AAT17588	Aat17588 Vector SC
19	1007.5	67.3	1382	2	AAT86989	Aat86989 SCE1 sing
20	1007.5	67.3	1382	8	ACA60744	Aca60744 Mouse MHC
21	1002	67.0	702	2	AAT60704	Aat60704 cDNA enco
22	996	66.6	588	2	AAT60701	Aat60701 Alphalalp
23	993.5	66.4	1385	2	AAT17586	Aat17586 Vector SS
24	993.5	66.4	1385	2	AAT86987	Aat86987 SSC1 sing
25	993.5	66.4	1385	8	ACA60742	Aca60742 Mouse MHC
26	983	65.7	1243	6	ABN84048	Abn84048 Single ch
27	982	65.6	2053	4	ABI99029	Abi99029 IAS MBP 9
28	982	65.6	2059	4	ABI99032	Abi99032 MBP 1-14
29	949.5	63.5	1701	4	ABI99028	Abi99028 IAS MBP 1
30	949.5	63.5	2346	4	ABI99027	Abi99027 IAS MBP 1
31	946	63.2	2343	4	ABI99033	Abi99033 MBP 90-10
32	944.5	63.1	1662	4	ABI99039	Abi99039 Murine pC
33	944.5	63.1	1680	4	ABI99021	Abi99021 I-As MBP.
34	944.5	63.1	1686	4	ABI99031	Abi99031 MBP 1-14
35	944.5	63.1	1698	4	ABI99038	Abi99038 Murine pC
36	941.5	62.9	1707	4	ABI99030	Abi99030 IAS MBP 9
37	821.5	54.9	768	14	AEB23395	Aeb23395 HLA-DQ al
38	818.5	54.7	768	14	AEB23394	Aeb23394 HLA-DQ al
39	818	54.7	765	14	AEB23392	Aeb23392 HLA-DQ al
40	813.5	54.4	768	6	ABQ74306	Abq74306 Human leu
41	813.5	54.4	768	14	ADV43942	Adv43942 Human psy
42	813.5	54.4	768	14	AEB23385	Aeb23385 HLA-DQ al
43	813.5	54.4	768	14	AEB23386	Aeb23386 HLA-DQ al
44	813.5	54.4	768	14	AEB23393	Aeb23393 HLA-DQ al
45	813.5	54.4	956	4	AAI58351	Aai58351 Human pol

ALIGNMENTS

RESULT 1
AAF55098
ID AAF55098 standard; DNA; 1484 BP.
XX
AC AAF55098;
XX
DT 15-MAY-2001 (first entry)
XX
DE DNA encoding a fusion protein comprising an alpha chain of MHC.
XX
KW Recombinant protein; alpha chain; beta chain; MHC; immunoglobulin;
KW major histocompatibility complex; Fc region; antigen; T lymphocyte;
KW immunostimulant; vaccine; infection; tumour; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1. .1482
FT /*tag= a
XX
PN WO200109194-A1.
XX
PD 08-FEB-2001.
XX
PF 28-JUL-2000; 2000WO-FR002193.
XX
PR 29-JUL-1999; 99FR-00009862.

(CNRS) CNRS CENT NAT RECH SCI.

Glaichenhaus N, Malherbe L;

WPI; 2001-182944/18.
P-PSDB; AAB67480.

New soluble recombinant protein, useful e.g. as immunostimulant, comprises dimeric major histocompatibility complex molecule fused to immunoglobulin Fc region.

Example 1; Page 31-33; 43pp; French.

The specification describes soluble recombinant proteins that comprise at least a dimer formed from the alpha and beta-chains of MHC (major histocompatibility complex) Class I and II molecules in which at least one chain has, attached to its C-terminus, at least part of the Fc region of an immunoglobulin. The recombinant proteins, when linked to an antigenic peptide, are used to count and/or purify antigen-reactive T lymphocytes and to characterize their phenotype, e.g. in preclinical evaluation of vaccines. They are also used as immunostimulants, particularly for vaccine development (against infections and tumours), to count and determine phenotype of autoreactive T cells in subjects with, or at risk of developing, autoimmune diseases, e.g. for staging or evaluating treatments, and (to purify and/or enrich Ag-reactive T cells from cell cultures or patient samples, for use in subsequent curative or preventative cellular therapy. The present sequence encodes a recombinant protein of the invention, comprising an alpha chain of MHC molecules

Sequence 1484 BP; 414 A; 394 C; 362 G; 314 T; 0 U; 0 Other;

nment Scores:

d. No.:	7.62e-140	Length:	1484
e:	1496.00	Matches:	278
ent Similarity:	100.0%	Conservative:	0
Local Similarity:	100.0%	Mismatches:	0
y Match:	100.0%	Indels:	0
	5	Gaps:	0

0-048-116B-2_COPY_1_278 (1-278) x AAF55098 (1-1484)

```
Qy        1 MetProCysSerArgAlaLeuIleLeuGlyValLeuAlaLeuAsnThrMetLeuSerLeu 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 ATGCCGTGCAGCAGAGCTCTGATTCTGGGGGTCCTCGCCCTGAACACCATGCTCAGCCTC 60

Qy       21 CysGlyGlyGluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrThrValTyr 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 TGCGGAGGTGAAGACGACATTGAGGCCGACCACGTAGGCTTCTATGGTACAACTGTTTAT 120

Qy       41 GlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 CAGTCTCCTGGAGACATTGGCCAGTACACACATGAATTTGATGGTGATGAGTTGTTCTAT 180

Qy       61 ValAspLeuAspLysLysLysThrValTrpArgLeuProGluPheGlyGlnLeuIleLeu 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GTGGACTTGGATAAGAAGAAAACTGTCTGGAGGCTTCCTGAGTTTGGCCAATTGATACTC 240

Qy       81 PheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 TTTGAGCCCCAAGGTGGACTGCAAAACATAGCTGCAGAAAAACACAACTTGGGAATCTTG 300

Qy      101 ThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPhePro 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 ACTAAGAGGTCAAATTTCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGTTCCCC 360

Qy      121 LysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhe 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 AAGTCCCCTGTGCTGCTGGGTCAGCCCAACACCCTTATCTGCTTTGTGGACAACATCTTC 420

Qy      141 ProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyr 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 CCACCTGTGATCAACATCACATGGCTCAGAAATAGCAAGTCAGTCACAGACGGCGTTTAT 480

Qy      161 GluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPhe 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 GAGACCAGCTTCCTCGTCAACCGTGACCATTCCTTCCACAAGCTGTCTTATCTCACCTTC 540

Qy      181 IleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluPro 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 ATCCCTTCTGATGATGACATTTATGACTGCAAGGTGGAGCACTGGGGCCTGGAGGAGCCG 600

Qy      201 ValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThrGly 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 GTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAAACTGGA 660

Qy      221 GlyGlyGlySerThrThrAlaProSerAlaGlnLeuGluLysGluLeuGlnAlaLeuGlu 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 GGTGGAGGATCCACTACAGCTCCATCAGCTCAGCTCGAAAAAGAGCTCCAGGCCCTGGAG 720

Qy      241 LysGluAsnAlaGlnLeuGluTrpGluLeuGlnAlaLeuGluLysGluLeuAlaGlnAla 260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 AAGGAAAATGCACAGCTGGAATGGGAGTTGCAAGCACTGGAAAAGGAACTGGCTCAGGCA 780

Qy      261 AlaSerGluProArgGlyProThrIleLysProCysProProCysLysCysPro 278
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 GCATCTGAGCCCAGAGGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCA 834
```

RESULT 2
ADQ31223
ID ADQ31223 standard; cDNA; 777 BP.
XX
AC ADQ31223;
XX
DT 07-OCT-2004 (first entry)
XX
DE Class II MHC-related I-Ab(alpha)-leucine zipper (LZ) fusion cDNA.
XX
KW class II major histocompatibility complex; MHC; CD4+ T-cell detection;
KW flow cytometry; mucous membrane invasive antigen;
KW I-Ab(alpha)-leucine zipper fusion; ss; gene.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT CDS 1. .777
FT /*tag= a
FT /product= "Class II MHC-related I-Ab(alpha)-leucine
FT zipper (LZ) fusion protein"
XX
PN JP2004196789-A.
XX
PD 15-JUL-2004.
XX
PF 03-DEC-2003; 2003JP-00404367.
XX
PR 03-DEC-2002; 2002JP-00351818.
XX
PA (SENT-) SENTAN KAGAKU GIJUTSU INCUBATION CENT KK.
XX
DR WPI; 2004-546819/53.
DR P-PSDB; ADQ31222.
XX
PT Peptide-Class II major histocompatibility complex (MHC) composite, useful
PT for detecting antigen specific CD4+ T-cell, comprises antigen peptide
PT containing epitope of mucous membrane invasive protein, and extracellular
PT region of MHC.
XX
PS Example 1; SEQ ID NO 8; 30pp; Japanese.
XX
CC The invention relates to a novel class II major histocompatibility
CC complex (MHC) antigenic peptide composite comprising a peptide containing
CC the T-cell antigenic determinant of a mucous membrane invasive protein
CC and the extracellular region of a class II MHC molecule or at least part
CC of the extracellular region of the class II MHC molecule having an amino
CC acid sequence comprising one or more deletions, substitutions or

additions. The molecule of the invention may be useful for detecting an antigen-specific CD4+ T-cell by flow cytometry and for presenting a microorganism-derived mucous membrane invasive protein as an antigen. The method of the invention enables efficient detection of antigen-specific activation of CD4+ T-cells in the mucous membrane. The current sequence is that of the class II major histocompatibility complex-related I-Ab(alpha)-leucine zipper (LZ) fusion cDNA of the invention.

Sequence 777 BP; 193 A; 207 C; 195 G; 182 T; 0 U; 0 Other;

ignment Scores:

ed. No.:	5.27e-112	Length:	777
ore:	1214.50	Matches:	232
rcent Similarity:	92.3%	Conservative:	7
st Local Similarity:	89.6%	Mismatches:	19
ery Match:	81.2%	Indels:	1
:	12	Gaps:	1

-10-048-116B-2_COPY_1_278 (1-278) x ADQ31223 (1-777)

```
          1 MetProCysSerArgAlaLeuIleLeuGlyValLeuAlaLeuAsnThrMetLeuSerLeu 20
            ||||||   ||||||||||||||||||||||||||||||||   ||||||||||||||||
          1 ATGCCGCGCAGCAGAGCTCTGATTCTGGGGGTCCTCGCCCTGACCACCATGCTCAGCCTC 60

         21 CysGlyGlyGluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrThrValTyr 40
            ||||||||||||||||||||||||||||||||||||||||   ||||||   :::||||||
         61 TGTGGAGGTGAAGACGACATTGAGGCCGACCACGTAGGCACCTATGGTATAAGTGTATAT 120

         41 GlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr 60
            ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
        121 CAGTCTCCTGGAGACATTGGCCAGTACACATTTGAATTTGATGGTGATGAGTTGTTCTAT 180

         61 ValAspLeuAspLysLysLysThrValTrpArgLeuProGluPheGlyGlnLeuIleLeu 80
            ||||||||||||||||||:::||||||||   ||||||||||||||||||||||||||||
        181 GTGGACTTGGATAAGAAGGAGACTGTCTGGATGCTTCCTGAGTTTGGCCAATTGGCAAGC 240

         81 PheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeu 100
            |||:::|||||||||||||||||||||||||||||||||||||||||||||||:::|||
        241 TTTGACCCCCAAGGTGGACTGCAAAACATAGCTGTAGTAAAACACAACTTGGGAGTCTTG 300

        101 ThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPhePro 120
            |||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
        301 ACTAAGAGGTCAAATTCCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGTTCCCC 360

        121 LysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhe 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        361 AAGTCCCCTGTGCTGCTGGGTCAGCCCAACACCCTCATCTGCTTTGTGGACAACATCTTC 420

        141 ProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyr 160
            ||||||||||||||||||||||||||||||||||||||||||   ||||||||||||||
        421 CCTCCTGTGATCAACATCACATGGCTCAGAAATAGCAAGTCAGTCGCAGACGGTGTTTAT 480

        161 GluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPhe 180
            |||||||||||||   ||||||||||:::||||||||||||||||||||||||||||||
        481 GAGACCAGCTTCTTCGTCAACCGTGACTATTCCTTCCACAAGCTGTCTTATCTCACCTTC 540

        181 IleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluPro 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        541 ATCCCTTCTGACGATGACATTTATGACTGCAAGGTGGAACACTGGGGCCTGGAGGAGCCG 600

        201 ValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThrGly 220
            ||||||||||||||||||||||||||||||||||||||||||||||   :::
        601 GTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCGTCA---GCAGACCTGGTT 657

        221 GlyGlyGlySerThrThrAlaProSerAlaGlnLeuGluLysGluLeuGlnAlaLeuGlu 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
        658 CCGCGCGGATCCACTACAGCTCCATCAGCTCAGCTCGAAAAAGAGCTCCAGGCCCTGCAG 717

        241 LysGluAsnAlaGlnLeuGluTrpGluLeuGlnAlaLeuGluLysGluLeuAlaGln 259
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        718 AAGGAAAATGCACAGCTGGAATGGGAGTTGCAAGCACTGGAAAAGGAACTGGCTCAG 774
```

SULT 3

AAV12067

ID AAV12067 standard; cDNA; 4713 BP.
XX
AC AAV12067;
XX
DT 08-JUN-1998 (first entry)
XX
DE Murine IAd alpha chain cDNA.
XX
KW Major histocompatibility class II antigen; MHC class II; T cell;
KW T lymphocyte; Th1; Th2; activation; CD4+; antigen presenting cell; APC;
KW autoimmune disease; diabetes; multiple sclerosis; autoimmune thyroiditis;
KW systemic lupus erythromatosus; myasthenia gravis; Crohn's disease;
KW inflammatory bowel disease; allergy; asthma; contact sensitivity;
KW immunotherapy; therapy; IAd alpha chain; mouse; ds; circular; cyclic.
XX
OS Mus musculus.
XX
PN WO9746256-A1.
XX
PD 11-DEC-1997.
XX
PF 22-MAY-1997; 97WO-US008697.
XX
PR 23-MAY-1996; 96US-0018175P.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Webb SR, Winqvist O, Karlsson L, Jackson MR, Peterson PA;
XX
DR WPI; 1998-041895/04.
XX
PT Synthetic antigen presenting cell for activating CD4+ T cells - useful to
PT treat autoimmune disease, e.g. diabetes, multiple sclerosis, Crohn's
PT disease and inflammatory bowel disease, or allergy, e.g. asthma and
PT contact sensitivity.
XX
PS Example 2; Page 92-94; 141pp; English.
XX
CC This nucleotide sequence comprises a PCR product obtained by
CC amplification of mouse splenocyte cDNA using primers (see AAV12063 and
CC AAV12064) designed for the amplification of IAd alpha chain full-length
CC cDNA. IAd beta chain cDNA (see AAV12068) has been similarly obtained. The
CC IAd sequences were cloned into metallothionein promoter (see AAV12062)-
CC driven vector pRmHa-3 prior to sequencing. Major histocompatibility
CC complex (MHC) class II IAd heterodimers were expressed at the cell
CC surface of transfected Drosophila Schneider 2 (ATCC CRL 10974) cells. The
CC invention relates to the preparation and use of synthetic antigen
CC presenting matrices, in particular antigen presenting cells such as
CC insect cells that have been transfected to produce MHC antigen presenting
CC molecules with one or more accessory molecules. The matrices are used to
CC activate naive CD4+ T cells and to shift the ongoing activation state
CC into a preferred differentiated population of Th1 or Th2 cells.
CC Applications include the treatment of autoimmune disease, e.g. diabetes,
CC multiple sclerosis, autoimmune thyroiditis, systemic lupus erythematosus,
CC myasthenia gravis, Crohn's disease and inflammatory bowel disease, or an
CC allergy, e.g. asthma and contact sensitivity
XX
SQ Sequence 4713 BP; 1211 A; 1166 C; 1152 G; 1184 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.15e-107	Length:	4713
Score:	1182.00	Matches:	219
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	79.0%	Indels:	0
DB:	2	Gaps:	0

US-10-048-116B-2_COPY_1_278 (1-278) x AAV12067 (1-4713)

```
Qy          1 MetProCysSerArgAlaLeuIleLeuGlyValLeuAlaLeuAsnThrMetLeuSerLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        459 ATGCCGTGCAGCAGAGCTCTGATTCTGGGGGTCCTCGCCCTGAACACCATGCTCAGCCTC 518
```

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 21 CysGlyGlyGluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrThrValTyr 40
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
519 TGCGGAGGTGAAGACGACATTGAGGCCGACCACGTAGGCTTCTATGGTACAACTGTTTAT 578

 41 GlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr 60
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
579 CAGTCTCCTGGAGACATTGGCCAGTACACACATGAATTTGATGGTGATGAGTTGTTCTAT 638

 61 ValAspLeuAspLysLysLysThrValTrpArgLeuProGluPheGlyGlnLeuIleLeu 80
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
639 GTGGACTTGGATAAGAAGAAAACTGTCTGGAGGCTTCCTGAGTTTGGCCAATTGATACTC 698

 81 PheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeu 100
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
699 TTTGAGCCCCAAGGTGGACTGCAAAACATAGCTGCAGAAAAACACAACTTGGGAATCTTG 758

101 ThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPhePro 120
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
759 ACTAAGAGGTCAAATTTCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGTTCCCC 818

121 LysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhe 140
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
819 AAGTCCCCTGTGCTGCTGGGTCAGCCCAACACCCTTATCTGCTTTGTGGACAACATCTTC 878

141 ProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyr 160
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
879 CCACCTGTGATCAACATCACATGGCTCAGGAATAGCAAGTCAGTCACAGACGGCGTTTAT 938

161 GluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPhe 180
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
939 GAGACCAGCTTCCTCGTCAACCGTGACCATTCCTTCCACAAGCTGTCTTATCTCACCTTC 998

181 IleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluPro 200
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
999 ATCCCTTCTGATGATGACATTTATGACTGCAAGGTGGAGCACTGGGGCCTGGAGGAGCCG 1058

201 ValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThr 219
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1059 GTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAAACT 1115
```

```
ULT 4
0705
  AAT60705 standard; cDNA; 1344 BP.

  AAT60705;

  27-AUG-2003  (revised)
  12-SEP-1997  (first entry)

  cDNA encoding soluble fused MHC heterodimer:peptide complex pLJ23.

  Soluble; fusion; major histocompatibility complex; MHC; heterodimer;
  complex; antigen; binding groove; tolerance; autoantigen; disease;
  insulin dependent; diabetes mellitus; IDDM; antagonist; T cell; anergy;
  presenting cell; ds.

  Mus sp.
  Synthetic.

  Key             Location/Qualifiers
  mat_peptide     1. .1344
                  /*tag= a

  WO9640944-A2.

  19-DEC-1996.

  07-JUN-1996;   96WO-US010102.

  07-JUN-1995;   95US-00480002.
  07-JUN-1995;   95US-00482133.
  07-JUN-1995;   95US-00483241.

  PR   27-OCT-1995;   95US-0005964P.
  XX
  PA   (ZYMO ) ZYMOGENETICS INC.
  PA   (ANER-) ANERGEN INC.
  XX
  PI   Kindsvogel W,  Reich EP,  Gross JA,  Deshpande S,  Sheppard PO;
  XX
  DR   WPI; 1997-052337/05.
  DR   P-PSDB; AAW10513.
  XX
  PT   Novel fused major histocompatibility complex:antigenic peptide complex -
  PT   useful to induce tolerance to an autoantigen-related disease e.g. insulin
  PT   -dependent diabetes mellitus.
  XX
  PS   Example 3; Page 129-132; 142pp; English.
  XX
  CC   The present sequence encodes a novel soluble fused major
  CC   histocompatibility complex (MHC) heterodimer:peptide complex, comprising
  CC   1st and 2nd MHC domains, linked by a 5-25 residue linker, an antigenic
  CC   peptide able to associate with a peptide binding groove of the MHC
  CC   molecule, linked in frame to the 2nd domain by a 5-25 residue linker and
  CC   a DNA encoding a 3rd MHC domain linked in frame to the DNA encoding the
  CC   antigenic peptide by a DNA encoding a 5-25 residue linker. The complex
  CC   can be used to induce immunological tolerance in adults susceptible to,
  CC   or suffering from an autoantigen related disease, e.g. insulin dependent
  CC   diabetes mellitus (IDDM), by antagonising the binding of particular T
  CC   cells and antigen presenting cells, to induce anergy (immunological non-
  CC   responsiveness) in the targeted T cell. As the heterodimers and
  CC   corresponding antigen are permanently linked into a single chain,
  CC   obviating the requirement for complex heterodimer truncation or
  CC   formation, the complex eliminates inefficient and non-specific peptide
  CC   loading. (Updated on 27-AUG-2003 to correct OS field.)
  XX
  SQ   Sequence 1344 BP; 326 A; 356 C; 390 G; 272 T; 0 U; 0 Other;

  Alignment Scores:
  Pred. No.:                1.07e-100      Length:          1344
  Score:                    1105.00        Matches:         203
  Percent Similarity:       100.0%         Conservative:    0
  Best Local Similarity:    100.0%         Mismatches:      0
  Query Match:              73.9%          Indels:          0
  DB:                       2              Gaps:            0

  US-10-048-116B-2_COPY_1_278 (1-278) x AAT60705 (1-1344)

  Qy        22 GlyGlyGluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrThrValTyrGln 41
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  Db       388 GGTGGCGAAGACGACATTGAGGCCGACCACGTAGGCTTCTATGGTACAACTGTTTATCAG 447

  Qy        42 SerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyrVal 61
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  Db       448 TCTCCTGGAGACATTGGCCAGTACACACATGAATTTGATGGTGATGAGTTGTTCTATGTG 507

  Qy        62 AspLeuAspLysLysLysThrValTrpArgLeuProGluPheGlyGlnLeuIleLeuPhe 81
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  Db       508 GACTTGGATAAGAAGAAAACTGTCTGGAGGCTTCCTGAGTTTGGCCAATTGATACTCTTT 567

  Qy        82 GluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeuThr 101
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  Db       568 GAGCCCCAAGGTGGACTGCAAAACATAGCTGCAGAAAAACACAACTTGGGAATCTTGACT 627

  Qy       102 LysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPheProLys 121
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  Db       628 AAGAGGTCAAATTTCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGTTCCCCAAG 687

  Qy       122 SerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhePro 141
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  Db       688 TCCCCTGTGCTGCTGGGTCAGCCCAACACCCTTATCTGCTTTGTGGACAACATCTTCCCA 747

  Qy       142 ProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyrGlu 161
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  Db       748 CCTGTGATCAACATCACATGGCTCAGAAATAGCAAGTCAGTCACAGACGGCGTTTATGAG 807
```

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162 ThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPheIle 181
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
808 ACCAGCTTCCTCGTCAACCGTGACCATTCCTTCCACAAGCTGTCTTATCTCACCTTCATC 867

182 ProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluProVal 201
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
868 CCTTCTGATGATGACATTTATGACTGCAAGGTGGAGCACTGGGGCCTGGAGGAGCCGGTT 927

202 LeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThrGlyGly 221
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
928 CTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAGACTGGCGGA 987

222 GlyGlySer 224
    |||||||||
988 GGTGGCTCA 996
```

SULT 5
I99041

ABI99041 standard; cDNA; 1676 BP.

ABI99041;

25-FEB-2002 (first entry)

Murine pCB223 coding sequence.

Mouse; MHC; major histocompatibility complex; MHC class II; multimer; single chain; immunosuppressive; antidiabetic; antiinflammatory; antianaemic; antirheumatoid; antiarthritic; neuroprotective; vaccine; autoimmune disease; insulin dependent diabetes; multiple sclerosis; myasthenia gravis; pernicious anaemia; autoimmune encephalomyelitis; rheumatoid arthritis; systemic lupus erythematosus; ss.

Mus sp.
Synthetic.

WO200170245-A1.

27-SEP-2001.

22-MAR-2001; 2001WO-US009616.

22-MAR-2000; 2000US-0191274P.
15-MAY-2000; 2000US-0204249P.
23-JAN-2001; 2001US-0264003P.

(CORI-) CORIXA CORP.

Carter D, Zhu S, Arimilli S, Wang A;

WPI; 2001-616371/71.
P-PSDB; ABB56471.

Multimeric complex for treating autoimmune diseases, comprises first and second single chain MHC class II molecules, each comprising alpha1 and beta1 domain linked through amino acid linker and multimerization domain.

Disclosure; Page 115; 147pp; English.

The invention relates to a multimeric complex comprising a first recombinant single chain major histocompatibility complex (MHC) class II molecule and a second recombinant single chain MHC class II molecule, each comprising an alpha1 domain and a beta1 domain linked through an amino acid linker and a multimerisation domain. The first and the second molecule are linked through the multimerisation domain to form a multimeric complex,. The complex is useful for treating autoimmune diseases. It is useful for treating insulin dependent diabetes, multiple sclerosis, myasthenia gravis, pernicious anaemia, autoimmune encephalomyelitis (EAE), rheumatoid arthritis and systemic lupus erythematosus. The present sequence encodes a single chain MHC class II molecule of the invention

Sequence 1676 BP; 438 A; 470 C; 407 G; 361 T; 0 U; 0 Other;

```
Alignment Scores:
Pred. No.:                 2.34e-98     Length:          1676
Score:                     1083.00      Matches:         215
Percent Similarity:        68.9%        Conservative:    13
Best Local Similarity:     65.0%        Mismatches:      39
Query Match:               72.4%        Indels:          64
DB:                        4            Gaps:            5

US-10-048-116B-2_COPY_1_278 (1-278) x ABI99041 (1-1676)

Qy      7 LeuIleLeuGlyValLeuAlaLeuAsnThrMetLeuSerLeuCysGly------GlyGlu 24
          |||:::          :::   :::       :::||||||     |||       |||||
Db     37 CTCCTCTCGGCTGCTGTGGTGGTGCTGATGGTGCTGAGCAGCCCAGGGACTGAGGGCGAA 96

Qy     25 AspAspIleGluAlaAspHisValGlyPheTyrGlyThrThrValTyrGlnSerProGly 44
          ||||||||||||||||||||||||||||     ||||||||||||||||||||||||||||
Db     97 GACGACATTGAGGCCGACCACGTAGGCGTCTATGGTACAACTGTATATCAGTCTCCTGGA 156

Qy     45 AspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyrValAspLeuAsp 64
          |||||||||||||||||||||||||||||||||||||||     ||||||||||||||||
Db    157 GACATTGGCCAGTACACACATGAATTTGATGGTGATGAGTGGTTCTATGTGGACTTGGAT 216

Qy     65 LysLysLysThrValTrpArgLeuProGluPheGlyGlnLeuIleLeuPheGluProGln 84
          ||||||:::|||:::|||   ||||||||||||||||||||||||     |||:::||||||
Db    217 AAGAAGGAGACTATCTGGATGCTTCCTGAGTTTGGCCAATTGACAAGCTTTGACCCCCAA 276

Qy     85 GlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeuThrLysArgSer 104
          ||||||||||||||||||||||||||      |||:::   ||||||||||||||||||||
Db    277 GGTGGACTGCAAAACATAGCTACAGGAAAATACACCTTGGGAATCTTGACTAAGAGGTCA 336

Qy    105 AsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPheProLysSerProVal 124
          |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    337 AATTCCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGTTCCCCAAGTCCCCTGTG 396

Qy    125 LeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePheProProValIle 144
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    397 CTGCTGGGTCAGCCCAACACCCTCATCTGCTTTGTGGACAACATCTTCCCTCCTGTGATC 456

Qy    145 AsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyrGluThrSerPhe 164
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    457 AACATCACATGGCTCAGAAATAGTAAGTCAGTCACAGACGGCGTTTATGAGACCAGCTTC 516

Qy    165 LeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPheIleProSerAsp 184
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    517 CTTGTCAACCGTGACCATTCCTTCCACAAGCTGTCTTATCTCACCTTCATCCCTTCTGAC 576

Qy    185 AspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluProValLeuLysHis 204
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    577 GATGATATTTATGACTGCAAGGTGGAGCACTGGGGCCTGGAGGAGCCGGTTCTGAAACAC 636

Qy    205 TrpGluProGluIleProAlaProMetSerGluLeuThrGluThrGlyGlyGlyGlySer 224
          |||||||||||||||||||||||||||||||||                  |||
Db    637 TGGGAACCTGAGATTCCAGCCCCCATGTCAGAA---------------GGATCTGCCAAA 681

Qy    225 ThrThrAlaProSer--------------------------------------------- 229
          |||||||||||||||
Db    682 ACAACAGCCCCATCGGTCTATCCACTGGCCCCTGTGTGTGGAGATACAACTGGCTCCTCG 741

Qy    229 ------------------------------------------------------------ 229

Db    742 GTGACTCTAGGATGCCTGGTCAAGGGTTATTTCCCTGAGCCAGTGACCTTGACCTGGAAC 801

Qy    230 ---------------------------------------AlaGlnLeuGluLysGluLeuGln 237
                                                 |||   |||:::   :::|||
Db    802 TCTGGATCCCTGTCCAGTGGTGTGCACACCTTCCCAGCTGTCCTGCAGTCTGACCTCTAC 861

Qy    238 AlaLeuGluLysGlu------AsnAlaGlnLeuGluTrpGluLeuGlnAlaLeuGluLys 255
             |||                             |||      |||::::::
Db    862 ACCCTCAGCAGCTCAGTGACTGTAACCTCGAGCACCTGGCCCAGCCAGTCCATCACCTGC 921

Qy    256 GluLeuAlaGlnAlaAlaSer------------------------GluProArgGlyPro 267
             :::|||      ||||||                        |||||||||||||||
```

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      922 AATGTGGCCCACCCGGCAAGCAGCACCAAGGTGGACAAGAAAATTGAGCCCAGAGGGCCC 981

      268 ThrIleLysProCysProProCysLysCysPro 278
          ||||||||||||||||||||||||||||||||||
      982 ACAATCAAGCCCTGTCCTCCATGCAAATGCCCA 1014

LT 6
3169
AAQ03169 standard; DNA; 776 BP.

AAQ03169;

25-MAR-2003  (revised)
31-OCT-2002  (revised)
23-AUG-1990  (first entry)

Sequence encoding the I-Ab-alpha chain of the Class II major
histocompatibility complex (MHC) antigens.

I-A (Class II) histocompatibility protein;
major histocompatibility complex antigen; MHC-II; acetylcholine receptor;
myasthenia gravis; autoantigen; autommune disease; epitope.

Unidentified.

WO8912459-A.

28-DEC-1989.

23-JUN-1989;   89WO-US002784.

23-JUN-1988;   88US-00210594.
21-JUN-1989;   89US-00367751.

(BIOS-) BIOSPAN CORP.

Sharma SD,  Lerch BL,  Clark BR;

WPI; 1990-022384/03.

New complexes of histo-compatible glyco:protein - with antigenic
peptide(s) and label or toxin, used to target antigen specific T helper
cells.

Figure 8; Page ?; 74pp; English.

The patent claims complexes of formulae (I), (II) and (III) which are as
follows: (I) X - MCH - peptide; (II) MCH - peptide - X; (III) MCH -
peptide. Where X = toxin or labelling gp.; MHC = effective portion of the
major histocompatibility glycoprotein; and the peptide includes an
epitope associated with one of the major autoimmune diseases. The MHC is
the N-terminal of alpha1, alpha2, beta1 or beta2 regions of MHC-II. The
complexes can be used to treat and monitor the autoimmune disease. In one
protocol, an oligonucleotide encoding the AChR peptide 195-212 - an
epitope in myasthenia gravis patients - was attached to the DNA encoding
the N-terminal of the I-Ab-alpha chain. (Updated on 31-OCT-2002 to add
missing OS field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated
on 25-MAR-2003 to correct PI field.)

Sequence 776 BP; 177 A; 205 C; 199 G; 195 T; 0 U; 0 Other;

nment Scores:
. No.:              2.56e-98        Length:         776
:e:                 1078.00         Matches:        201
ent Similarity:     94.1%           Conservative:   5
 Local Similarity:  91.8%           Mismatches:     13
y Match:            72.1%           Indels:         0
                    2               Gaps:           0

0-048-116B-2_COPY_1_278 (1-278) x AAQ03169 (1-776)

        1 MetProCysSerArgAlaLeuIleLeuGlyValLeuAlaLeuAsnThrMetLeuSerLeu 20
          |||||||  ||||||||||||||||||||||||||||||||||  ||||||||||||||||

Db          6 ATGCCGCGCAGCAGAGCTCTGATTCTGGGGGTCCTCGCCCTGACCACCATGCTCAGCCTC 65

Qy         21 CysGlyGlyGluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrThrValTyr 40
              ||||||||||||||||||||||||||||||||||||||||  ||||||  :::||||||
Db         66 TGTGGAGGTGAAGACGACATTGAGGCCGACCACGTAGGCACCTATGGTATAAGTGTATAT 125

Qy         41 GlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr 60
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db        126 CAGTCTCCTGGAGACATTGGCCAGTACACATTTGAATTTGATGGTGATGAGTTGTTCTAT 185

Qy         61 ValAspLeuAspLysLysLysThrValTrpArgLeuProGluPheGlyGlnLeuIleLeu 80
              ||||||||||||||||||:::||||||||||  ||||||||||||||||||||||||||
Db        186 GTGGACTTGGATAAGAAGGAGACTGTCTGGATGCTTCCTGAGTTTGGCCAATTGGCAAGC 245

Qy         81 PheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeu 100
              |||:::||||||||||||||||||||||||||||||  ||||||||||||||:::|||
Db        246 TTTGACCCCCAAGGTGGACTGCAAAACATAGCTGTAGTAAAACACAACTTGGGAGTCTTG 305

Qy        101 ThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPhePro 120
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db        306 ACTAAGAGGTCAAATTCCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGTTCCCC 365

Qy        121 LysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 AAGTCCCCTGTGCTGCTGGGTCAGCCCAACACCCTCATCTGCTTTGTGGACAACATCTTC 425

Qy        141 ProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||
Db        426 CCTCCTGTGATCAACATCACATGGCTCAGAAATAGCAAGTCAGTCGCAGACGGTGTTTAT 485

Qy        161 GluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPhe 180
              ||||||||||||  ||||||||||||:::||||||||||||||||||||||||||||||
Db        486 GAGACCAGCTTCTTCGTCAACCGTGACTATTCCTTCCACAAGCTGTCTTATCTCACCTTC 545

Qy        181 IleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluPro 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 ATCCCTTCTGACGATGACATTTATGACTGCAAGGTGGAACACTGGGGCCTGGAGGAGCCG 605

Qy        201 ValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThr 219
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 GTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAGACT 662

RESULT 7
ADX26089
ID   ADX26089 standard; DNA; 978 BP.
XX
AC   ADX26089;
XX
DT   05-MAY-2005  (first entry)
XX
DE   Novel cell pain response detection method-related mouse gene SeqID435.
XX
KW   pain; animal disease model; expression; analgesic; antiaddictive;
KW   nootropic; anticonvulsant; vasotropic; neuroprotective; tranquilizer;
KW   antiasthmatic; antirheumatic; antiarthritic; osteopathic;
KW   ophthalmological; antiinflammatory; antipruritic; dermatological;
KW   antiulcer; gastrointestinal-Gen.; nephrotropic; gynecological;
KW   hepatotropic; antiparkinsonian; neuroleptic; laxative; gene therapy;
KW   neuropathic pain; Alzheimers disease; Parkinsons disease;
KW   motor neurone disease; Huntingtons disease; schizophrenia; gene; ds.
XX
OS   Mus sp.
XX
PN   WO2005014849-A2.
XX
PD   17-FEB-2005.
XX
PF   06-JUL-2004; 2004WO-US023166.
XX
PR   03-JUL-2003; 2003US-0485101P.
XX
PA   (EURO-) EUROCELTIQUE SA.
XX
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Tong J, Jin G, Ji R, Xu Y, Chiang LW, Lavery DJ;

WPI; 2005-163258/17.

Detecting pain responses in a cell, useful in identifying potential therapeutic and diagnostic candidates for treating pain, by identifying genes that are differentially expressed in a model of neuropathic pain.

Example 1; SEQ ID NO 435; 173pp; English.

This invention relates to a novel method of detecting a pain response in a cell which comprises determining the expression level in a test cell of at least one nucleic acid molecule and comparing the expression level to a level in an animal model of pain, where similar or identical expression levels indicate a pain response in the test cell. The invention may be useful for the development of compounds with an analgesic, antiaddictive, nootropic, anticonvulsant, vasotropic, neuroprotective, tranquilizer, antiasthmatic, antirheumatic, antiarthritic, osteopathic, ophthalmological, antiinflammatory, antipruritic, dermatological, antiulcer, gastrointestinal-Gen., nephrotropic, gynecological, hepatotropic, antiparkinsonian, neuroleptic or laxative activity whilst the disclosed sequences may prove useful for gene therapy. The methods and compositions of the present invention are useful for identifying agonists and antagonists for the gene or gene products as potential therapeutic and diagnostic candidates for treating pain, including neuropathic pain, nociceptive pain, chronic pain, inflammatory pain, pain associated with cancer, and pain associated with rheumatic disease, and also for addiction, seizure, stroke, ischemia, a neurodegenerative disorder, anxiety, depression, headache, asthma, rheumatic disease, osteoarthritis, retinopathy, inflammatory eye disorders, pruritus, ulcer, gastric lesions, uncontrollable urination, an inflammatory or unstable bladder disorder, inflammatory bowel disease, irritable bowel syndrome (IBS), irritable bowel disease (IBD), gastroesophageal reflux disease (GERD), functional dyspepsia, functional chest pain of presumed esophageal origin, functional dysphagia, non-cardiac chest pain, symptomatic gastroesophageal disease, gastritis, aerophagia, functional constipation, functional diarrhea, burbulence, chronic functional abdominal pain, recurrent abdominal pain (RAP), function abdominal bloating, functional biliary pain, functional incontinence, functional ano-rectal disorder, cholecystalgia, interstitial cystitis, dysmenorrhea, or dyspareunia. They can also be used diagnosing or treating Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, Huntington's disease and schizophrenia. The present sequence is that of a mouse gene which demonstrated homology to a human gene whose expression level analysed in the method of the invention.

Sequence 978 BP; 218 A; 263 C; 247 G; 250 T; 0 U; 0 Other;

ignment Scores:

el. No.:	7.05e-98	Length:	978
ore:	1075.00	Matches:	203
rcent Similarity:	93.6%	Conservative:	2
st Local Similarity:	92.7%	Mismatches:	14
ery Match:	71.9%	Indels:	0
:	14	Gaps:	0

-10-048-116B-2_COPY_1_278 (1-278) x ADX26089 (1-978)

```
          1 MetProCysSerArgAlaLeuIleLeuGlyValLeuAlaLeuAsnThrMetLeuSerLeu 20
            |||||||  ||||||||||||||||||||||||||||||||  ||||||||||||||||
         24 ATGCCGCGCAGCAGAGCTCTGATTCTGGGGGTCCTCGCCCTGACCACCATGCTCAGCCTC 83

         21 CysGlyGlyGluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrThrValTyr 40
            ||||||||||||||||||||||||||||||||||||||||    ||||||   |||||||||
         84 TGCGGAGGTGAAGACGACATTGAGGCCGACCACGTAGGCTCCTATGGTATAACTGTATAT 143

         41 GlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr 60
            |||||||||||||||||||||||||||||||    ||||||||||||||||||||||||||
        144 CAGTCTCCTGGAGACATTGGCCAGTACACATTTGAATTTGATGGTGATGAGTTGTTCTAT 203

         61 ValAspLeuAspLysLysLysThrValTrpArgLeuProGluPheGlyGlnLeuIleLeu 80
            ||||||||||||||||:::|||||||||   ||||||||||||   ||||||
        204 GTGGACTTGGATAAGAAGGAGACTGTCTGGATGCTTCCTGAGTTTGCTCAACTGAGAAGA 263

Qy          81 PheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeu 100
               ||||||||||||||||||||||||||||||||||||||||  ||||||||||||  ||||||
Db         264 TTTGAGCCCCAAGGTGGACTGCAAAACATAGCTACAGGAAAACACAACTTGGAAATCTTG 323

Qy         101 ThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPhePro 120
               |||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db         324 ACTAAGAGGTCAAATTCCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGTTCCCC 383

Qy         121 LysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhe 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         384 AAGTCTCCTGTGCTGCTGGGTCAGCCCAACACCCTTATCTGCTTTGTGGACAACATCTTC 443

Qy         141 ProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyr 160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         444 CCTCCTGTGATCAACATCACATGGCTCAGAAATAGCAAGTCAGTCACAGACGGCGTTTAT 503

Qy         161 GluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPhe 180
               |||||||||||  |||||||||||:::||||||||||||||||||||||||||||||||
Db         504 GAAACCAGCTTCTTCGTCAACCGTGACTATTCCTTCCACAAGCTGTCTTATCTCACCTTC 563

Qy         181 IleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluPro 200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         564 ATCCCTTCTGACGATGACATTTATGACTGCAAGGTGGAGCACTGGGGCCTGGAGGAGCCG 623

Qy         201 ValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThr 219
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         624 GTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAGACT 680
```

RESULT 8
AAT06285
ID AAT06285 standard; DNA; 776 BP.
XX
AC AAT06285;
XX
DT 10-APR-1996 (first entry)
XX
DE I-Ab-alpha chain DNA.
XX
KW I-Ab-alpha-chain; acetylcholine receptor; myelin basic protein;
KW autoantigen; MHC class II; major histocompatibility complex;
KW autoimmunity; autoimmune disease; rheumatoid arthritis;
KW myasthenia gravis; multiple sclerosis; allograft rejection; vaccine; ds.
XX
OS Mus musculus.
XX
PN US5468481-A.
XX
PD 21-NOV-1995.
XX
PF 14-APR-1992; 92US-00869293.
XX
PR 23-JUN-1988; 88US-00210594.
PR 21-JUN-1989; 89US-00367751.
PR 30-AUG-1990; 90US-00576084.
PR 28-DEC-1990; 90US-00635840.
PR 23-APR-1991; 91US-00690840.
XX
PA (ANER-) ANERGEN INC.
XX
PI Sharma SD, Lerch BL, Clark BR;
XX
DR WPI; 1993-036056/04.
XX
PT Pure major MHC-peptide complex - useful in treating deleterious immune
PT response such as auto:immunity.
XX
PS Disclosure; Fig 8; 47pp; English.
XX
CC A sequence (AAT06285) encoding the I-Ab-alpha chain is utilised in the
CC construction of novel MHC class II conjugates. An autoantigen peptide,
CC derived e.g. from the acetylcholine receptor alpha chain (AAR86421) or
CC myelin basic protein (AAR86422), is attached to the N-terminal end of an

appropriate MHC molecule via the I-Ab-alpha (or -beta) chain sequence. The resulting conjugate is used in the treatment of autoimmune diseases

Sequence 776 BP; 177 A; 205 C; 199 G; 194 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.:	1.02e-97	Length:	776
Score:	1072.00	Matches:	200
Percent Similarity:	93.6%	Conservative:	5
Best Local Similarity:	91.3%	Mismatches:	14
Query Match:	71.7%	Indels:	0
DB:	2	Gaps:	0

US-10-048-116B-2_COPY_1_278 (1-278) x AAT06285 (1-776)

```
        1 MetProCysSerArgAlaLeuIleLeuGlyValLeuAlaLeuAsnThrMetLeuSerLeu 20
          ||||||  ||||||||||||||||||||||||||||||||||  ||||||||||||||||
        6 ATGCCGCGCAGCAGAGCTCTGATTCTGGGGGTCCTCGCCCTGACCACCATGCTCAGCCTC 65

       21 CysGlyGlyGluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrThrValTyr 40
          ||||||||||||||||||||||||||||||||||||  ||||||   :::||||||
       66 TGTGGAGGTGAAGACGACATTGAGGCCGACCACGTAGGCACCTATGGTATAAGTGTATAT 125

       41 GlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr 60
          ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
      126 CAGTCTCCTGGAGACATTGGCCAGTACACATTTGAATTTGATGGTGATGAGTTGTTCTAT 185

       61 ValAspLeuAspLysLysLysThrValTrpArgLeuProGluPheGlyGlnLeuIleLeu 80
          ||||||||||||||||:::||||||||||  ||||||||||||||||||||||
      186 GTGGACTTGGATAAGAAGGAGACTGTCTGGATGCTTCCTGAGTTTGGCCAATTGGCAAGC 245

       81 PheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeu 100
          |||:::|||||||||||||||||||||||||||||||  ||||||||||||||:::|||
      246 TTTGACCCCCAAGGTGGACTGCAAAACATAGCTGTAGTAAAACACAACTTGGGAGTCTTG 305

      101 ThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPhePro 120
          ||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
      306 ACTAAGAGGTCAAATTCCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGTTCCCC 365

      121 LysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhe 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      366 AAGTCCCCTGTGCTGCTGGGTCAGCCCAACACCCTCATCTGCTTTGTGGACAACATCTTC 425

      141 ProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyr 160
          ||||||||||||||||||||||||||||||  ||||||||||||  ||||||||||||
      426 CCTCCTGTGATCAACATCACATGGCTCAGAAAARAGCAAGTCAGTCGCAGACGGTGTTTAT 485

      161 GluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPhe 180
          ||||||||||||  ||||||||||||:::||||||||||||||||||||||||||||||
      486 GAGACCAGCTTCTTCGTCAACCGTGACTATTCCTTCCACAAGCTGTCTTATCTCACCTTC 545

      181 IleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluPro 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      546 ATCCCTTCTGACGATGACATTTATGACTGCAAGGTGGAACACTGGGGCCTGGAGGAGCCG 605

      201 ValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThr 219
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      606 GTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAGACT 662
```

LT 9
6919
AAQ56919 standard; DNA; 776 BP.

AAQ56919;

25-MAR-2003 (revised)
08-JUL-1994 (first entry)

Mouse I-Ab-alpha chain.

MHC; major histocompatibility complex; toxic conjugate; autoimmunity; autoimmune disease; helper T-cell; T-lymphocyte; acetylcholine receptor; myelin basic protein; I-Ab; ds.

XX
OS Mus sp.
XX
PN US5284935-A.
XX
PD 08-FEB-1994.
XX
PF 28-DEC-1990; 90US-00635840.
XX
PR 23-JUN-1988; 88US-00210594.
PR 21-JUN-1989; 89US-00367751.
PR 30-AUG-1990; 90US-00576084.
XX
PA (ANER-) ANERGEN INC.
XX
PI Sharma SD, Lerch BL, Clark BR;
XX
DR WPI; 1994-056406/07.
DR P-PSDB; AAR45948.
XX
PT MHC-mediated toxic peptide conjugates - useful for ameliorating auto-
PT immunity.
XX
PS Disclosure; Fig 8.1-8.2; 42pp; English.
XX
CC The acetylcholine receptor alpha subunit given in sequence AAR45946
CC (corresponding mRNA in AAQ56918) and the myelin basic protein given in
CC AAR45947 are antigenic peptides associated with autoantigens. They have
CC been conjugated with MHC class II components such as I-Ab- alpha chain
CC (encoded by sequene AAQ56919) and I-Ab-beta chain, (encoded by AAQ56920)
CC and a toxin or label to form conjugates used to target helper T-cells for
CC the treatment of autoimmune diseases. (Updated on 25-MAR-2003 to correct
CC PF field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 776 BP; 177 A; 205 C; 199 G; 194 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.:	1.02e-97	Length:	776
Score:	1072.00	Matches:	200
Percent Similarity:	93.6%	Conservative:	5
Best Local Similarity:	91.3%	Mismatches:	14
Query Match:	71.7%	Indels:	0
DB:	2	Gaps:	0

US-10-048-116B-2_COPY_1_278 (1-278) x AAQ56919 (1-776)

```
Qy          1 MetProCysSerArgAlaLeuIleLeuGlyValLeuAlaLeuAsnThrMetLeuSerLeu 20
              ||||||  ||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db          6 ATGCCGCGCAGCAGAGCTCTGATTCTGGGGGTCCTCGCCCTGACCACCATGCTCAGCCTC 65

Qy         21 CysGlyGlyGluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrThrValTyr 40
              ||||||||||||||||||||||||||||||||||||  ||||||   :::||||||
Db         66 TGTGGAGGTGAAGACGACATTGAGGCCGACCACGTAGGCACCTATGGTATAAGTGTATAT 125

Qy         41 GlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr 60
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        126 CAGTCTCCTGGAGACATTGGCCAGTACACATTTGAATTTGATGGTGATGAGTTGTTCTAT 185

Qy         61 ValAspLeuAspLysLysLysThrValTrpArgLeuProGluPheGlyGlnLeuIleLeu 80
              ||||||||||||||||:::||||||||||  ||||||||||||||||||||||
Db        186 GTGGACTTGGATAAGAAGGAGACTGTCTGGATGCTTCCTGAGTTTGGCCAATTGGCAAGC 245

Qy         81 PheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeu 100
              |||:::|||||||||||||||||||||||||||||||  ||||||||||||||:::|||
Db        246 TTTGACCCCCAAGGTGGACTGCAAAACATAGCTGTAGTAAAACACAACTTGGGAGTCTTG 305

Qy        101 ThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPhePro 120
              ||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        306 ACTAAGAGGTCAAATTCCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGTTCCCC 365

Qy        121 LysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 AAGTCCCCTGTGCTGCTGGGTCAGCCCAACACCCTCATCTGCTTTGTGGACAACATCTTC 425
```

```
       141 ProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyr 160
           ||||||||||||||||||||||||||||||   ||||||||||||   ||||||||||||
       426 CCTCCTGTGATCAACATCACATGGCTCAGAAARAGCAAGTCAGTCGCAGACGGTGTTTAT 485

       161 GluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPhe 180
           ||||||||||||   ||||||||||||:::||||||||||||||||||||||||||||||
       486 GAGACCAGCTTCTTCGTCAACCGTGACTATTCCTTCCACAAGCTGTCTTATCTCACCTTC 545

       181 IleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluPro 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       546 ATCCCTTCTGACGATGACATTTATGACTGCAAGGTGGAACACTGGGGCCTGGAGGAGCCG 605

       201 ValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThr 219
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       606 GTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAGACT 662

SULT 10
T17587
   AAT17587 standard; DNA; 1508 BP.

   AAT17587;

   26-SEP-1996  (first entry)

   Vector SCT1-derived single chain gene encoding MHC fusion complex.

   MHC; major histocompatibility complex; PCR; polymerase chain reaction;
   T cell activity modulator; antagonist; immune disorder; allergy;
   multiple sclerosis; insulin-dependent diabetes mellitus;
   rheumatoid arthritis; myasthenia gravis; ds.

   Synthetic.

   Key             Location/Qualifiers
   CDS             6. .1508
                   /*tag= a
   sig_peptide     6. .86
                   /*tag= b
                   /label= I-Ad_beta_chain_leader
                   /note= "murine MHC class II I-Ad gene beta chain leader
                   sequence"
   misc_feature    87. .137
                   /*tag= c
                   /label= OVA_323-339
                   /note= "chicken ovalbumin residues 323-339"
   misc_feature    138. .167
                   /*tag= d
                   /note= "10 residue linker peptide"
   misc_feature    168. .452
                   /*tag= e
                   /label= I-Ad_beta1
                   /note= "murine MHC class II I-Ad gene beta-1 domain"
   misc_feature    453. .734
                   /*tag= f
                   /label= I-Ad_beta2
                   /note= "murine MHC class II I-Ad gene beta-2 domain"
   misc_feature    735. .806
                   /*tag= g
                   /note= "24 residue peptide linker"
   misc_feature    807. .1067
                   /*tag= h
                   /label= I-Ad_alpha1
                   /note= "murine MHC class II I-Ad gene alpha-2 domain"
   misc_feature    1068. .1352
                   /*tag= i
                   /label= I-Ad_alpha2
                   /note= "murine MHC class II I-Ad gene alpha-2 domain"
   misc_feature    1353. .1505
                   /*tag= j
                   /label= I-Ad_alpha-TM
                   /note= "murine MHC class II I-Ad gene alpha-transmembrane
                   domain"

   XX
   PN   WO9604314-A1.
   XX
   PD   15-FEB-1996.
   XX
   PF   31-JUL-1995;   95WO-US009816.
   XX
   PR   29-JUL-1994;   94US-00283302.
   PR   01-FEB-1995;   95US-00382454.
   XX
   PA   (DADE-) DADE INT INC.
   XX
   PI   Wong HC,  Rhode PR,  Weidanz JA,  Grammer S,  Edwards AC;
   PI   Chavaillaz P,  Jiao J;
   XX
   DR   WPI; 1996-129343/13.
   DR   P-PSDB; AAR98906.
   XX
   PT   Major histocompatability complex fusion complex for modulating T cell
   PT   activity - used in the treatment of immune disorders, e.g. multiple
   PT   sclerosis, IDDM and rheumatoid arthritis.
   XX
   PS   Example 17; Fig 28; 210pp; English.
   XX
   CC   AAT17587 encodes a murine MHC fusion complex capable of modulating T cell
   CC   activity encoded by the vector SCT1. The MHC fusion complex comprises at
   CC   least one MHC molecule containing a peptide-binding groove and a
   CC   presenting peptide covalently linked to the MHC molecule and opt. a
   CC   transmembrane domain. DNA encoding a MHC fusion complex may be cloned
   CC   into a host cell to express the complex. The transformed cells may then
   CC   be used to identify peptides that modulate, pref. antagonise, T cell
   CC   activity. DNA encoding a MHC fusion complex or a single chain fusion
   CC   molecule may be used to vaccinate a mammal against a targeted disorder.
   CC   The fusion complexes may be used to suppress an immune response in an
   CC   animal suffering from an immune disorder e.g. multiple sclerosis, insulin
   CC   -dependent diabetes mellitus, rheumatoid arthritis, myasthenia gravis or
   CC   chronic allergies. The complexes may also be used in the treatment of
   CC   livestock and pets such as cats and dogs. The MHC fusion complexes can be
   CC   produced such that they contain a single antigenic peptide including one
   CC   of known structure, additionally a wide range of peptides can be
   CC   presented for T cell interaction
   XX
   SQ   Sequence 1508 BP; 337 A; 414 C; 440 G; 317 T; 0 U; 0 Other;

   Alignment Scores:
   Pred. No.:                1.15e-96        Length:          1508
   Score:                    1065.50         Matches:         198
   Percent Similarity:       98.5%           Conservative:    0
   Best Local Similarity:    98.5%           Mismatches:      0
   Query Match:              71.2%           Indels:          3
   DB:                       2               Gaps:            1

   US-10-048-116B-2_COPY_1_278 (1-278) x AAT17587 (1-1508)

   Qy          22 GlyGly---------GluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrThr 38
                  ||||||         ||||||||||||||||||||||||||||||||||||||||||
   Db         792 GGCGGTTCCTCGAGTGAAGACGACATTGAGGCCGACCACGTAGGCTTCTATGGTACAACT 851

   Qy          39 ValTyrGlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeu 58
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   Db         852 GTTTATCAGTCTCCTGGAGACATTGGCCAGTACACACATGAATTTGATGGTGATGAGTTG 911

   Qy          59 PheTyrValAspLeuAspLysLysLysThrValTrpArgLeuProGluPheGlyGlnLeu 78
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   Db         912 TTCTATGTGGACTTGGATAAGAAGAAAACTGTCTGGAGGCTTCCTGAGTTTGGCCAATTG 971

   Qy          79 IleLeuPheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGly 98
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   Db         972 ATACTCTTTGAGCCCCAAGGTGGACTGCAAAACATAGCTGCAGAAAAACACAACTTGGGA 1031

   Qy          99 IleLeuThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrVal 118
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   Db        1032 ATCTTGACTAAGAGGTCAAATTTCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTG 1091
```

```
      119 PheProLysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsn 138
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     1092 TTCCCCAAGTCCCCTGTGCTGCTGGGTCAGCCCAACACCCTTATCTGCTTTGTGGACAAC 1151

      139 IlePheProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGly 158
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     1152 ATCTTCCCACCTGTGATCAACATCACATGGCTCAGAAATAGCAAGTCAGTCACAGACGGC 1211

      159 ValTyrGluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeu 178
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     1212 GTTTATGAGACCAGCTTCCTCGTCAACCGTGACCATTCCTTCCACAAGCTGTCTTATCTC 1271

      179 ThrPheIleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGlu 198
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     1272 ACCTTCATCCCTTCTGATGATGACATTTATGACTGCAAGGTGGAGCACTGGGGCCTGGAG 1331

      199 GluProValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGlu 218
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     1332 GAGCCGGTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAA 1391

      219 Thr 219
          |||
     1392 ACT 1394
```

LT 11
6988
AAT86988 standard; DNA; 1508 BP.

AAT86988;

27-MAR-1998 (first entry)

SCT1 single chain gene.

Construction; major histocompatibility complex; MHC; fusion complex; SCT1 single chain gene; ss.

Synthetic.

Key	Location/Qualifiers
CDS	6. .1508
	/*tag= a

WO9728191-A1.

07-AUG-1997.

30-JAN-1997; 97WO-US001617.

31-JAN-1996; 96US-00596387.

(DADE-) DADE INT INC.

Rhode PR, Jiao J, Burkhardt M, Wong HC;

WPI; 1997-402555/37.
P-PSDB; AAW29213.

Single chain major histocompatibility complex comprising linked alpha and beta chains - useful for suppressing an immune response to an auto:immune disease, e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, etc.

Example 17; Page 137-139; 217pp; English.

The present sequence was used in the construction of major histocompatibility complex (MHC) fusion complexes

Sequence 1508 BP; 337 A; 413 C; 441 G; 317 T; 0 U; 0 Other;

nment Scores:
d. No.: 1.15e-96 Length: 1508

Score:	1065.50	Matches:	198
Percent Similarity:	98.5%	Conservative:	0
Best Local Similarity:	98.5%	Mismatches:	0
Query Match:	71.2%	Indels:	3
DB:	2	Gaps:	1

US-10-048-116B-2_COPY_1_278 (1-278) x AAT86988 (1-1508)

```
Qy         22 GlyGly---------GluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrThr 38
              ||||||         ||||||||||||||||||||||||||||||||||||||||||||
Db        792 GGCGGTTCCTCGAGTGAAGACGACATTGAGGCCGACCACGTAGGCTTCTATGGTACAACT 851

Qy         39 ValTyrGlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeu 58
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        852 GTTTATCAGTCTCCTGGAGACATTGGCCAGTACACACATGAATTTGATGGTGATGAGTTG 911

Qy         59 PheTyrValAspLeuAspLysLysLysThrValTrpArgLeuProGluPheGlyGlnLeu 78
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        912 TTCTATGTGGACTTGGATAAGAAGAAAACTGTCTGGAGGCTTCCTGAGTTTGGCCAATTG 971

Qy         79 IleLeuPheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGly 98
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        972 ATACTCTTTGAGCCCCAAGGTGGACTGCAAAACATAGCTGCAGAAAAACACAACTTGGGA 1031

Qy         99 IleLeuThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrVal 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1032 ATCTTGACTAAGAGGTCAAATTTCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTG 1091

Qy        119 PheProLysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsn 138
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1092 TTCCCCAAGTCCCCTGTGCTGCTGGGTCAGCCCAACACCCTTATCTGCTTTGTGGACAAC 1151

Qy        139 IlePheProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGly 158
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1152 ATCTTCCCACCTGTGATCAACATCACATGGCTCAGAAATAGCAAGTCAGTCACAGACGGC 1211

Qy        159 ValTyrGluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeu 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1212 GTTTATGAGACCAGCTTCCTCGTCAACCGTGACCATTCCTTCCACAAGCTGTCTTATCTC 1271

Qy        179 ThrPheIleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGlu 198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1272 ACCTTCATCCCTTCTGATGATGACATTTATGACTGCAAGGTGGAGCACTGGGGCCTGGAG 1331

Qy        199 GluProValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGlu 218
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1332 GAGCCGGTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAA 1391

Qy        219 Thr 219
              |||
Db       1392 ACT 1394
```

RESULT 12
AAX89069
ID AAX89069 standard; DNA; 1508 BP.
XX
AC AAX89069;
XX
DT 14-SEP-1999 (first entry)
XX
DE Single chain IAd/OVA 323-229 MHC fusion protein encoding DNA.
XX
KW Major histocompatibility complex; MHC; single chain MHC; sc-MHC; Ig;
KW peptide binding groove; immunoglobulin; T cell receptor; immune response;
KW immune-related disorder; antigenic peptide; fusion protein; ss.
XX
OS Synthetic.
XX
PN WO9921572-A1.
XX
PD 06-MAY-1999.
XX
PF 13-OCT-1998; 98WO-US021520.

29-OCT-1997; 97US-00960190.

(SUNO-) SUNOL MOLECULAR CORP.

Rhode PR, Acevedo J, Burkhardt M, Jiao J, Wong HC;

WPI; 1999-418411/35.
P-PSDB; AAY27111.

Single chain major histocompatibility complex class I complexes.

Example 1; Fig 1; 148pp; English.

The invention relates to new single chain major histocompatibility complex (sc-MHC) class II complexes that comprise a peptide binding groove, and a modified class II beta 2 chain or covalently linked immunoglobulin (Ig) light chain constant (C1) region. The MHC complexes are useful for detection and analysis of peptide ligands, pathogenic T-cells, for functional, cellular and molecular assays. They can be used to identify and isolate T cell receptor and/or MHC agonists and antagonists. They can be used in vivo to compete with pathogenic antigen presenting cells involved in immune-related disorders. They can also be used to raise antibodies and to screen immune cells. It is also use in a method of suppressing an immune response in mammals. The sc-MHC complexes comprising modified class II beta 2 chains and/or Ig-C1 regions are soluble and provide enhanced yield. These MHC complexes also can contain single antigenic peptides readily isolated from expressing cells in significant quantities. The polyspecific MHC complexes also provide a means to detect cells expressing multiple target structures with a single complex. The present sequence represents a DNA encoding a single chain IAd/OVA 323-229 MHC fusion protein

Sequence 1508 BP; 337 A; 413 C; 441 G; 317 T; 0 U; 0 Other;

ignment Scores:
ed. No.: 1.15e-96 Length: 1508
ore: 1065.50 Matches: 198
rcent Similarity: 98.5% Conservative: 0
st Local Similarity: 98.5% Mismatches: 0
ery Match: 71.2% Indels: 3
: 2 Gaps: 1

-10-048-116B-2_COPY_1_278 (1-278) x AAX89069 (1-1508)

```
Qy         22 GlyGly---------GluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrThr 38
              ||||||         ||||||||||||||||||||||||||||||||||||||||||||
Db        792 GGCGGTTCCTCGAGTGAAGACGACATTGAGGCCGACCACGTAGGCTTCTATGGTACAACT 851

Qy         39 ValTyrGlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeu 58
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        852 GTTTATCAGTCTCCTGGAGACATTGGCCAGTACACACATGAATTTGATGGTGATGAGTTG 911

Qy         59 PheTyrValAspLeuAspLysLysLysThrValTrpArgLeuProGluPheGlyGlnLeu 78
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        912 TTCTATGTGGACTTGGATAAGAAGAAAACTGTCTGGAGGCTTCCTGAGTTTGGCCAATTG 971

Qy         79 IleLeuPheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGly 98
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        972 ATACTCTTTGAGCCCCAAGGTGGACTGCAAAACATAGCTGCAGAAAAACACAACTTGGGA 1031

Qy         99 IleLeuThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrVal 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1032 ATCTTGACTAAGAGGTCAAATTTCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTG 1091

Qy        119 PheProLysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsn 138
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1092 TTCCCCAAGTCCCCTGTGCTGCTGGGTCAGCCCAACACCCTTATCTGCTTTGTGGACAAC 1151

Qy        139 IleProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGly 158
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1152 ATCTTCCCACCTGTGATCAACATCACATGGCTCAGAAATAGCAAGTCAGTCACAGACGGC 1211

Qy        159 ValTyrGluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeu 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1212 GTTTATGAGACCAGCTTCCTCGTCAACCGTGACCATTCCTTCCACAAGCTGTCTTATCTC 1271

Qy        179 ThrPheIleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGlu 198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1272 ACCTTCATCCCTTCTGATGATGACATTTATGACTGCAAGGTGGAGCACTGGGGCCTGGAG 1331

Qy        199 GluProValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGlu 218
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1332 GAGCCGGTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAA 1391

Qy        219 Thr 219
              |||
Db       1392 ACT 1394
```

RESULT 13
ACA60743
ID ACA60743 standard; DNA; 1508 BP.
XX
AC ACA60743;
XX
DT 16-JUN-2003 (first entry)
XX
DE Mouse MHC I-Ad/Ova 323-339 synthetic gene SCT1.
XX
KW MHC; major histocompatibility complex; gene therapy; fusion complex;
KW peptide-binding groove; T cell modulation; class II MHC; vaccine;
KW autoimmune disorder; multiple sclerosis; rheumatoid arthritis;
KW insulin-dependent diabetes mellitus; myasthenia gravis; immunogen;
KW chronic allergy; mouse; ds; I-Ad; gene.
XX
OS Mus sp.
OS Synthetic.
XX
PN US2002198144-A1.
XX
PD 26-DEC-2002.
XX
PF 06-JUL-2001; 2001US-00900379.
XX
PR 29-JUL-1994; 94US-00283302.
PR 01-FEB-1995; 95US-00382454.
PR 17-JAN-1997; 97US-00776084.
XX
PA (DADE-) DADE INT INC.
XX
PI Wong HC, Rhode PR, Weidanz JA, Grammer S, Edwards AC;
PI Chavaillaz P, Jiao JJJ;
XX
DR WPI; 2003-341126/32.
DR P-PSDB; ABU72107.
XX
PT Novel major histocompatibility complex fusion complex having presenting
PT peptide covalently linked to MHC molecule containing peptide-binding
PT groove, used for suppressing immune response in multiple sclerosis,
PT allergies.
XX
PS Example 17; Fig 28; 126pp; English.
XX
CC The invention relates to a major histocompatibility complex (MHC) fusion
CC complex (I) comprising an MHC molecule that contains a peptide-binding
CC groove, and a presenting peptide covalently (e.g. an antigenic peptide)
CC linked to the MHC molecule, where (I) is capable of modulating the
CC activity of a T cell. Also included are a DNA construct coding for the
CC complex, where the MHC molecule is a class II MHC (e.g. mouse I-Ad or I-
CC As, or human HLA-DR1 (human leukocyte antigen-DR1)), a multivalent MHC
CC fusion complex comprising two or more linked complexes, identifying a
CC peptide that can modulate the activity of T cells (involving introducing
CC into host cells cloning vectors that each contain the fusion complex DNA,
CC culturing the host cells under conditions suitable for expression of the
CC MHC fusion complex, and selecting host cells that express MHC fusion
CC complex that modulate the activity of T cells), a single recombinant

expression vector comprising DNA that codes for the alpha and beta chains of the fusion complex MHC protein, a single recombinant expression vector comprising DNA that codes for a T cell costimulatory factor and the alpha and beta chains of the MHC fusion complex. The DNA constructs can contain heterologous leader peptide sequences and Kozak sequence for efficient expression of the fusion complex. Also included are inducing an immune response in a mammal (including vaccinating a mammal against a targeted disorder, by administering DNA sequence comprising a fusion complex, or DNA sequence coding for a fusion complex which is a single chain fusion molecule) and suppressing an immune response in a mammal by administering to the mammal a DNA sequence comprising an expression vector, encoding a full length MHC molecule that contains a transmembrane domain, and a presenting peptide that is a T cell receptor (TCR) antagonist or partial agonist and is covalently linked to the MHC protein, or DNA sequence coding for the fusion complex which is a single chain fusion molecule. The methods are useful for identifying a peptide that can modulate the activity of T cells, inducing an immune response in a mammal (including vaccinating a mammal against a targeted disorder) and for suppressing an immune response in a mammal. The disorders include an autoimmune disorder such as multiple sclerosis, insulin-dependent diabetes mellitus, rheumatoid arthritis, myasthenia gravis or chronic allergies. The present sequence encodes a mouse MHC class II I-Ad fusion complex of the invention

Sequence 1508 BP; 337 A; 413 C; 441 G; 317 T; 0 U; 0 Other;

nment Scores:			
. No.:	1.15e-96	Length:	1508
e:	1065.50	Matches:	198
ent Similarity:	98.5%	Conservative:	0
Local Similarity:	98.5%	Mismatches:	0
y Match:	71.2%	Indels:	3
	8	Gaps:	1

0-048-116B-2_COPY_1_278 (1-278) x ACA60743 (1-1508)

```
      22 GlyGly---------GluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrThr 38
         ||||||         ||||||||||||||||||||||||||||||||||||||||||||
     792 GGCGGTTCCTCGAGTGAAGACGACATTGAGGCCGACCACGTAGGCTTCTATGGTACAACT 851

      39 ValTyrGlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeu 58
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     852 GTTTATCAGTCTCCTGGAGACATTGGCCAGTACACACATGAATTTGATGGTGATGAGTTG 911

      59 PheTyrValAspLeuAspLysLysLysThrValTrpArgLeuProGluPheGlyGlnLeu 78
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     912 TTCTATGTGGACTTGGATAAGAAGAAAACTGTCTGGAGGCTTCCTGAGTTTGGCCAATTG 971

      79 IleLeuPheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGly 98
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     972 ATACTCTTTGAGCCCCAAGGTGGACTGCAAAACATAGCTGCAGAAAAACACAACTTGGGA 1031

      99 IleLeuThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrVal 118
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    1032 ATCTTGACTAAGAGGTCAAATTTCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTG 1091

     119 PheProLysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsn 138
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    1092 TTCCCCAAGTCCCCTGTGCTGCTGGGTCAGCCCAACACCCTTATCTGCTTTGTGGACAAC 1151

     139 IleProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGly 158
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    1152 ATCTTCCCACCTGTGATCAACATCACATGGCTCAGAAATAGCAAGTCAGTCACAGACGGC 1211

     159 ValTyrGluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeu 178
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    1212 GTTTATGAGACCAGCTTCCTCGTCAACCGTGACCATTCCTTCCACAAGCTGTCTTATCTC 1271

     179 ThrPheIleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGlu 198
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    1272 ACCTTCATCCCTTCTGATGATGACATTTATGACTGCAAGGTGGAGCACTGGGGCCTGGAG 1331

     199 GluProValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGlu 218
```

```
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1332 GAGCCGGTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAA 1391

Qy     219 Thr 219
           |||
Db    1392 ACT 1394
```

RESULT 14
AAT60698
ID AAT60698 standard; cDNA; 588 BP.
XX
AC AAT60698;
XX
DT 27-AUG-2003 (revised)
DT 12-SEP-1997 (first entry)
XX
DE Alpha1alpha2 region of Class II NOD mouse MHC (IAg7) cDNA.
XX
KW Soluble; fusion; major histocompatibility complex; MHC; region;
KW heterodimer; complex; alpha2; antigen; binding groove; tolerance;
KW autoantigen; disease; insulin dependent; diabetes mellitus; IDDM;
KW antagonist; T cell; anergy; presenting cell; NOD mouse; Class II; alpha1;
KW ds.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT mat_peptide 1. .588
FT /*tag= a
XX
PN WO9640944-A2.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US010102.
XX
PR 07-JUN-1995; 95US-00480002.
PR 07-JUN-1995; 95US-00482133.
PR 07-JUN-1995; 95US-00483241.
PR 27-OCT-1995; 95US-0005964P.
XX
PA (ZYMO) ZYMOGENETICS INC.
PA (ANER-) ANERGEN INC.
XX
PI Kindsvogel W, Reich EP, Gross JA, Deshpande S, Sheppard PO;
XX
DR WPI; 1997-052337/05.
DR P-PSDB; AAW10505.
XX
PT Novel fused major histocompatibility complex:antigenic peptide complex -
PT useful to induce tolerance to an autoantigen-related disease e.g. insulin
PT -dependent diabetes mellitus.
XX
PS Example 3; Page 132-133; 142pp; English.
XX
CC A novel soluble fused major histocompatibility complex (MHC)
CC heterodimer:peptide complex, comprises DNA encoding 1st and 2nd MHC
CC domains, e.g. the present sequence, linked by DNA encoding a 5-25 residue
CC linker, and a DNA encoding an antigenic peptide able to associate with a
CC peptide binding groove of the MHC molecule, linked in frame to the DNA
CC encoding the 2nd domain by a DNA encoding a 5-25 residue linker. The
CC complex can be used to induce immunological tolerance in adults
CC susceptible to, or suffering from an autoantigen related disease, e.g.
CC insulin dependent diabetes mellitus (IDDM), by antagonising the binding
CC of particular T cells and antigen presenting cells, to induce anergy
CC (immunological non-responsiveness) in the targeted T cell. As the
CC heterodimers and corresponding antigen are permanently linked into a
CC single chain, obviating the requirement for complex heterodimer
CC truncation or formation, the complex eliminates inefficient and non-
CC specific peptide loading. (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 588 BP; 153 A; 153 C; 136 G; 146 T; 0 U; 0 Other;

```
ignment Scores:
ed. No.:                3.51e-97        Length:         588
ore:                    1065.00         Matches:        196
rcent Similarity:       100.0%          Conservative:   0
st Local Similarity:    100.0%          Mismatches:     0
ery Match:              71.2%           Indels:         0
:                       2               Gaps:           0

-10-048-116B-2_COPY_1_278 (1-278) x AAT60698 (1-588)

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            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          1 GAAGACGACATTGAGGCCGACCACGTAGGCTTCTATGGTACAACTGTTTATCAGTCTCCT 60

         44 GlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyrValAspLeu 63
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         61 GGAGACATTGGCCAGTACACACATGAATTTGATGGTGATGAGTTGTTCTATGTGGACTTG 120

         64 AspLysLysLysThrValTrpArgLeuProGluPheGlyGlnLeuIleLeuPheGluPro 83
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        121 GATAAGAAGAAAACTGTCTGGAGGCTTCCTGAGTTTGGCCAATTGATACTCTTTGAGCCC 180

         84 GlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeuThrLysArg 103
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        181 CAAGGTGGACTGCAAAACATAGCTGCAGAAAAACACAACTTGGGAATCTTGACTAAGAGG 240

        104 SerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPheProLysSerPro 123
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        241 TCAAATTTCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGTTCCCCAAGTCCCCT 300

        124 ValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIleProProVal 143
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        301 GTGCTGCTGGGTCAGCCCAACACCCTTATCTGCTTTGTGGACAACATCTTCCCACCTGTG 360

        144 IleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyrGluThrSer 163
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        361 ATCAACATCACATGGCTCAGAAATAGCAAGTCAGTCACAGACGGCGTTTATGAGACCAGC 420

        164 PheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPheIleProSer 183
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        421 TTCCTCGTCAACCGTGACCATTCCTTCCACAAGCTGTCTTATCTCACCTTCATCCCTTCT 480

        184 AspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluProValLeuLys 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        481 GATGATGACATTTATGACTGCAAGGTGGAGCACTGGGGCCTGGAGGAGCCGGTTCTGAAA 540

        204 HisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThr 219
            ||||||||||||||||||||||||||||||||||||||||||||||||||
        541 CACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAGACT 588

SULT 15
Q35054
   AAQ35054 standard; DNA; 776 BP.

   AAQ35054;

   25-MAR-2003  (revised)
   21-MAY-1993  (first entry)

   IAB alpha chain (known).

   Acetylcholine receptor; epitope; myasthenia gravis; MG; antigen;
   binding site; MHC; IAB; alpha; beta; ds.

   Synthetic.

   WO9218150-A1.

   29-OCT-1992.

   23-APR-1992;   92WO-US003391.

   23-APR-1991;   91US-00690840.

PR   14-APR-1992;   92US-00869293.
XX
PA   (ANER-) ANERGEN INC.
XX
PI   Clark BR,  Sharma SD,  Lerch BL;
XX
DR   WPI; 1993-036056/04.
XX
PT   Pure major MHC-peptide complex - useful in treating deleterious immune
PT   response such as auto:immunity.
XX
PS   Disclosure; Fig 8; 93pp; English.
XX
CC   The AChR peptide 195-215, which has been characterised as an epitope in
CC   myasthenia gravis (MG) in humans and in mice, may be connected to the N-
CC   terminal antigen binding site of a polypeptide derived from an MHC
CC   antigen associated with MG. For example, if the recombinant complex is to
CC   be used in mice, the AChR peptide may be incorporated into a sequence
CC   encoding either the I-Ab-alpha or I-Ab-beta chain (see AAQ35054-55
CC   respectively). If the AChR peptide is to be incorporated into the beta
CC   chain, for example, the oligonucleotide may be inserted as a replacement
CC   for the leader sequence. (Updated on 25-MAR-2003 to correct PN field.)
CC   (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 776 BP; 178 A; 211 C; 192 G; 194 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.:              1.04e-95        Length:         776
Score:                  1052.00         Matches:        195
Percent Similarity:     93.2%           Conservative:   9
Best Local Similarity:  89.0%           Mismatches:     15
Query Match:            70.3%           Indels:         0
DB:                     2               Gaps:           0

US-10-048-116B-2_COPY_1_278 (1-278) x AAQ35054 (1-776)

Qy          1 MetProCysSerArgAlaLeuIleLeuGlyValLeuAlaLeuAsnThrMetLeuSerLeu 20
              |||||| |||||||||||||||||||:::|||||||||  |||||||||:::|||
Db          6 ATGCCGCGCAGCAGAGCTCTGATTCTGGGGCTCCTCGCCCTGACCACCATGCTCACCCTC 65

Qy         21 CysGlyGlyGluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrThrValTyr 40
              |||  ||||||||||||||||||||||||||||||  ||||||  :::||||||
Db         66 TGTGCAGGTGAAGACGACATTGAGGCCGACCACGTAGGCACCTATGGTATAAGTGTATAT 125

Qy         41 GlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr 60
              |||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        126 CAGTCTCCTGGAGACATTGGCCAGTACACATTTGAATTTGATGGTGATGAGTTGTTCTAT 185

Qy         61 ValAspLeuAspLysLysLysThrValTrpArgLeuProGluPheGlyGlnLeuIleLeu 80
              ||||||||||||||||:::|||||||||  ||||||||||||||||||||||||||||
Db        186 GTGGACTTGGATAAGAAGGAGACTGTCTGGATGCTTCCTGAGTTTGGCCAATTGCCAAGC 245

Qy         81 PheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeu 100
              |||:::|||||||||||||||||||||||||||||||||||||||||:::|||
Db        246 TTTGACCCCCAAGGTGGACTGCAAAACATAGCTGTAGTAAAACACAACTTGGGAGTCTTG 305

Qy        101 ThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPhePro 120
              |||||||||||||||  ||||||||||||||:::|||||||||||||||:::||||||
Db        306 ACTAAGAGGTCAAATTCCACCCCAGCTACCAATGACGCTCCTCAAGCGACTCTGTTCCCC 365

Qy        121 LysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 AAGTCCCCTGTGCTGCTGGGTCAGCCCAACACCCTCATCTGCTTTGTGGACAACATCTTC 425

Qy        141 ProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyr 160
              |||||||||||||||||||||||||||  ||||||||||  ||||||||||
Db        426 CCTCCTGTGATCAACATCACATGGCTCAGAAAAAGCAARTCAGTCGCAGACGGTGTTTAT 485

Qy        161 GluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPhe 180
              ||||||||||||  ||||||||||:::|||||||||||||||||||||||||||||||
Db        486 GAGACCAGCTTCTTCGTCAACCGTGACTATTCCTTCCACAAGCTGTCTTATCTCACCTTC 545

Qy        181 IleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluPro 200
```

```
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
546 ATCCCTTCTGACGATGACATTTATGACTGCAAGGTGGAACACTGGGGCCTGGAGGAGCCG 605

201 ValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThr 219
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
606 GTTCTGAAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAGACT 662
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GenCore version 5.1.8

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1484	99.9	1484	2	AX081280	AX081280 Sequence
2	957.6	64.5	1446	2	BD137962	BD137962 Monovalen
3	701.2	47.2	1045	2	CQ806515	CQ806515 Sequence
4	701.2	47.2	1108	2	CQ806531	CQ806531 Sequence
5	701.2	47.2	1108	2	CQ806532	CQ806532 Sequence
6	700.6	47.2	990	6	MMU294738	AJ294738 Mus muscu
7	700.6	47.2	1095	6	MMIGG6	V00798 Mouse mRNA
8	700.6	47.2	1341	2	I07390	I07390 Sequence 4
9	700.6	47.2	1401	2	CS138860	CS138860 Sequence
10	700.6	47.2	1407	6	AF466698	AF466698 Mus muscu
11	700.6	47.2	1570	2	A22261	A22261 M.musculus
12	700.6	47.2	1570	2	AR029102	AR029102 Sequence
13	700.6	47.2	1570	2	BD057272	BD057272 Gene enco
14	700.6	47.2	1570	2	AR409372	AR409372 Sequence
15	700.6	47.2	1570	2	AR559698	AR559698 Sequence
16	700.6	47.2	1570	6	AB097847	AB097847 Mus muscu
17	700.6	47.2	3973	2	CQ897414	CQ897414 Sequence
18	700.2	47.2	729	2	AR650819	AR650819 Sequence
19	700	47.1	1158	2	AR160140	AR160140 Sequence
20	700	47.1	1188	2	AR160149	AR160149 Sequence
21	700	47.1	6729	2	AX080954	AX080954 Sequence
22	700	47.1	7528	2	AX080953	AX080953 Sequence
23	699.4	47.1	1530	2	CS121774	CS121774 Sequence
24	699	47.1	699	2	CS251282	CS251282 Sequence
25	699	47.1	708	2	CS121762	CS121762 Sequence
26	699	47.1	1413	2	CS121778	CS121778 Sequence
27	699	47.1	1431	2	CS121780	CS121780 Sequence
28	699	47.1	1581	2	A78881	A78881 Sequence 1
29	699	47.1	1581	6	MMIGHC2AA	X70423 M.musculus
30	698.4	47.0	1131	2	BD022361	BD022361 Multi-fun
31	698.4	47.0	1131	2	AR772537	AR772537 Sequence
32	698.4	47.0	1194	2	BD022360	BD022360 Multi-fun
33	698.4	47.0	1194	2	AR772536	AR772536 Sequence
34	698.4	47.0	1473	2	CQ889913	CQ889913 Sequence
35	698.4	47.0	1473	2	CQ889975	CQ889975 Sequence
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39	697.4	47.0	1407	2	CS126190	CS126190 Sequence
40	697.4	47.0	1570	2	A77138	A77138 Sequence 6
41	697.4	47.0	1707	2	AR650821	AR650821 Sequence
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43	695.4	46.8	1278	2	AR393789	AR393789 Sequence
44	695.4	46.8	1278	2	AX084107	AX084107 Sequence
45	695.4	46.8	2709	2	AR393797	AR393797 Sequence

ALIGNMENTS

RESULT 1
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LOCUS AX081280 1484 bp DNA linear PAT 27-FEB-2001
DEFINITION Sequence 1 from Patent WO0109194.
ACCESSION AX081280
VERSION AX081280.1 GI:13170129
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Glaichenhaus,N. and Malherbe,L.
TITLE Recombinant proteins and molecular complexes derived therefrom, analogous to molecules involved in immune responses
JOURNAL Patent: WO 0109194-A 1 08-FEB-2001;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
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ETSFLVNRDHSFHKLSYLTFIPSDDDIYDCKVEHWGLEEPVLKHWEPEIPAPMSELTE
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CPAPNLLGGPSVFIFPPPKIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHT
AQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKGSVR
APQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDG
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ORIGIN

Query Match 99.9%; Score 1484; DB 2; Length 1484;
Best Local Similarity 100.0%; Pred. No. 0;

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itches 1484;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

        1 ATGCCGTGCAGCAGAGCTCTGATTCTGGGGGTCCTCGCCCTGAACACCATGCTCAGCCTC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        1 ATGCCGTGCAGCAGAGCTCTGATTCTGGGGGTCCTCGCCCTGAACACCATGCTCAGCCTC 60

       61 TGCGGAGGTGAAGACGACATTGAGGCCGACCACGTAGGCTTCTATGGTACAACTGTTTAT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       61 TGCGGAGGTGAAGACGACATTGAGGCCGACCACGTAGGCTTCTATGGTACAACTGTTTAT 120

      121 CAGTCTCCTGGAGACATTGGCCAGTACACACATGAATTTGATGGTGATGAGTTGTTCTAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      121 CAGTCTCCTGGAGACATTGGCCAGTACACACATGAATTTGATGGTGATGAGTTGTTCTAT 180

      181 GTGGACTTGGATAAGAAGAAAACTGTCTGGAGGCTTCCTGAGTTTGGCCAATTGATACTC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      181 GTGGACTTGGATAAGAAGAAAACTGTCTGGAGGCTTCCTGAGTTTGGCCAATTGATACTC 240

      241 TTTGAGCCCCAAGGTGGACTGCAAAACATAGCTGCAGAAAAACACAACTTGGGAATCTTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      241 TTTGAGCCCCAAGGTGGACTGCAAAACATAGCTGCAGAAAAACACAACTTGGGAATCTTG 300

      301 ACTAAGAGGTCAAATTTCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGTTCCCC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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      361 AAGTCCCCTGTGCTGCTGGGTCAGCCCAACACCCTTATCTGCTTTGTGGACAACATCTTC 420
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      361 AAGTCCCCTGTGCTGCTGGGTCAGCCCAACACCCTTATCTGCTTTGTGGACAACATCTTC 420

      421 CCACCTGTGATCAACATCACATGGCTCAGAAATAGCAAGTCAGTCACAGACGGCGTTTAT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      421 CCACCTGTGATCAACATCACATGGCTCAGAAATAGCAAGTCAGTCACAGACGGCGTTTAT 480

      481 GAGACCAGCTTCCTCGTCAACCGTGACCATTCCTTCCACAAGCTGTCTTATCTCACCTTC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      481 GAGACCAGCTTCCTCGTCAACCGTGACCATTCCTTCCACAAGCTGTCTTATCTCACCTTC 540

      541 ATCCCTTCTGATGATGACATTTATGACTGCAAGGTGGAGCACTGGGGCCTGGAGGAGCCG 600
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      541 ATCCCTTCTGATGATGACATTTATGACTGCAAGGTGGAGCACTGGGGCCTGGAGGAGCCG 600

      601 GTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAAACTGGA 660
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      661 GGTGGAGGATCCACTACAGCTCCATCAGCTCAGCTCGAAAAAGAGCTCCAGGCCCTGGAG 720
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      661 GGTGGAGGATCCACTACAGCTCCATCAGCTCAGCTCGAAAAAGAGCTCCAGGCCCTGGAG 720

      721 AAGGAAAATGCACAGCTGGAATGGGAGTTGCAAGCACTGGAAAAGGAACTGGCTCAGGCA 780
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      721 AAGGAAAATGCACAGCTGGAATGGGAGTTGCAAGCACTGGAAAAGGAACTGGCTCAGGCA 780

      781 GCATCTGAGCCCAGAGGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCAGCACCT 840
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      781 GCATCTGAGCCCAGAGGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCAGCACCT 840

      841 AACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      841 AACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATG 900

      901 ATCTCCCTGAGCCCCATAGTCACATGTGTGGTGGTGGATGTGAGCGAGGATGACCCAGAT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      901 ATCTCCCTGAGCCCCATAGTCACATGTGTGGTGGTGGATGTGAGCGAGGATGACCCAGAT 960

      961 GTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAAACCCAT 1020
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     1021 AGAGAGGATTACAACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGAC 1080
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     1021 AGAGAGGATTACAACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGAC 1080
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Qy      1081 TGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAAGACCTCCCAGCGCCCATC 1140
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Db      1081 TGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAAGACCTCCCAGCGCCCATC 1140

Qy      1141 GAGAGAACCATCTCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTTGCCT 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 GAGAGAACCATCTCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTTGCCT 1200

Qy      1201 CCACCAGAAGAAGAGATGACTAAGAAACAGGTCACTCTGACCTGCATGGTCACAGACTTC 1260
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Qy      1261 ATGCCTGAAGACATTTACGTGGAGTGGACCAACAACGGGAAAACAGAGCTAAACTACAAG 1320
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Db      1261 ATGCCTGAAGACATTTACGTGGAGTGGACCAACAACGGGAAAACAGAGCTAAACTACAAG 1320

Qy      1321 AACACTGAACCAGTCCTGGACTCTGATGGTTCTTACTTCATGTACAGCAAGCTGAGAGTG 1380
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Db      1321 AACACTGAACCAGTCCTGGACTCTGATGGTTCTTACTTCATGTACAGCAAGCTGAGAGTG 1380

Qy      1381 GAAAAGAAGAACTGGGTGGAAAGAAATAGCTACTCCTGTTCAGTGGTCCACGAGGGTCTG 1440
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Db      1381 GAAAAGAAGAACTGGGTGGAAAGAAATAGCTACTCCTGTTCAGTGGTCCACGAGGGTCTG 1440

Qy      1441 CACAATCACCACACGACTAAGAGCTTCTCCCGGACTCCGGGTAA 1484
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RESULT 2
BD137962
LOCUS       BD137962               1446 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Monovalent MHC-binding domain fused proteins and conjugates,
            polyvalent MHC-binding domain fused proteins and conjugates,
            polymer MHC-binding domain fused proteins and conjugates, and
            utilization therefor.
ACCESSION   BD137962
VERSION     BD137962.1  GI:23232907
KEYWORDS    JP 2002504342-A/7.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 1446)
  AUTHORS   Wucherpfennig,K.W. and Strominger,J.L.
  TITLE     Monovalent MHC-binding domain fused proteins and conjugates,
            polyvalent MHC-binding domain fused proteins and conjugates,
            polymer MHC-binding domain fused proteins and conjugates, and
            utilization
  JOURNAL   Patent: JP 2002504342-A 7 12-FEB-2002;
            PRESIDENT AND FELLOWS OF HARVARD COLLEGE
COMMENT     OS   Artificial Sequence
            PN   JP 2002504342-A/7
            PD   12-FEB-2002
            PF   19-FEB-1999 JP 2000532537
            PR   19-FEB-1998 US    60/075351
            PI   KAI W WUCHERPFENNIG,JACK L STROMINGER
            PC   C12N15/09,A61K35/14,A61K47/48,C07K14/705,C07K16/00,C07K19/00,
            PC   C12Q1/02,
            PC   G01N33/53,C12N15/00
            CC   Description of Artificial Sequence: DR2-IgG fusion CC   3' end
            of secretory signal
            CC   DRA*0101 extracellular domain
            CC   Linker
            CC   Fos leucine zipper domain
            CC   IgG domain
            FH   Key             Location/Qualifiers
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            FT   misc_feature    (1). .(15)
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                  /organism="synthetic construct"
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IGIN

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Best Local Similarity  81.8%;  Pred. No. 1.5e-249;
Matches 1136;  Conservative    0;  Mismatches  234;  Indels   18;  Gaps    2;

Qy      116 TTTATCAGTCTCCTGGAGACATTGGCCAGTACACACATGAATTTGATGGTGATGAGTTGT 175
            | |||| |  |||||   |    ||| |||  |    ||| ||||||||||||||| | |
Db       50 TCTATCTGAATCCTGACCAATCAGGCGAGTTTATGTTTGACTTTGATGGTGATGAGATTT 109

Qy      176 TCTATGTGGACTTGGATAAGAAGAAAACTGTCTGGAGGCTTCCTGAGTTTGGCCAATTGA 235
            || |||||||  |||  ||||||  | ||  |||||| |||||   || |||||  | |||
Db      110 TCCATGTGGATATGGCAAAGAAGGAGACGGTCTGGCGGCTTGAAGAATTTGGACGATTTG 169

Qy      236 TACTCTTTGAGCCCCAAGGTGGACTGCAAAACATAGCTGCAGAAAAACAGAACTTGGGAA 295
            |||||||  | |||||||  | ||   ||||||||||  || |||  |||||||| ||
Db      170 CCAGCTTTGAGGCTCAAGGTGCATTGGCCAACATAGCTGTGGACAAAGCCAACTTGGAAA 229

Qy      296 TCTTGACTAAGAGGTCAAATTTCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGT 355
            || |||| ||| | || || |  || ||    |||||||   ||||  | |  ||||||
Db      230 TCATGACAAAGCGCTCCAACTATACTCCGATCACCAATGTACCTCCAGAGGTAACTGTGC 289

Qy      356 TCCCCAAGTCCCCTGTGCTGCTGGGTCAGCCCAACACCCTTATCTGCTTTGTGGACAACA 415
            || | ||   |||||||   |||  |  ||||||||  ||| |||||  ||  | |||||
Db      290 TCACGAACAGCCCTGTGGAACTGAGAGAGCCCAACGTCCTCATCTGTTTCATAGACAAGT 349

Qy      416 TCTTCCCACCTGTGATCAACATCACATGGCTCAGAAATAGCAAGTCAGTCACAGACGGCG 475
            ||  ||||||  ||| ||||  |||| |||||  |||||  | ||  | |||||    || |
Db      350 TCACCCCACCAGTGGTCAATGTCACGTGGCTTCGAAATGGAAAACCTGTCACCACAGGAG 409

Qy      476 TTTATGAGACCAGCTTCCTCGTCAACCGTGACCATTCCTTCCACAAGCTGTCTTATCTCA 535
            | |  |||||   ||||||   ||     |||||     |||| |||| |    ||||||
Db      410 TGTCAGAGACAGTCTTCCTGCCCAGGGAAGACCACCTTTTCCGCAAGTTCCACTATCTCC 469

Qy      536 CCTTCATCCCTTCTGATGATGACATTTATGACTGCAAGGTGGAGCACTGGGGCCTGGAGG 595
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Db      470 CCTTCCTGCCCTCAACTGAGGACGTTTACGACTGCAGGGTGGAGCACTGGGGCTTGGATG 529

Qy      596 AGCCGGTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAAA 655
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Db      530 AGCCTCTTCTCAAGCACTGGGAGTTTGATGCTCCAAGCCCTCTCCCAGAGACTACAGAGG 589

Qy      656 CTGGAGGTGGAGGATCCACT---------------ACAGCTCCATCAGCTCAGCTCGAAA 700
              |  || || ||   |  |                  |||     ||| ||| || |||
Db      590 TCGACGGAGGTGGCGGCGGTTTAACTGATACACTCCAAGCGGAGACAGATCAACTTGAAG 649

Qy      701 AAGAGCTCCAGGCCCTGGAGAAGGAAAATGCACAGCTGGAATGGGAGTTGCAAGCACTGG 760
            | |||      ||  || |||  || | |||  | ||       |||  | ||  |||||
Db      650 ACGAGAAGTCTGCGTTGCAGACCGAGATTGCCAATCTACTGAAAGAGAAGGAAAAACTGG 709

Qy      761 AAAAGGAACTG---GCTCAGGCAGCATCTGAGCCCAGAGGGCCCACAATCAAGCCCTGTC 817
            |      |||   || || ||||||||||||||||||||||||||||||||||||||||||
Db      710 AGTTCATCCTGGCCGCCCATGCAGCATCTGAGCCCAGAGGGCCCACAATCAAGCCCTGTC 769

Qy      818 CTCCATGCAAATGCCCAGCACCTAACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCTC 877
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Db      770 CTCCATGCAAATGCCCAGCACCTAACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCTC 829

Qy      878 CAAAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCATAGTCACATGTGTGGTGGTGG 937
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Db      830 CAAAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCATAGTCACATGTGTGGTGGTGG 889

Qy      938 ATGTGAGCGAGGATGACCCAGATGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTAC 997
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      890 ATGTGAGCGAGGATGACCCAGATGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTAC 949

Qy      998 ACACAGCTCAGACACAAACCCATAGAGAGGATTACAACAGTACTCTCCGGGTGGTCAGTG 1057
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Db       950 ACACAGCTCAGACACAAACCCATAGAGAGGATTACAACAGTACTCTCCGGGTGGTCAGTG 1009

Qy      1058 CCCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACA 1117
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1010 CCCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACA 1069

Qy      1118 ACAAAGACCTCCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGGTCAGTAAGAG 1177
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1070 ACAAAGACCTCCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGGTCAGTAAGAG 1129

Qy      1178 CTCCACAGGTATATGTCTTGCCTCCACCAGAAGAAGAGATGACTAAGAAACAGGTCACTC 1237
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Db      1130 CTCCACAGGTATATGTCTTGCCTCCACCAGAAGAAGAGATGACTAAGAAACAGGTCACTC 1189

Qy      1238 TGACCTGCATGGTCACAGACTTCATGCCTGAAGACATTTACGTGGAGTGGACCAACAACG 1297
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1190 TGACCTGCATGGTCACAGACTTCATGCCTGAAGACATTTACGTGGAGTGGACCAACAACG 1249

Qy      1298 GGAAAACAGAGCTAAACTACAAGAACACTGAACCAGTCCTGGACTCTGATGGTTCTTACT 1357
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1250 GGAAAACAGAGCTAAACTACAAGAACACTGAACCAGTCCTGGACTCTGATGGTTCTTACT 1309

Qy      1358 TCATGTACAGCAAGCTGAGAGTGGAAAAGAAGAACTGGGTGGAAAGAAATAGCTACTCCT 1417
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Db      1310 TCATGTACAGCAAGCTGAGAGTGGAAAAGAAGAACTGGGTGGAAAGAAATAGCTACTCCT 1369

Qy      1418 GTTCAGTGGTCCACGAGGGTCTGCACAATCACCACACGACTAAGAGCTTCTCCCGGACTC 1477
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Qy      1478 CGGGTAAA 1485
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Db      1430 CGGGTAAA 1437
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RESULT 3
CQ806515
LOCUS       CQ806515                1045 bp    DNA     linear   PAT 10-MAY-2004
DEFINITION  Sequence 10 from Patent WO2004035622.
ACCESSION   CQ806515
VERSION     CQ806515.1  GI:47111911
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Dreher,I. and Moll,T.
  TITLE     Antagonists il-15
  JOURNAL   Patent: WO 2004035622-A 10 29-APR-2004;
            F. HOFFMANN-LA ROCHE AG (CH)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DNA for fusionprotein"
ORIGIN

  Query Match            47.2%;  Score 701.2;  DB 2;  Length 1045;
  Best Local Similarity  93.3%;  Pred. No. 1.3e-179;
  Matches  733;  Conservative    0;  Mismatches   53;  Indels    0;  Gaps    0;

Qy      700 AAAGAGCTCCAGGCCCTGGAGAAGGAAAATGCACAGCTGGAATGGGAGTTGCAAGCACTG 759
            |||||      |||  |||||| |  |||||     |        | | ||       | ||
Db      256 AAAGAATGTGAGGAACTGGAGGAAAAAAATATTAAAGAATTTTTGCAGAGTTTTGTACAT 315

Qy      760 GAAAAGGAACTGGCTCAGGCAGCATCTGAGCCCAGAGGGCCCACAATCAAGCCCTGTCCT 819
                  || ||          | || || ||||||||||||||||||||||||||||||
Db      316 ATTGTCCAAATGTTCATCAACACTTCGGATCCCAGAGGGCCCACAATCAAGCCCTGTCCT 375

Qy      820 CCATGCAAATGCCCAGCACCTAACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCTCCA 879
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      376 CCATGCAAATGCCCAGCACCTAACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCTCCA 435
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       880 AAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCATAGTCACATGTGTGGTGGTGGAT 939
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       436 AAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCATAGTCACATGTGTGGTGGTGGAT 495

       940 GTGAGCGAGGATGACCCAGATGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTACAC 999
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       496 GTGAGCGAGGATGACCCAGATGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTACAC 555

      1000 ACAGCTCAGACACAAACCCATAGAGAGGATTACAACAGTACTCTCCGGGTGGTCAGTGCC 1059
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       556 ACAGCTCAGACACAAACCCATAGAGAGGATTACAACAGTACTCTCCGGGTGGTCAGTGCC 615

      1060 CTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAAC 1119
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      1120 AAAGACCTCCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGGTCAGTAAGAGCT 1179
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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      1300 AAAACAGAGCTAAACTACAAGAACACTGAACCAGTCCTGGACTCTGATGGTTCTTACTTC 1359
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       856 AAAACAGAGCTAAACTACAAGAACACTGAACCAGTCCTGGACTCTGATGGTTCTTACTTC 915

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       916 ATGTACAGCAAGCTGAGAGTGGAAAAGAAGAACTGGGTGGAAAGAAATAGCTACTCCTGT 975

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      1480 GGTAAA 1485
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LT 4
6531
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NITION  Sequence 26 from Patent WO2004035622.
SSION   CQ806531
ION     CQ806531.1  GI:47111925
ORDS    .
CE      Homo sapiens (human)
GANISM  Homo sapiens
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
        Hominidae; Homo.
RENCE   1
THORS   Dreher,I. and Moll,T.
TLE     Antagonists il-15
URNAL   Patent: WO 2004035622-A 26 29-APR-2004;
        F. HOFFMANN-LA ROCHE AG (CH)
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ery Match             47.2%;  Score 701.2;  DB 2;  Length 1108;
st Local Similarity   93.3%;  Pred. No. 1.3e-179;
tches  733;  Conservative    0;  Mismatches   53;  Indels    0;  Gaps    0;
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Qy       700 AAAGAGCTCCAGGCCCTGGAGAAGGAAAATGCACAGCTGGAATGGGAGTTGCAAGCACTG 759
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Db       319 AAAGAATGTGAGGAACTGGAGGAAAAAAAATATTAAAGAATTTTTGGACAGTTTTGTACAT 378

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Qy       880 AAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCATAGTCACATGTGTGGTGGTGGAT 939
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Qy      1060 CTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAAC 1119
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Qy      1240 ACCTGCATGGTCACAGACTTCATGCCTGAAGACATTTACGTGGAGTGGACCAACAACGGG 1299
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Qy      1300 AAAACAGAGCTAAACTACAAGAACACTGAACCAGTCCTGGACTCTGATGGTTCTTACTTC 1359
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CQ806532
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DEFINITION  Sequence 27 from Patent WO2004035622.
ACCESSION   CQ806532
VERSION     CQ806532.1  GI:47111926
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Dreher,I. and Moll,T.
  TITLE     Antagonists il-15
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ULT 6
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INITION  Mus musculus partial mRNA for immunoglobulin heavy chain constant
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ACCESSION   AJ294738
VERSION     AJ294738.1  GI:12055401
KEYWORDS    constant region; gamma 2a; IGHG2A gene; immunoglobulin heavy chain.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   McLean,G.R., Nakouzi,A., Casadevall,A. and Green,N.S.
  TITLE     Human and murine immunoglobulin expression vector cassettes
  JOURNAL   Mol. Immunol. 37 (14), 837-845 (2000)
   PUBMED   11257305
REFERENCE   2  (bases 1 to 990)
  AUTHORS   McLean,G.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-SEP-2000) McLean G.R., Cell Biology, Albert Einstein
            College of Medicine, 1300 Morris Park Avenue, Bronx, New York
            10461, USA
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ORIGIN

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Qy        846 CTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTC 905
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LT 7
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NITION  Mouse mRNA for gamma-2a-immunoglobulin heavy-chain.
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ION     V00798.1  GI:51835
ORDS    complementary DNA; gamma-immunoglobulin; immunoglobulin.
CE      Mus musculus (house mouse)
GANISM  Mus musculus
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
        Sciurognathi; Muroidea; Muridae; Murinae; Mus.
RENCE   1  (bases 1 to 1095)
THORS   Sikorav,J.L., Auffray,C. and Rougeon,F.
TLE     Structure of the constant and 3' untranslated regions of the murine
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URNAL   Nucleic Acids Res. 8 (14), 3143-3155 (1980)
UBMED   6777755
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IN

ery Match             47.2%;  Score 700.6;  DB 6;  Length 1095;
st Local Similarity   100.0%;  Pred. No. 1.9e-179;
tches  700;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        846 CTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTC 905
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DEFINITION  Sequence 4 from Patent EP 0338767.
ACCESSION   I07390
VERSION     I07390.1  GI:589918
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1341)
  AUTHORS   Beavers,L.S., Bumol,T.F., Gadski,R.A. and Weigel,B.J.
  TITLE     Novel recombinant and chimeric antibodies directed against a human
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  JOURNAL   Patent: EP 0338767-A2 4 25-OCT-1989;
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ORIGIN

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INITION Sequence 1 from Patent WO2005068503.
CESSION CS138860
SION CS138860.1 GI:73530223
WORDS .
RCE Mus musculus (house mouse)
RGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
ERENCE 1
UTHORS Liu,C.
ITLE M-csf-specific monoclonal antibody and uses thereof
OURNAL Patent: WO 2005068503-A 1 28-JUL-2005;
CHIRON CORPORATION (US); Liu, Cheng (US)
TURES Location/Qualifiers
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IGIN

uery Match 47.2%; Score 700.6; DB 2; Length 1401;

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Best Local Similarity 100.0%; Pred. No. 1.9e-179;
Matches 700; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 786 TGAGCCCAGAGGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCAGCACCTAACCT 845
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Qy 1026 GGATTACAACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGACTGGAT 1085
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Qy 1386 GAAGAACTGGGTGGAAAGAAATAGCTACTCCTGTTCAGTGGTCCACGAGGGTCTGCACAA 1445
Db 1302 GAAGAACTGGGTGGAAAGAAATAGCTACTCCTGTTCAGTGGTCCACGAGGGTCTGCACAA 1361

Qy 1446 TCACCACACGACTAAGAGCTTCTCCCGGACTCCGGGTAAA 1485
Db 1362 TCACCACACGACTAAGAGCTTCTCCCGGACTCCGGGTAAA 1401
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RESULT 10
AF466698
LOCUS AF466698 1407 bp mRNA linear ROD 17-DEC-2002
DEFINITION Mus musculus strain BALB/c immunoglobulin heavy chain mRNA, partial cds.
ACCESSION AF466698
VERSION AF466698.1 GI:27127159
KEYWORDS .
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1407)
AUTHORS Lai,Y.S., John,J.A.C., Guo,I.C., Chen,S.C., Fang,K. and Chang,C.Y.
TITLE In vitro efficiency of intra- and extracellular immunization with mouse anti-YGNNV antibody against yellow grouper nervous necrosis virus
JOURNAL Vaccine 20 (25-26), 3221-3229 (2002)
PUBMED 12163274
REFERENCE 2 (bases 1 to 1407)

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THORS   Lai,Y.-S., John,C., Guo,I.-C., Chen,S.-C., Fang,K. and Chang,C.-Y.
TLE     Direct Submission
URNAL   Submitted (08-JAN-2002) Institute of Zoology, Academia Sinica, 128
        Academia Road, NanKang, Taipei 11529, Taiwan, ROC
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st Local Similarity   100.0%;  Pred. No. 1.9e-179;
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      786 TGAGCCCAGAGGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCAGCACCTAACCT 845
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      708 TGAGCCCAGAGGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCAGCACCTAACCT 767

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     1026 GGATTACAACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGACTGGAT 1085
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     1206 AGAAGAAGAGATGACTAAGAAACAGGTCACTCTGACCTGCATGGTCACAGACTTCATGCC 1265
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     1386 GAAGAACTGGGTGGAAAGAAATAGCTACTCCTGTTCAGTGGTCCACGAGGGTCTGCACAA 1445
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Qy       1446 TCACCACACGACTAAGAGCTTCTCCCGGACTCCGGGTAAA 1485
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Db       1368 TCACCACACGACTAAGAGCTTCTCCCGGACTCCGGGTAAA 1407


RESULT 11
A22261
LOCUS       A22261                  1570 bp    DNA     linear   PAT 16-NOV-2004
DEFINITION  M.musculus OKT3 heavy chain.
ACCESSION   A22261
VERSION     A22261.1  GI:21727143
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
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REFERENCE   1  (bases 1 to 1570)
  AUTHORS   .
  TITLE     HUMANISED ANTIBODIES
  JOURNAL   Patent: WO 9109967-A 3 11-JUL-1991;
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ORIGIN

  Query Match             47.2%;  Score 700.6;  DB 2;  Length 1570;
  Best Local Similarity   100.0%;  Pred. No. 2e-179;
  Matches  700;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        786 TGAGCCCAGAGGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCAGCACCTAACCT 845
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Qy        846 CTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTC 905
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Db        805 CTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTC 864

Qy        906 CCTGAGCCCCATAGTCACATGTGTGGTGGTGGATGTGAGCGAGGATGACCCAGATGTCCA 965
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Db        865 CCTGAGCCCCATAGTCACATGTGTGGTGGTGGATGTGAGCGAGGATGACCCAGATGTCCA 924

Qy        966 GATCAGCTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAAACCCATAGAGA 1025
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Db        925 GATCAGCTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAAACCCATAGAGA 984

Qy       1026 GGATTACAACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGACTGGAT 1085
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Qy       1086 GAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAAGACCTCCCAGCGCCCATCGAGAG 1145
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Qy       1146 AACCATCTCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACC 1205
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INITION  Sequence 6 from patent US 5859205.
SSION   AR029102
SION    AR029102.1  GI:5941075
WORDS   .
RCE     Unknown.
RGANISM  Unknown.
        Unclassified.
ERENCE  1  (bases 1 to 1570)
UTHORS  Adair,J.Robert., Athwal,D.Singh. and Emtage,J.Spencer.
ITLE    Humanised antibodies
OURNAL  Patent: US 5859205-A 6 12-JAN-1999;
TURES             Location/Qualifiers
   source         1. .1570
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IGIN

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est Local Similarity   100.0%;  Pred. No. 2e-179;
atches  700;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db       1405 TCACCACACGACTAAGAGCTTCTCCCGGACTCCGGGTAAA 1444


RESULT 13
BD057272
LOCUS       BD057272                1570 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Gene encoding antimalathion monoclonal antibody.
ACCESSION   BD057272
VERSION     BD057272.1  GI:22602878
KEYWORDS    JP 2001275682-A/9.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 1570)
  AUTHORS   Okawa,H., Nakata,M. and Yuasa,Y.
  TITLE     Gene encoding antimalathion monoclonal antibody
  JOURNAL   Patent: JP 2001275682-A 9 09-OCT-2001;
            KANKYO MENEKI GIJUTSU KENKYUSYO KK
COMMENT     PN   JP 2001275682-A/9
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ORIGIN

  Query Match             47.2%;  Score 700.6;  DB 2;  Length 1570;
  Best Local Similarity   100.0%;  Pred. No. 2e-179;
  Matches  700;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       786 TGAGCCCAGAGGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCAGCACCTAACCT 845
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Qy       846 CTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTC 905
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Qy       966 GATCAGCTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAAACCCATAGAGA 1025
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     1280 TGAACCAGTCCTGGACTCTGATGGTTCTTACTTCATGTACAGCAAGCTGAGAGTGGAAAA 1339

     1386 GAAGAACTGGGTGGAAAGAAATAGCTACTCCTGTTCAGTGGTCCACGAGGGTCTGCACAA 1445
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LT 14
9372
S       AR409372                1570 bp    mRNA    linear   PAT 18-DEC-2003
NITION  Sequence 6 from patent US 6632927.
SSION   AR409372
ION     AR409372.1  GI:40160268
ORDS    .
CE      Unknown.
GANISM  Unknown.
        Unclassified.
RENCE   1  (bases 1 to 1570)
THORS   Adair,J.R., Athwal,D.S. and Emtage,J.S.
TLE     Humanized antibodies
URNAL   Patent: US 6632927-A 6 14-OCT-2003;
        Celltech Therapeutics Limited; Berkshire;
        GBX;
URES             Location/Qualifiers
 source          1. .1570
                 /organism="unknown"
                 /mol_type="mRNA"
IN

ery Match             47.2%;  Score 700.6;  DB 2;  Length 1570;
st Local Similarity   100.0%;  Pred. No. 2e-179;
tches  700;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

      786 TGAGCCCAGAGGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCAGCACCTAACCT 845
      745 TGAGCCCAGAGGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCAGCACCTAACCT 804

      846 CTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTC 905
      805 CTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTC 864

      906 CCTGAGCCCCATAGTCACATGTGTGGTGGTGGATGTGAGCGAGGATGACCCAGATGTCCA 965
      865 CCTGAGCCCCATAGTCACATGTGTGGTGGTGGATGTGAGCGAGGATGACCCAGATGTCCA 924
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Qy       966 GATCAGCTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAAACCCATAGAGA 1025
Db       925 GATCAGCTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAAACCCATAGAGA 984

Qy      1026 GGATTACAACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGACTGGAT 1085
Db       985 GGATTACAACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGACTGGAT 1044

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Db      1105 AACCATCTCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACC 1164

Qy      1206 AGAAGAAGAGATGACTAAGAAACAGGTCACTCTGACCTGCATGGTCACAGACTTCATGCC 1265
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Db      1225 TGAAGACATTTACGTGGAGTGGACCAACAACGGGAAAACAGAGCTAAACTACAAGAACAC 1284

Qy      1326 TGAACCAGTCCTGGACTCTGATGGTTCTTACTTCATGTACAGCAAGCTGAGAGTGGAAAA 1385
Db      1285 TGAACCAGTCCTGGACTCTGATGGTTCTTACTTCATGTACAGCAAGCTGAGAGTGGAAAA 1344

Qy      1386 GAAGAACTGGGTGGAAAGAAATAGCTACTCCTGTTCAGTGGTCCACGAGGGTCTGCACAA 1445
Db      1345 GAAGAACTGGGTGGAAAGAAATAGCTACTCCTGTTCAGTGGTCCACGAGGGTCTGCACAA 1404

Qy      1446 TCACCACACGACTAAGAGCTTCTCCCGGACTCCGGGTAAA 1485
Db      1405 TCACCACACGACTAAGAGCTTCTCCCGGACTCCGGGTAAA 1444
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DEFINITION  Sequence 6 from patent US 6750325.
ACCESSION   AR559698
VERSION     AR559698.1  GI:53969764
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1570)
  AUTHORS   Jolliffe,L.K., Zivin,R.A., Adair,J.R. and Athwal,D.S.
  TITLE     CD3 specific recombinant antibody
  JOURNAL   Patent: US 6750325-A 6 15-JUN-2004;
            Celltech R&D Limited; Slough;
            GBX;
FEATURES             Location/Qualifiers
     source          1. .1570
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             47.2%;  Score 700.6;  DB 2;  Length 1570;
  Best Local Similarity   100.0%;  Pred. No. 2e-179;
  Matches  700;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       786 TGAGCCCAGAGGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCAGCACCTAACCT 845
Db       745 TGAGCCCAGAGGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCAGCACCTAACCT 804

Qy       846 CTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTC 905
Db       805 CTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTC 864

Qy       906 CCTGAGCCCCATAGTCACATGTGTGGTGGTGGATGTGAGCGAGGATGACCCAGATGTCCA 965
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  966 GATCAGCTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAAACCCATAGAGA 1025
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  925 GATCAGCTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAAACCCATAGAGA 984

 1026 GGATTACAACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGACTGGAT 1085
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  985 GGATTACAACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGACTGGAT 1044

 1086 GAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAAGACCTCCCAGCGCCCATCGAGAG 1145
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1045 GAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAAGACCTCCCAGCGCCCATCGAGAG 1104

 1146 AACCATCTCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACC 1205
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1105 AACCATCTCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACC 1164

 1206 AGAAGAAGAGATGACTAAGAAACAGGTCACTCTGACCTGCATGGTCACAGACTTCATGCC 1265
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1165 AGAAGAAGAGATGACTAAGAAACAGGTCACTCTGACCTGCATGGTCACAGACTTCATGCC 1224

 1266 TGAAGACATTTACGTGGAGTGGACCAACAACGGGAAAACAGAGCTAAACTACAAGAACAC 1325
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1225 TGAAGACATTTACGTGGAGTGGACCAACAACGGGAAAACAGAGCTAAACTACAAGAACAC 1284

 1326 TGAACCAGTCCTGGACTCTGATGGTTCTTACTTCATGTACAGCAAGCTGAGAGTGGAAAA 1385
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: time : 8835.58 secs

GenCore version 5.1.8

nucleic - nucleic search, using sw model

on: May 31, 2006, 23:41:05 ; Search time 1026.58 Seconds
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Maximum Match 100%
Listing first 45 summaries

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14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	% Query Match	Length	DB	ID	Description
1	1484	99.9	1484	5	AAF55098	Aaf55098 DNA encod
2	1067.4	71.9	1676	4	ABI99041	Abi99041 Murine pC
3	957.6	64.5	1446	2	AAT99707	Aat99707 DR2-IgG f
4	957.6	64.5	1446	2	AAX87813	Aax87813 HLA-DR2 a
5	957.6	64.5	1446	14	ADW44282	Adw44282 DR2-IgG f
6	726.2	48.9	2346	4	ABI99027	Abi99027 IAS MBP 1
7	723.2	48.7	2343	4	ABI99033	Abi99033 MBP 90-10
8	701.2	47.2	1045	12	ADO07566	Ado07566 Fusion pr
9	701.2	47.2	1108	12	ADO07578	Ado07578 Fusion pr
10	701.2	47.2	1108	12	ADO07577	Ado07577 Fusion pr
11	700.6	47.2	990	12	ADL15694	Adl15694 Murine im
12	700.6	47.2	1401	14	AEC20762	Aec20762 M-CSF spe
13	700.6	47.2	1560	14	AED19725	Aed19725 Anti-PrP
14	700.6	47.2	1569	14	ADV26108	Adv26108 Mouse OKT
15	700.6	47.2	1569	14	ADW71834	Adw71834 Murine OK
16	700.6	47.2	1570	2	AAQ12637	Aaq12637 Monoclona
17	700.6	47.2	1570	12	ADQ91058	Adq91058 Murine OK
18	700.6	47.2	3973	13	ADT77690	Adt77690 Monoclona
19	700.4	47.2	1509	14	AEE21942	Aee21942 Single ch
20	700.2	47.2	729	3	AAZ35704	Aaz35704 Human gly
21	700.2	47.2	1140	10	ADE85817	Ade85817 Murine in
22	700	47.1	1158	2	AAT59350	Aat59350 1-153 del
23	700	47.1	1188	2	AAT59349	Aat59349 1-153 c-m
24	700	47.1	6729	4	AAF30341	Aaf30341 Bicistron
25	700	47.1	7528	4	AAF30316	Aaf30316 Bicistron
26	699.4	47.1	1530	14	AEB12356	Aeb12356 Fusion pr
27	699.4	47.1	1530	14	AED64236	Aed64236 mFc-hOGH-
28	699	47.1	699	15	AEF05391	Aef05391 Human mFc
29	699	47.1	708	14	AEB12344	Aeb12344 Immunoglo
30	699	47.1	708	14	AED64224	Aed64224 Murine im
31	699	47.1	1341	1	AAN91659	Aan91659 Chimeric
32	699	47.1	1413	14	AEB12360	Aeb12360 Fusion pr
33	699	47.1	1413	14	AED64240	Aed64240 hTSH-mFC-
34	699	47.1	1431	14	AEB12362	Aeb12362 Fusion pr
35	699	47.1	1431	14	AED64242	Aed64242 hOGH-mFC-
36	699	47.1	1581	2	AAQ48037	Aaq48037 Monoclona
37	699	47.1	1645	2	AAQ54652	Aaq54652 T84.12 He
38	698.4	47.0	1131	2	AAV55416	Aav55416 Chimeric
39	698.4	47.0	1194	2	AAV55415	Aav55415 Chimeric
40	698.4	47.0	1275	2	AAT62850	Aat62850 Mouse sol
41	698.4	47.0	1473	13	ADS31748	Ads31748 DNA encod
42	698.4	47.0	1473	13	ADS92750	Ads92750 DNA encod
43	697.8	47.0	1524	14	AEE21946	Aee21946 Single ch
44	697.4	47.0	699	3	AAZ51300	Aaz51300 Murine im
45	697.4	47.0	699	3	AAA50055	Aaa50055 Mouse imm

ALIGNMENTS

RESULT 1
AAF55098
ID AAF55098 standard; DNA; 1484 BP.
XX
AC AAF55098;
XX
DT 15-MAY-2001 (first entry)
XX
DE DNA encoding a fusion protein comprising an alpha chain of MHC.
XX
KW Recombinant protein; alpha chain; beta chain; MHC; immunoglobulin;
KW major histocompatibility complex; Fc region; antigen; T lymphocyte;
KW immunostimulant; vaccine; infection; tumour; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1. .1482
FT /*tag= a
XX
PN WO200109194-A1.
XX
PD 08-FEB-2001.
XX
PF 28-JUL-2000; 2000WO-FR002193.
XX
PR 29-JUL-1999; 99FR-00009862.
XX
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
PI Glaichenhaus N, Malherbe L;
XX
DR WPI; 2001-182944/18.
DR P-PSDB; AAB67480.
XX
PT New soluble recombinant protein, useful e.g. as immunostimulant,
PT comprises dimeric major histocompatibility complex molecule fused to
PT immunoglobulin Fc region.
XX
PS Example 1; Page 31-33; 43pp; French.
XX

The specification describes soluble recombinant proteins that comprise at least a dimer formed from the alpha and beta-chains of MHC (major histocompatibility complex) Class I and II molecules in which at least one chain has, attached to its C-terminus, at least part of the Fc region of an immunoglobulin. The recombinant proteins, when linked to an antigenic peptide, are used to count and/or purify antigen-reactive T lymphocytes and to characterize their phenotype, e.g. in preclinical evaluation of vaccines. They are also used as immunostimulants, particularly for vaccine development (against infections and tumours), to count and determine phenotype of autoreactive T cells in subjects with, or at risk of developing, autoimmune diseases, e.g. for staging or evaluating treatments, and (to purify and/or enrich Ag-reactive T cells from cell cultures or patient samples, for use in subsequent curative or preventative cellular therapy. The present sequence encodes a recombinant protein of the invention, comprising an alpha chain of MHC molecules

Sequence 1484 BP; 414 A; 394 C; 362 G; 314 T; 0 U; 0 Other;

ery Match 99.9%; Score 1484; DB 5; Length 1484;
st Local Similarity 100.0%; Pred. No. 0;
tches 1484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 ATGCCGTGCAGCAGAGCTCTGATTCTGGGGGTCCTCGCCCTGAACACCATGCTCAGCCTC 60

Qy         61 TGCGGAGGTGAAGACGACATTGAGGCCGACCACGTAGGCTTCTATGGTACAACTGTTTAT 120
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Db         61 TGCGGAGGTGAAGACGACATTGAGGCCGACCACGTAGGCTTCTATGGTACAACTGTTTAT 120

Qy        121 CAGTCTCCTGGAGACATTGGCCAGTACACACATGAATTTGATGGTGATGAGTTGTTCTAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAGTCTCCTGGAGACATTGGCCAGTACACACATGAATTTGATGGTGATGAGTTGTTCTAT 180

Qy        181 GTGGACTTGGATAAGAAGAAAACTGTCTGGAGGCTTCCTGAGTTTGGCCAATTGATACTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACTTGGATAAGAAGAAAACTGTCTGGAGGCTTCCTGAGTTTGGCCAATTGATACTC 240

Qy        241 TTTGAGCCCCAAGGTGGACTGCAAAACATAGCTGCAGAAAAACACAACTTGGGAATCTTG 300
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Qy        301 ACTAAGAGGTCAAATTTCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGTTCCCC 360
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Qy        361 AAGTCCCCTGTGCTGCTGGGTCAGCCCAACACCCTTATCTGCTTTGTGGACAACATCTTC 420
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Db        361 AAGTCCCCTGTGCTGCTGGGTCAGCCCAACACCCTTATCTGCTTTGTGGACAACATCTTC 420

Qy        421 CCACCTGTGATCAACATCACATGGCTCAGAAATAGCAAGTCAGTCACAGACGGCGTTTAT 480
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Qy        481 GAGACCAGCTTCCTCGTCAACCGTGACCATTCCTTCCACAAGCTGTCTTATCTCACCTTC 540
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Qy        541 ATCCCTTCTGATGATGACATTTATGACTGCAAGGTGGAGCACTGGGGCCTGGAGGAGCCG 600
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Qy        601 GTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAAACTGGA 660
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Db        601 GTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAAACTGGA 660

Qy        661 GGTGGAGGATCCACTACAGCTCCATCAGCTCAGCTCGAAAAAGAGCTCCAGGCCCTGGAG 720
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Qy        781 GCATCTGAGCCCAGAGGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCAGCACCT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        841 AACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATG 900

Qy        901 ATCTCCCTGAGCCCCATAGTCACATGTGTGGTGGTGGATGTGAGCGAGGATGACCCAGAT 960
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Db        901 ATCTCCCTGAGCCCCATAGTCACATGTGTGGTGGTGGATGTGAGCGAGGATGACCCAGAT 960

Qy        961 GTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAAACCCAT 1020
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Db        961 GTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAAACCCAT 1020

Qy       1021 AGAGAGGATTACAACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGAC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGAGAGGATTACAACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGAC 1080

Qy       1081 TGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAAGACCTCCCAGCGCCCATC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1141 GAGAGAACCATCTCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTTGCCT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GAGAGAACCATCTCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTTGCCT 1200

Qy       1201 CCACCAGAAGAAGAGATGACTAAGAAACAGGTCACTCTGACCTGCATGGTCACAGACTTC 1260
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Db       1201 CCACCAGAAGAAGAGATGACTAAGAAACAGGTCACTCTGACCTGCATGGTCACAGACTTC 1260

Qy       1261 ATGCCTGAAGACATTTACGTGGAGTGGACCAACAACGGGAAAACAGAGCTAAACTACAAG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 ATGCCTGAAGACATTTACGTGGAGTGGACCAACAACGGGAAAACAGAGCTAAACTACAAG 1320

Qy       1321 AACACTGAACCAGTCCTGGACTCTGATGGTTCTTACTTCATGTACAGCAAGCTGAGAGTG 1380
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Qy       1381 GAAAAGAAGAACTGGGTGGAAAGAAATAGCTACTCCTGTTCAGTGGTCCACGAGGGTCTG 1440
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RESULT 2
ABI99041
ID ABI99041 standard; cDNA; 1676 BP.
XX
AC ABI99041;
XX
DT 25-FEB-2002 (first entry)
XX
DE Murine pCB223 coding sequence.
XX
KW Mouse; MHC; major histocompatibility complex; MHC class II; multimer;
KW single chain; immunosuppressive; antidiabetic; antiinflammatory;
KW antianaemic; antirheumatoid; antiarthritic; neuroprotective; vaccine;
KW autoimmune disease; insulin dependent diabetes; multiple sclerosis;
KW myasthenia gravis; pernicious anaemia; autoimmune encephalomyelitis;
KW rheumatoid arthritis; systemic lupus erythematosus; ss.
XX
OS Mus sp.
OS Synthetic.
XX
PN WO200170245-A1.
XX
PD 27-SEP-2001.

22-MAR-2001; 2001WO-US009616.

22-MAR-2000; 2000US-0191274P.
15-MAY-2000; 2000US-0204249P.
23-JAN-2001; 2001US-0264003P.

(CORI-) CORIXA CORP.

Carter D, Zhu S, Arimilli S, Wang A;

WPI; 2001-616371/71.
P-PSDB; ABB56471.

Multimeric complex for treating autoimmune diseases, comprises first and second single chain MHC class II molecules, each comprising alpha1 and beta1 domain linked through amino acid linker and multimerization domain.

Disclosure; Page 115; 147pp; English.

The invention relates to a multimeric complex comprising a first recombinant single chain major histocompatibility complex (MHC) class II molecule and a second recombinant single chain MHC class II molecule, each comprising an alpha1 domain and a beta1 domain linked through an amino acid linker and a multimerisation domain. The first and the second molecule are linked through the multimerisation domain to form a multimeric complex,. The complex is useful for treating autoimmune diseases. It is useful for treating insulin dependent diabetes, multiple sclerosis, myasthenia gravis, pernicious anaemia, autoimmune encephalomyelitis (EAE), rheumatoid arthritis and systemic lupus erythematosus. The present sequence encodes a single chain MHC class II molecule of the invention

Sequence 1676 BP; 438 A; 470 C; 407 G; 361 T; 0 U; 0 Other;

Query Match 71.9%; Score 1067.4; DB 4; Length 1676;
Best Local Similarity 83.5%; Pred. No. 2.9e-277;
Matches 1319; Conservative 0; Mismatches 96; Indels 164; Gaps 3;

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Qy      67 GGTGAAGACGACATTGAGGCCGACCACGTAGGCTTCTATGGTACAACTGTTTATCAGTCT 126
           || |||||||||||||||||||||||||||||| ||||||||||||||| |||||||||
Db      91 GGCGAAGACGACATTGAGGCCGACCACGTAGGCGTCTATGGTACAACTGTATATCAGTCT 150

Qy     127 CCTGGAGACATTGGCCAGTACACACATGAATTTGATGGTGATGAGTTGTTCTATGTGGAC 186
           ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db     151 CCTGGAGACATTGGCCAGTACACACATGAATTTGATGGTGATGAGTGGTTCTATGTGGAC 210

Qy     187 TTGGATAAGAAGAAAACTGTCTGGAGGCTTCCTGAGTTTGGCCAATTGATACTCTTTGAG 246
           |||||||||||| | ||| |||||| |||||||||||||||||||||| |  ||||||
Db     211 TTGGATAAGAAGGAGACTATCTGGATGCTTCCTGAGTTTGGCCAATTGACAAGCTTTGAC 270

Qy     247 CCCCAAGGTGGACTGCAAAACATAGCTGCAGAAAAACACAACTTGGGAATCTTGACTAAG 306
           |||||||||||||||||||||||||| ||| |||| ||| ||||||||||||||||||
Db     271 CCCCAAGGTGGACTGCAAAACATAGCTACAGGAAAATACACCTTGGGAATCTTGACTAAG 330

Qy     307 AGGTCAAATTTCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGTTCCCCAAGTCC 366
           |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db     331 AGGTCAAATTCCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGTTCCCCAAGTCC 390

Qy     367 CCTGTGCTGCTGGGTCAGCCCAACACCCTTATCTGCTTTGTGGACAACATCTTCCCACCT 426
           |||||||||||||||||||||||||||||| |||||||||||||||||||||||||| |||
Db     391 CCTGTGCTGCTGGGTCAGCCCAACACCCTCATCTGCTTTGTGGACAACATCTTCCCTCCT 450

Qy     427 GTGATCAACATCACATGGCTCAGAAATAGCAAGTCAGTCACAGACGGCGTTTATGAGACC 486
           |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db     451 GTGATCAACATCACATGGCTCAGAAATAGTAAGTCAGTCACAGACGGCGTTTATGAGACC 510

Qy     487 AGCTTCCTCGTCAACCGTGACCATTCCTTCCACAAGCTGTCTTATCTCACCTTCATCCCT 546
           |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     511 AGCTTCCTTGTCAACCGTGACCATTCCTTCCACAAGCTGTCTTATCTCACCTTCATCCCT 570

Qy     547 TCTGATGATGACATTTATGACTGCAAGGTGGAGCACTGGGGCCTGGAGGAGCCGGTTCTG 606
           ||||| ||||| ||||||||||||||||||||||||||||||||||||||||||||||||
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Db     571 TCTGACGATGATATTTATGACTGCAAGGTGGAGCACTGGGGCCTGGAGGAGCCGGTTCTG 630

Qy     607 AAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAAACTGGAGGTGGA 666
           |||||||||||||||||||||||||||||||||||||||||||||| | | | | | |
Db     631 AAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAAGGATCTGCCAAAACAACAGCC 690

Qy     667 GGAT---------------------------------------------------------- 670
           ||
Db     691 CCATCGGTCTATCCACTGGCCCCTGTGTGTGGAGATACAACTGGCTCCTCGGTGACTCTA 750

Qy     671 ---------------------------------------------------------- 670

Db     751 GGATGCCTGGTCAAGGGTTATTTCCCTGAGCCAGTGACCTTGACCTGGAACTCTGGATCC 810

Qy     671 ----------------------------------------------CCACTACAGCTCCATC 686
                                                          || ||||| |  || |
Db     811 CTGTCCAGTGGTGTGCACACCTTCCCAGCTGTCCTGCAGTCTGACCTCTACACCCTCAGC 870

Qy     687 AGCTCAGCTCGAAAAAGAGCTCCAGGCCCTGGAGAAGGAAAATGCACAGCTGGAATGGGA 746
           |||||||  ||     | ||| ||  |||||   ||  |      || ||| |||| |
Db     871 AGCTCAG--TGACTGTAACCTCGAGCACCTGGCCCAGCCAGTCCATCACCTGCAATGTGG 928

Qy     747 GTTGCAAGCACTGGAAAAGGAACTGGCTCAGGCAGCATCTGAGCCCAGAGGGCCCACAAT 806
           | | | | | |  ||  |  || | |  | ||||||||||||||||||||
Db     929 CCCACCCGGCAAGCAGCACCAAGGTGGACAAGAA--AATTGAGCCCAGAGGGCCCACAAT 986

Qy     807 CAAGCCCTGTCCTCCATGCAAATGCCCAGCACCTAACCTCTTGGGTGGACCATCCGTCTT 866
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     987 CAAGCCCTGTCCTCCATGCAAATGCCCAGCACCTAACCTCTTGGGTGGACCATCCGTCTT 1046

Qy     867 CATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCATAGTCACATG 926
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1047 CATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCATAGTCACATG 1106

Qy     927 TGTGGTGGTGGATGTGAGCGAGGATGACCCAGATGTCCAGATCAGCTGGTTTGTGAACAA 986
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1107 TGTGGTGGTGGATGTGAGCGAGGATGACCCAGATGTCCAGATCAGCTGGTTTGTGAACAA 1166

Qy     987 CGTGGAAGTACACACAGCTCAGACACAAACCCATAGAGAGGATTACAACAGTACTCTCCG 1046
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1167 CGTGGAAGTACACACAGCTCAGACACAAACCCATAGAGAGGATTACAACAGTACTCTCCG 1226

Qy    1047 GGTGGTCAGTGCCCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATG 1106
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1227 GGTGGTCAGTGCCCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATG 1286

Qy    1107 CAAGGTCAACAACAAAGACCTCCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGG 1166
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1287 CAAGGTCAACAACAAAGACCTCCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGG 1346

Qy    1167 GTCAGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACCAGAAGAAGAGATGACTAAGAA 1226
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1347 GTCAGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACCAGAAGAAGAGATGACTAAGAA 1406

Qy    1227 ACAGGTCACTCTGACCTGCATGGTCACAGACTTCATGCCTGAAGACATTTACGTGGAGTG 1286
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1407 ACAGGTCACTCTGACCTGCATGGTCACAGACTTCATGCCTGAAGACATTTACGTGGAGTG 1466

Qy    1287 GACCAACAACGGGAAAACAGAGCTAAACTACAAGAACACTGAACCAGTCCTGGACTCTGA 1346
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1467 GACCAACAACGGGAAAACAGAGCTAAACTACAAGAACACTGAACCAGTCCTGGACTCTGA 1526

Qy    1347 TGGTTCTTACTTCATGTACAGCAAGCTGAGAGTGGAAAAGAAGAACTGGGTGGAAAGAAA 1406
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1527 TGGTTCTTACTTCATGTACAGCAAGCTGAGAGTGGAAAAGAAGAACTGGGTGGAAAGAAA 1586

Qy    1407 TAGCTACTCCTGTTCAGTGGTCCACGAGGGTCTGCACAATCACCACACGACTAAGAGCTT 1466
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1587 TAGCTACTCCTGTTCAGTGGTCCACGAGGGTCTGCACAATCACCACACGACTAAGAGCTT 1646

Qy    1467 CTCCCGGACTCCGGGTAAA 1485
           ||||||||||||||||||
Db    1647 CTCCCGGACTCCGGGTAAA 1665
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LT 3
9707
AAT99707 standard; cDNA; 1446 BP.

AAT99707;

17-OCT-2003 (revised)
17-AUG-1998 (first entry)

DR2-IgG fusion construct.

Major histocompatibility complex class II; MHC class II; human; mouse; fusion protein; HLA-DR2; DRA*0101; binding domain; Fos; dimerisation domain; IgG; allergy; autoimmune disease; vaccine; multiple sclerosis; therapy; ss.

Homo sapiens.
Mus musculus.
Chimeric.

WO9806749-A2.

19-FEB-1998.

15-AUG-1997; 97WO-US014503.

16-AUG-1996; 96US-0024077P.

(HARD) HARVARD COLLEGE.

Wucherpfennig KW, Strominger JL;

WPI; 1998-159459/14.

New Class II MHC fusion proteins - comprising a MHC Class II binding domain and a dimerisation domain or an immunoglobulin region used for modulating immune responses.

Example; Page 49; 76pp; English.

This nucleotide sequences codes for a bivalent DR2 fusion protein obtained by fusion of the Fc portion of IgG2a to the 3' end of a DR-alpha -Fos cDNA construct (see AAV16866). The Fc portion was amplified by RT-PCR from mouse hybridoma L243. The PCR product was then fused in frame with the DR-alpha-Fos construct by overlapping PCR. The DR2-IgG fusion was expressed in the Drosophila Schneider cell system. The invention relates to new soluble monovalent and multivalent Class II MHC fusion proteins comprising a MHC Class II binding domain and a dimerisation domain or an immunoglobulin region that can be used for the treatment of allergic and autoimmune diseases (e.g. multiple sclerosis), for tolerising a subject to foreign tissue before or after organ or tissue transplantation, or for vaccination against pathogens. (Updated on 17-OCT -2003 to standardise OS field)

Sequence 1446 BP; 414 A; 375 C; 356 G; 301 T; 0 U; 0 Other;

ery Match 64.5%; Score 957.6; DB 2; Length 1446;
st Local Similarity 81.8%; Pred. No. 1.2e-247;
tches 1136; Conservative 0; Mismatches 234; Indels 18; Gaps 2;

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Qy   116 TTTATCAGTCTCCTGGAGACATTGGCCAGTACACACATGAATTTGATGGTGATGAGTTGT 175
Db    50 TCTATCTGAATCCTGACCAATCAGGCGAGTTTATGTTTGACTTTGATGGTGATGAGATTT 109

Qy   176 TCTATGTGGACTTGGATAAGAAGAAAACTGTCTGGAGGCTTCCTGAGTTTGGCCAATTGA 235
Db   110 TCCATGTGGATATGGCAAAGAAGGAGACGGTCTGGCGGCTTGAAGAATTTGGACGATTTG 169

Qy   236 TACTCTTTGAGCCCCAAGGTGGACTGCAAAACATAGCTGCAGAAAAACACAACTTGGGAA 295
Db   170 CCAGCTTTGAGGCTCAAGGTGCATTGGCCAACATAGCTGTGGACAAAGCCAACTTGGAAA 229

Qy   296 TCTTGACTAAGAGGTCAAATTTCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGT 355
Db   230 TCATGACAAAGCGCTCCAACTATACTCCGATCACCAATGTACCTCCAGAGGTAACTGTGC 289

Qy   356 TCCCCAAGTCCCCTGTGCTGCTGGGTCAGCCCAACACCCTTATCTGCTTTGTGGACAACA 415
Db   290 TCACGAACAGCCCTGTGGAACTGAGAGAGCCCAACGTCCTCATCTGTTTCATAGACAAGT 349

Qy   416 TCTTCCCACCTGTGATCAACATCACATGGCTCAGAAATAGCAAGTCAGTCACAGACGGCG 475
Db   350 TCACCCCACCAGTGGTCAATGTCACGTGGCTTCGAAATGGAAAACCTGTCACCACAGGAG 409

Qy   476 TTTATGAGACCAGCTTCCTCGTCAACCGTGACCATTCCTTCCACAAGCTGTCTTATCTCA 535
Db   410 TGTCAGAGACAGTCTTCCTGCCCAGGGAAGACCACCTTTTCCGCAAGTTCCACTATCTCC 469

Qy   536 CCTTCATCCCTTCTGATGATGACATTTATGACTGCAAGGTGGAGCACTGGGGCCTGGAGG 595
Db   470 CCTTCCTGCCCTCAACTGAGGACGTTTACGACTGCAGGGTGGAGCACTGGGGCTTGGATG 529

Qy   596 AGCCGGTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAAA 655
Db   530 AGCCTCTTCTCAAGCACTGGGAGTTTGATGCTCCAAGCCCTCTCCCAGAGACTACAGAGG 589

Qy   656 CTGGAGGTGGAGGATCCACT--------------ACAGCTCCATCAGCTCAGCTCGAAA 700
Db   590 TCGACGGAGGTGGCGGCGGTTTAACTGATACACTCCAAGCGGAGACAGATCAACTTGAAG 649

Qy   701 AAGAGCTCCAGGCCCTGGAGAAGGAAAATGCACAGCTGGAATGGGAGTTGCAAGCACTGG 760
Db   650 ACGAGAAGTCTGCGTTGCAGACCGAGATTGCCAATCTACTGAAAGAGAAGGAAAAACTGG 709

Qy   761 AAAAGGAACTG---GCTCAGGCAGCATCTGAGCCCAGAGGGCCCACAATCAAGCCCTGTC 817
Db   710 AGTTCATCCTGGCCGCCCATGCAGCATCTGAGCCCAGAGGGCCCACAATCAAGCCCTGTC 769

Qy   818 CTCCATGCAAATGCCCAGCACCTAACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCTC 877
Db   770 CTCCATGCAAATGCCCAGCACCTAACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCTC 829

Qy   878 CAAAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCATAGTCACATGTGTGGTGGTGG 937
Db   830 CAAAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCATAGTCACATGTGTGGTGGTGG 889

Qy   938 ATGTGAGCGAGGATGACCCAGATGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTAC 997
Db   890 ATGTGAGCGAGGATGACCCAGATGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTAC 949

Qy   998 ACACAGCTCAGACACAAACCCATAGAGAGGATTACAACAGTACTCTCCGGGTGGTCAGTG 1057
Db   950 ACACAGCTCAGACACAAACCCATAGAGAGGATTACAACAGTACTCTCCGGGTGGTCAGTG 1009

Qy  1058 CCCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACA 1117
Db  1010 CCCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACA 1069

Qy  1118 ACAAAGACCTCCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGGTCAGTAAGAG 1177
Db  1070 ACAAAGACCTCCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGGTCAGTAAGAG 1129

Qy  1178 CTCCACAGGTATATGTCTTGCCTCCACCAGAAGAAGAGATGACTAAGAAACAGGTCACTC 1237
Db  1130 CTCCACAGGTATATGTCTTGCCTCCACCAGAAGAAGAGATGACTAAGAAACAGGTCACTC 1189

Qy  1238 TGACCTGCATGGTCACAGACTTCATGCCTGAAGACATTTACGTGGAGTGGACCAACAACG 1297
Db  1190 TGACCTGCATGGTCACAGACTTCATGCCTGAAGACATTTACGTGGAGTGGACCAACAACG 1249

Qy  1298 GGAAAACAGAGCTAAACTACAAGAACACTGAACCAGTCCTGGACTCTGATGGTTCTTACT 1357
Db  1250 GGAAAACAGAGCTAAACTACAAGAACACTGAACCAGTCCTGGACTCTGATGGTTCTTACT 1309
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      1358 TCATGTACAGCAAGCTGAGAGTGGAAAAGAAGAACTGGGTGGAAAGAAATAGCTACTCCT 1417
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1310 TCATGTACAGCAAGCTGAGAGTGGAAAAGAAGAACTGGGTGGAAAGAAATAGCTACTCCT 1369

      1418 GTTCAGTGGTCCACGAGGGTCTGCACAATCACCACACGACTAAGAGCTTCTCCCGGACTC 1477
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1370 GTTCAGTGGTCCACGAGGGTCTGCACAATCACCACACGACTAAGAGCTTCTCCCGGACTC 1429

      1478 CGGGTAAA 1485
           ||||||||
      1430 CGGGTAAA 1437


:ULT 4
:87813
   AAX87813 standard; DNA; 1446 BP.

   AAX87813;

   09-NOV-1999  (first entry)

   HLA-DR2 alpha-Fos-IgG fusion construct.

   Major histocompatability complex Class II; MHC; binding domain; HLA-DR2;
   leucine zipper; Fos; IgG; Fc; immunoglobulin; antibody; fusion protein;
   multiple sclerosis; rheumatoid arthritis; graft rejection; allergy;
   autoimmune disease; pemphigus vulgaris; systemic lupus erythematosus;
   T lymphocyte; T cell; diagnosis; therapy; adoptive immunotherapy; ss.

   Homo sapiens.
   Saccharomyces cerevisiae.
   Synthetic.
   Chimeric.

   Key             Location/Qualifiers
   CDS             1. .1440
                   /*tag=  a
   sig_peptide     1. .15
                   /*tag=  b
                   /note= "alpha-mating factor secretion signal"
   mat_peptide     16. .1437
                   /*tag=  c
                   /product= "DR2-Fos-Fc"

   WO9942597-A1.

   26-AUG-1999.

   19-FEB-1999;   99WO-US003603.

   19-FEB-1998;   98US-0075351P.

   (HARD ) HARVARD COLLEGE.

   Wucherpfennig KW,  Strominger JL;

   WPI; 1999-527481/44.
   P-PSDB; AAY31654.

   New HMC Class II binding domain fusion proteins and conjugates - used
   for, e.g. treating allergic and autoimmune diseases or detecting,
   isolating, activating or killing specific T cells.

   Example 7; Page 100-102; 113pp; English.

   This nucleotide sequence codes for a divalent HLA-DR2 MHC binding domain
   fusion protein (see AAY31654) comprising an alpha-mating factor secretion
   signal, the extracellular domain of the HLA-DR2 alpha chain (residues 1-
   191 of DRA*0101), a 7-amino acid linker, the 40-amino acid leucine zipper
   dimerization domain of Fos, and the Fc portion of IgG2a. The DR-alpha-Fc
   chain corresponds to an antibody heavy chain. The invention provides new
   monovalent, multivalent and multimeric MHC Class II binding domain fusion
   proteins and conjugates comprising at least a binding domain of an MHC
CC   Class II alpha or beta chain and a dimerization domain, especially a Fos
CC   or Jun leucine zipper domain. The MHC fusion proteins and conjugates can
CC   be used: for detecting and isolating T cells having a defined MHC/peptide
CC   complex specificity (claimed); to confer to a subject adoptive immunity
CC   to a defined MHC/peptide complex (claimed); to stimulate or activate T
CC   cells reactive to a defined MHC/peptide complex (claimed); for selective
CC   killing of T cells reactive to a defined MHC complex (claimed); to
CC   tolerize a subject to a defined MHC/peptide complex (claimed); to treat
CC   allergic and autoimmune diseases, e.g. multiple sclerosis, rheumatoid
CC   arthritis, pemphigus vulgaris, and systemic lupus erythematosus; and to
CC   prevent organ or tissue transplant rejection. The DR2-IgG design was
CC   chosen to increase the affinity for the T cell receptor by increasing
CC   valency, and to attach an effector domain, the Fc region of IgG2a.
CC   Complement fixation may result in the lysis of target T cells following
CC   binding of DR2-IgG molecules to the T cell receptor. DR2-IgG molecules
CC   may therefore be useful for the selective depletion of autoaggressive T
CC   cells
XX
SQ   Sequence 1446 BP; 414 A; 375 C; 356 G; 301 T; 0 U; 0 Other;

  Query Match             64.5%;  Score 957.6;  DB 2;  Length 1446;
  Best Local Similarity   81.8%;  Pred. No. 1.2e-247;
  Matches 1136;  Conservative    0;  Mismatches  234;  Indels   18;  Gaps    2;

Qy       116 TTTATCAGTCTCCTGGAGACATTGGCCAGTACACACATGAATTTGATGGTGATGAGTTGT 175
             | |||| |  |||||   |    ||| |||  |    ||| ||||||||||||||| | |
Db        50 TCTATCTGAATCCTGACCAATCAGGCGAGTTTATGTTTGACTTTGATGGTGATGAGATTT 109

Qy       176 TCTATGTGGACTTGGATAAGAAGAAAACTGTCTGGAGGCTTCCTGAGTTTGGCCAATTGA 235
             || ||||||| |||  |||||| | || |||||| ||||   || ||||| | |||
Db       110 TCCATGTGGATATGGCAAAGAAGGAGACGGTCTGGCGGCTTGAAGAATTTGGACGATTTG 169

Qy       236 TACTCTTTGAGCCCCAAGGTGGACTGCAAAACATAGCTGCAGAAAAACACAACTTGGGAA 295
             |||||||| | ||||||| | ||   |||||||||| || |||  |||||||| ||
Db       170 CCAGCTTTGAGGCTCAAGGTGCATTGGCCAACATAGCTGTGGACAAAGCCAACTTGGAAA 229

Qy       296 TCTTGACTAAGAGGTCAAATTTCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGT 355
             || |||| ||| | || || |  || ||    |||||||   ||||  | |  ||||||
Db       230 TCATGACAAAGCGCTCCAACTATACTCCGATCACCAATGTACCTCCAGAGGTAACTGTGC 289

Qy       356 TCCCCAAGTCCCCTGTGCTGCTGGGTCAGCCCAACACCCTTATCTGCTTTGTGGACAACA 415
             || | ||   |||||||   ||| |  |||||||  ||| |||||  ||  | |||||
Db       290 TCACGAACAGCCCTGTGGAACTGAGAGAGCCCAACGTCCTCATCTGTTTCATAGACAAGT 349

Qy       416 TCTTCCCACCTGTGATCAACATCACATGGCTCAGAAATAGCAAGTCAGTCACAGACGGCG 475
             ||  |||||| ||| ||||  |||| |||||  |||||  | ||  | |||||    || |
Db       350 TCACCCCACCAGTGGTCAATGTCACGTGGCTTCGAAATGGAAAACCTGTCACCACAGGAG 409

Qy       476 TTTATGAGACCAGCTTCCTCGTCAACCGTGACCATTCCTTCCACAAGCTGTCTTATCTCA 535
             | |  |||||   ||||||   ||      |||||    |||| |||| |    ||||||
Db       410 TGTCAGAGACAGTCTTCCTGCCCAGGGAAGACCACCTTTTCCGCAAGTTCCACTATCTCC 469

Qy       536 CCTTCATCCCTTCTGATGATGACATTTATGACTGCAAGGTGGAGCACTGGGGCCTGGAGG 595
             ||||| | || ||   ||| ||| |||| ||||||| ||||||||||||||| |||| |
Db       470 CCTTCCTGCCCTCAACTGAGGACGTTTACGACTGCAGGGTGGAGCACTGGGGCTTGGATG 529

Qy       596 AGCCGGTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAAA 655
             ||||  |||| || ||||||||   |||   ||||  |||  |  |||||   |||||
Db       530 AGCCTCTTCTCAAGCACTGGGAGTTTGATGCTCCAAGCCCTCTCCCAGAGACTACAGAGG 589

Qy       656 CTGGAGGTGGAGGATCCACT--------------ACAGCTCCATCAGCTCAGCTCGAAA 700
             |  || || ||   |  |                 |||    ||| ||| || |||
Db       590 TCGACGGAGGTGGCGGCGGTTTAACTGATACACTCCAAGCGGAGACAGATCAACTTGAAG 649

Qy       701 AAGAGCTCCAGGCCCTGGAGAAGGAAAATGCACAGCTGGAATGGGAGTTGCAAGCACTGG 760
             | |||      ||  || ||| || | |||  | ||      |||  | ||  |||||
Db       650 ACGAGAAGTCTGCGTTGCAGACCGAGATTGCCAATCTACTGAAAGAGAAGGAAAAACTGG 709

Qy       761 AAAAGGAACTG---GCTCAGGCAGCATCTGAGCCCAGAGGGCCCACAATCAAGCCCTGTC 817
             |       |||   || || ||||||||||||||||||||||||||||||||||||||||
Db       710 AGTTCATCCTGGCCGCCCATGCAGCATCTGAGCCCAGAGGGCCCACAATCAAGCCCTGTC 769

Qy       818 CTCCATGCAAATGCCCAGCACCTAACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCTC 877
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      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  770 CTCCATGCAAATGCCCAGCACCTAACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCTC 829

  878 CAAAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCATAGTCACATGTGTGGTGGTGG 937
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  830 CAAAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCATAGTCACATGTGTGGTGGTGG 889

  938 ATGTGAGCGAGGATGACCCAGATGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTAC 997
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  890 ATGTGAGCGAGGATGACCCAGATGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTAC 949

  998 ACACAGCTCAGACACAAACCCATAGAGAGGATTACAACAGTACTCTCCGGGTGGTCAGTG 1057
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  950 ACACAGCTCAGACACAAACCCATAGAGAGGATTACAACAGTACTCTCCGGGTGGTCAGTG 1009

 1058 CCCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACA 1117
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1010 CCCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACA 1069

 1118 ACAAAGACCTCCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGGTCAGTAAGAG 1177
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1070 ACAAAGACCTCCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGGTCAGTAAGAG 1129

 1178 CTCCACAGGTATATGTCTTGCCTCCACCAGAAGAAGAGATGACTAAGAAACAGGTCACTC 1237
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1130 CTCCACAGGTATATGTCTTGCCTCCACCAGAAGAAGAGATGACTAAGAAACAGGTCACTC 1189

 1238 TGACCTGCATGGTCACAGACTTCATGCCTGAAGACATTTACGTGGAGTGGACCAACAACG 1297
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1190 TGACCTGCATGGTCACAGACTTCATGCCTGAAGACATTTACGTGGAGTGGACCAACAACG 1249

 1298 GGAAAACAGAGCTAAACTACAAGAACACTGAACCAGTCCTGGACTCTGATGGTTCTTACT 1357
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1250 GGAAAACAGAGCTAAACTACAAGAACACTGAACCAGTCCTGGACTCTGATGGTTCTTACT 1309

 1358 TCATGTACAGCAAGCTGAGAGTGGAAAAGAAGAACTGGGTGGAAAGAAATAGCTACTCCT 1417
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1310 TCATGTACAGCAAGCTGAGAGTGGAAAAGAAGAACTGGGTGGAAAGAAATAGCTACTCCT 1369

 1418 GTTCAGTGGTCCACGAGGGTCTGCACAATCACCACACGACTAAGAGCTTCTCCCGGACTC 1477
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1370 GTTCAGTGGTCCACGAGGGTCTGCACAATCACCACACGACTAAGAGCTTCTCCCGGACTC 1429

 1478 CGGGTAAA 1485
      ||||||||
 1430 CGGGTAAA 1437
```

LT 5
4282
ADW44282 standard; DNA; 1446 BP.

ADW44282;

24-MAR-2005 (first entry)

DR2-IgG fusion protein encoding DNA.

Major histocompatibility complex; fusion protein; immunoconjugate; adoptive immunotherapy; dermatological; immunosuppressive; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; autoimmune diseases; pemphigus vulgaris; rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus; immune disorder; DR2-IgG protein; gene; ds.

Homo sapiens.
Chimeric.
Unidentified.

Key	Location/Qualifiers
CDS	1. .1440
	/*tag= b
	/product= "DR2-IgG fusion protein"
	/partial
FT	/note= "No start codon"
FT misc_feature	1. .15
FT	/*tag= a
FT	/note= "3' end of secretory signal"
FT misc_feature	16. .588
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FT	/note= "DRA*0101extracellular domain"
FT misc_feature	589. .609
FT	/*tag= d
FT	/note= "Linker sequence"
FT misc_feature	610. .729
FT	/*tag= e
FT	/note= "Fos Leucine zipper domain"
FT misc_feature	730. .1437
FT	/*tag= f
FT	/note= "IgG domain"

XX
PN US2005003431-A1.
XX
PD 06-JAN-2005.
XX
PF 21-JUL-2004; 2004US-00895543.
XX
PR 16-AUG-1996; 96US-0024077P.
PR 15-AUG-1997; 97WO-US014503.
PR 19-FEB-1998; 98US-0075351P.
PR 12-FEB-1999; 99US-00248964.
XX
PA (WUCH/) WUCHERPFENNIG K W.
PA (STRO/) STROMINGER J L.
XX
PI Wucherpfennig KW, Strominger JL;
XX
DR WPI; 2005-089945/10.
DR P-PSDB; ADW44283.
XX
PT Novel class II major histocompatibility complex (MHC) fusion protein
PT having MHC class II binding domain of MHC class II alpha chain, and
PT dimerization domain, useful for treating pemphigus vulgaris, rheumatoid
PT arthritis.
XX
PS Example; SEQ ID NO 11; 55pp; English.
XX
CC The present invention relates to the class II major histocompatibility
CC complex (MHC) fusion protein having MHC class II binding domain of MHC
CC class II alpha chain and a dimerization domain. The invention is useful
CC in adoptive immunotherapy and tolerizing against foreign tissue. The
CC invention is also useful for treating autoimmune diseases such as
CC pemphigus vulgaris, rheumatoid arthritis, multiple sclerosis and systemic
CC lupus erythematosus. The present sequence is the DR2-IgG fusion protein
CC encoding DNA.
XX
SQ Sequence 1446 BP; 414 A; 375 C; 356 G; 301 T; 0 U; 0 Other;

Query Match 64.5%; Score 957.6; DB 14; Length 1446;
Best Local Similarity 81.8%; Pred. No. 1.2e-247;
Matches 1136; Conservative 0; Mismatches 234; Indels 18; Gaps 2;

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Qy       116 TTTATCAGTCTCCTGGAGACATTGGCCAGTACACACATGAATTTGATGGTGATGAGTTGT 175
             | |||| |  |||||   |    ||| |||  |    ||| ||||||||||||||| | |
Db        50 TCTATCTGAATCCTGACCAATCAGGCGAGTTTATGTTTGACTTTGATGGTGATGAGATTT 109

Qy       176 TCTATGTGGACTTGGATAAGAAGAAAACTGTCTGGAGGCTTCCTGAGTTTGGCCAATTGA 235
             || |||||||  |||  ||||||  | ||  ||||||  |||||    ||  |||||  | |||
Db       110 TCCATGTGGATATGGCAAAGAAGGAGACGGTCTGGCGGCTTGAAGAATTTGGACGATTTG 169

Qy       236 TACTCTTTGAGCCCCAAGGTGGACTGCAAAACATAGCTGCAGAAAAACACAACTTGGGAA 295
               |||||||  | |||||||  | ||   ||||||||||   ||  |||  ||||||||  ||
Db       170 CCAGCTTTGAGGCTCAAGGTGCATTGGCCAACATAGCTGTGGACAAAGCCAACTTGGAAA 229

Qy       296 TCTTGACTAAGAGGTCAAATTTCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGT 355
             ||  ||||  |||  |  ||  ||  |  ||  ||     |||||||    ||||   |  |  ||||||
Db       230 TCATGACAAAGCGCTCCAACTATACTCCGATCACCAATGTACCTCCAGAGGTAACTGTGC 289
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 356 TCCCCAAGTCCCCTGTGCTGCTGGGTCAGCCCAACACCCTTATCTGCTTTGTGGACAACA 415
     || | ||   |||||||   ||| |  ||||||||  ||| |||||  ||  | |||||
 290 TCACGAACAGCCCTGTGGAACTGAGAGAGCCCAACGTCCTCATCTGTTTCATAGACAAGT 349

 416 TCTTCCCACCTGTGATCAACATCACATGGCTCAGAAATAGCAAGTCAGTCACAGACGGCG 475
     ||  |||||| ||| ||||  |||| |||||  |||||  | ||  | |||||    || |
 350 TCACCCCACCAGTGGTCAATGTCACGTGGCTTCGAAATGGAAAACCTGTCACCACAGGAG 409

 476 TTTATGAGACCAGCTTCCTCGTCAACCGTGACCATTCCTTCCACAAGCTGTCTTATCTCA 535
     | |  |||||   ||||||   ||      |||||    |||| ||||  |    ||||||
 410 TGTCAGAGACAGTCTTCCTGCCCAGGGAAGACCACCTTTTCCGCAAGTTCCACTATCTCC 469

 536 CCTTCATCCCTTCTGATGATGACATTTATGACTGCAAGGTGGAGCACTGGGGCCTGGAGG 595
     |||||  | ||  ||   ||| |||  |||| |||||||  |||||||||||||||  |||| |
 470 CCTTCCTGCCCTCAACTGAGGACGTTTACGACTGCAGGGTGGAGCACTGGGGCTTGGATG 529

 596 AGCCGGTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAAA 655
     ||||  ||||  ||  |||||||||   |||   ||||  |||  |  |||||   |||||
 530 AGCCTCTTCTCAAGCACTGGGAGTTTGATGCTCCAAGCCCTCTCCCAGAGACTACAGAGG 589

 656 CTGGAGGTGGAGGATCCACT----------------ACAGCTCCATCAGCTCAGCTCGAAA 700
     |  || || ||   |  |                   |||     ||| ||| ||  |||
 590 TCGACGGAGGTGGCGGCGGTTTAACTGATACACTCCAAGCGGAGACAGATCAACTTGAAG 649

 701 AAGAGCTCCAGGCCCTGGAGAAGGAAAATGCACAGCTGGAATGGGAGTTGCAAGCACTGG 760
     | |||      ||  || |||  || | |||  | ||       |||  | ||  |||||
 650 ACGAGAAGTCTGCGTTGCAGACCGAGATTGCCAATCTACTGAAAGAGAAGGAAAAACTGG 709

 761 AAAAGGAACTG---GCTCAGGCAGCATCTGAGCCCAGAGGGCCCACAATCAAGCCCTGTC 817
     |       |||   || || ||||||||||||||||||||||||||||||||||||||||||
 710 AGTTCATCCTGGCCGCCCATGCAGCATCTGAGCCCAGAGGGCCCACAATCAAGCCCTGTC 769

 818 CTCCATGCAAATGCCCAGCACCTAACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCTC 877
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 770 CTCCATGCAAATGCCCAGCACCTAACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCTC 829

 878 CAAAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCATAGTCACATGTGTGGTGGTGG 937
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 830 CAAAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCATAGTCACATGTGTGGTGGTGG 889

 938 ATGTGAGCGAGGATGACCCAGATGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTAC 997
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 890 ATGTGAGCGAGGATGACCCAGATGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTAC 949

 998 ACACAGCTCAGACACAAACCCATAGAGAGGATTACAACAGTACTCTCCGGGTGGTCAGTG 1057
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 950 ACACAGCTCAGACACAAACCCATAGAGAGGATTACAACAGTACTCTCCGGGTGGTCAGTG 1009

1058 CCCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACA 1117
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1010 CCCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACA 1069

1118 ACAAAGACCTCCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGGTCAGTAAGAG 1177
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1070 ACAAAGACCTCCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGGTCAGTAAGAG 1129

1178 CTCCACAGGTATATGTCTTGCCTCCACCAGAAGAAGAGATGACTAAGAAACAGGTCACTC 1237
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1130 CTCCACAGGTATATGTCTTGCCTCCACCAGAAGAAGAGATGACTAAGAAACAGGTCACTC 1189

1238 TGACCTGCATGGTCACAGACTTCATGCCTGAAGACATTTACGTGGAGTGGACCAACAACG 1297
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1190 TGACCTGCATGGTCACAGACTTCATGCCTGAAGACATTTACGTGGAGTGGACCAACAACG 1249

1298 GGAAAACAGAGCTAAACTACAAGAACACTGAACCAGTCCTGGACTCTGATGGTTCTTACT 1357
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1250 GGAAAACAGAGCTAAACTACAAGAACACTGAACCAGTCCTGGACTCTGATGGTTCTTACT 1309

1358 TCATGTACAGCAAGCTGAGAGTGGAAAAGAAGAACTGGGTGGAAAGAAATAGCTACTCCT 1417
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1310 TCATGTACAGCAAGCTGAGAGTGGAAAAGAAGAACTGGGTGGAAAGAAATAGCTACTCCT 1369
```

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Qy       1418 GTTCAGTGGTCCACGAGGGTCTGCACAATCACCACACGACTAAGAGCTTCTCCCGGACTC 1477
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1370 GTTCAGTGGTCCACGAGGGTCTGCACAATCACCACACGACTAAGAGCTTCTCCCGGACTC 1429

Qy       1478 CGGGTAAA 1485
              ||||||||
Db       1430 CGGGTAAA 1437
```

RESULT 6
ABI99027
ID ABI99027 standard; cDNA; 2346 BP.
XX
AC ABI99027;
XX
DT 25-FEB-2002 (first entry)
XX
DE IAS MBP 1-14 CH1.CH2.CH3 coding sequence.
XX
KW Mouse; MHC; major histocompatibility complex; MHC class II; multimer;
KW single chain; immunosuppressive; antidiabetic; antiinflammatory;
KW antianaemic; antirheumatoid; antiarthritic; neuroprotective; vaccine;
KW autoimmune disease; insulin dependent diabetes; multiple sclerosis;
KW myasthenia gravis; pernicious anaemia; autoimmune encephalomyelitis;
KW rheumatoid arthritis; systemic lupus erythematosus; ss.
XX
OS Mus sp.
OS Synthetic.
XX
PN WO200170245-A1.
XX
PD 27-SEP-2001.
XX
PF 22-MAR-2001; 2001WO-US009616.
XX
PR 22-MAR-2000; 2000US-0191274P.
PR 15-MAY-2000; 2000US-0204249P.
PR 23-JAN-2001; 2001US-0264003P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Carter D, Zhu S, Arimilli S, Wang A;
XX
DR WPI; 2001-616371/71.
DR P-PSDB; ABB56457.
XX
PT Multimeric complex for treating autoimmune diseases, comprises first and
PT second single chain MHC class II molecules, each comprising alpha1 and
PT beta1 domain linked through amino acid linker and multimerization domain.
XX
PS Disclosure; Page 91-92; 147pp; English.
XX
CC The invention relates to a multimeric complex comprising a first
CC recombinant single chain major histocompatibility complex (MHC) class II
CC molecule and a second recombinant single chain MHC class II molecule,
CC each comprising an alpha1 domain and a beta1 domain linked through an
CC amino acid linker and a multimerisation domain. The first and the second
CC molecule are linked through the multimerisation domain to form a
CC multimeric complex,. The complex is useful for treating autoimmune
CC diseases. It is useful for treating insulin dependent diabetes, multiple
CC sclerosis, myasthenia gravis, pernicious anaemia, autoimmune
CC encephalomyelitis (EAE), rheumatoid arthritis and systemic lupus
CC erythematosus. The present sequence encodes a single chain MHC class II
CC molecule of the invention
XX
SQ Sequence 2346 BP; 560 A; 663 C; 646 G; 477 T; 0 U; 0 Other;

  Query Match   48.9%; Score 726.2; DB 4; Length 2346;
  Best Local Similarity 70.5%; Pred. No. 4.1e-185;
  Matches 1095; Conservative   0; Mismatches 323; Indels 135; Gaps   4;

```
Qy         68 GTGAAGACGACATTGAGGCCGACCACGTAGGCTTCTATGGTACAACTGTTTATCAGTCTC 127
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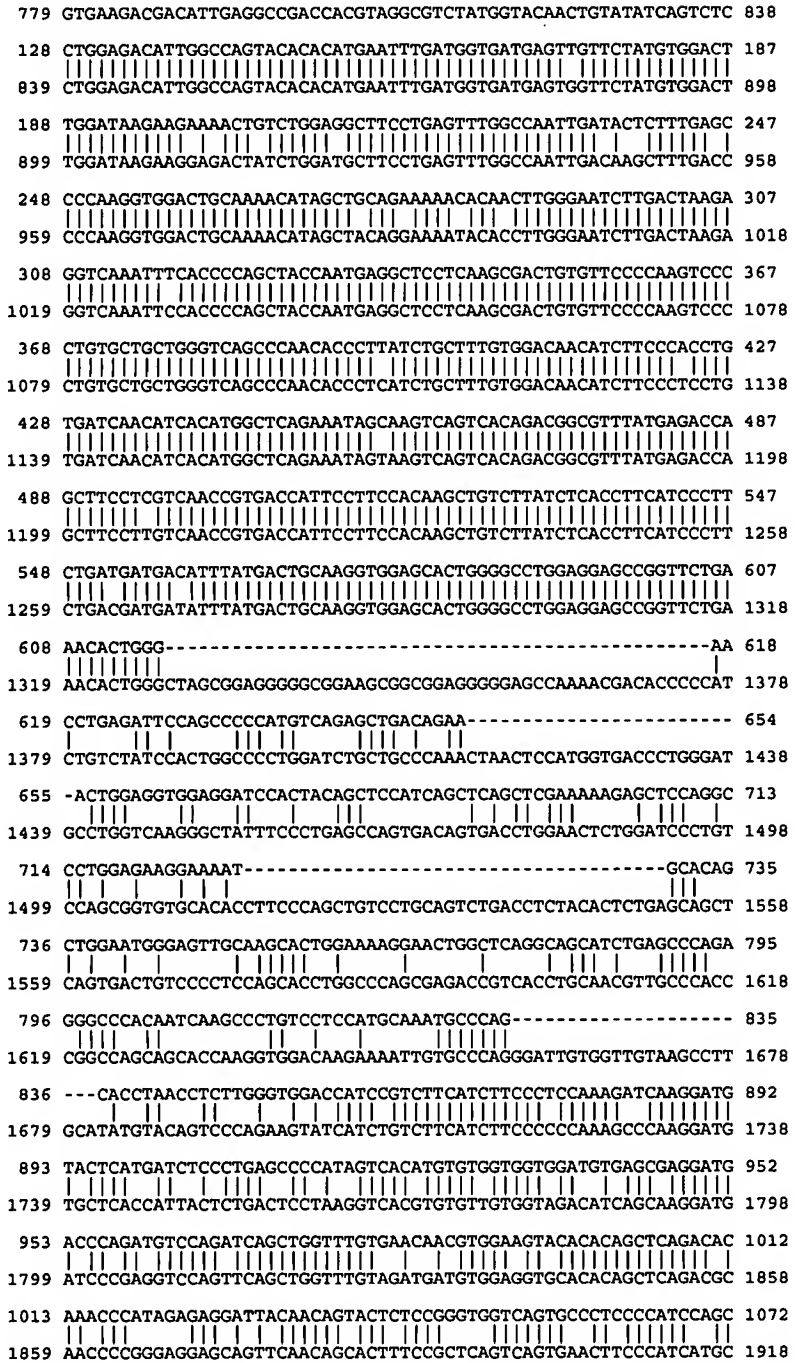

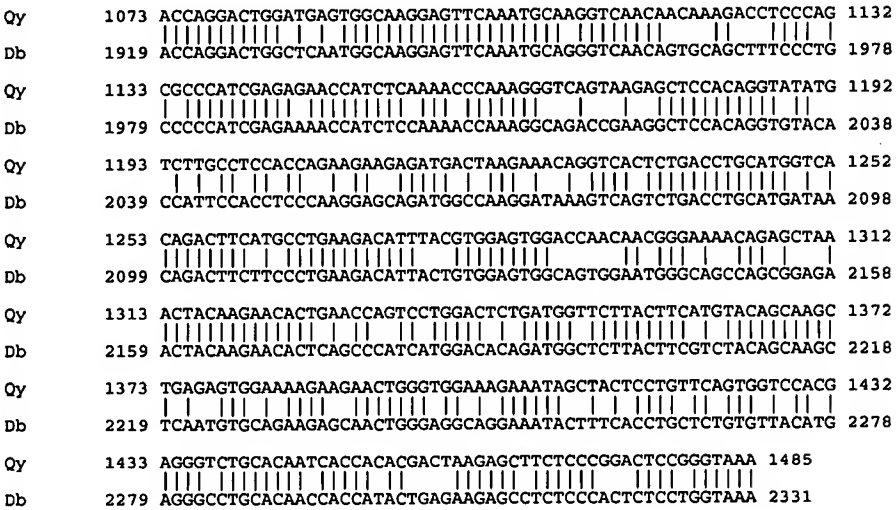

RESULT 7
ABI99033
ID ABI99033 standard; cDNA; 2343 BP.
XX
AC ABI99033;
XX
DT 25-FEB-2002 (first entry)
XX
DE MBP 90-101 CH1.H.CH2.CH3 coding sequence.
XX
KW Mouse; MHC; major histocompatibility complex; MHC class II; multimer;
KW single chain; immunosuppressive; antidiabetic; antiinflammatory;
KW antianaemic; antirheumatoid; antiarthritic; neuroprotective; vaccine;
KW autoimmune disease; insulin dependent diabetes; multiple sclerosis;
KW myasthenia gravis; pernicious anaemia; autoimmune encephalomyelitis;
KW rheumatoid arthritis; systemic lupus erythematosus; ss.
XX
OS Mus sp.
OS Synthetic.
XX
PN WO200170245-A1.
XX
PD 27-SEP-2001.
XX
PF 22-MAR-2001; 2001WO-US009616.
XX
PR 22-MAR-2000; 2000US-0191274P.
PR 15-MAY-2000; 2000US-0204249P.
PR 23-JAN-2001; 2001US-0264003P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Carter D, Zhu S, Arimilli S, Wang A;
XX
DR WPI; 2001-616371/71.
DR P-PSDB; ABB56463.
XX
PT Multimeric complex for treating autoimmune diseases, comprises first and
PT second single chain MHC class II molecules, each comprising alpha1 and
PT beta1 domain linked through amino acid linker and multimerization domain.
XX
PS Disclosure; Page 96; 147pp; English.
XX

The invention relates to a multimeric complex comprising a first recombinant single chain major histocompatibility complex (MHC) class II molecule and a second recombinant single chain MHC class II molecule, each comprising an alpha1 domain and a beta1 domain linked through an amino acid linker and a multimerisation domain. The first and the second molecule are linked through the multimerisation domain to form a multimeric complex,. The complex is useful for treating autoimmune diseases. It is useful for treating insulin dependent diabetes, multiple sclerosis, myasthenia gravis, pernicious anaemia, autoimmune encephalomyelitis (EAE), rheumatoid arthritis and systemic lupus erythematosus. The present sequence encodes a single chain MHC class II molecule of the invention

Sequence 2343 BP; 562 A; 665 C; 635 G; 481 T; 0 U; 0 Other;

Query Match 48.7%; Score 723.2; DB 4; Length 2343;
Best Local Similarity 70.4%; Pred. No. 2.6e-184;
Matches 1095; Conservative 0; Mismatches 323; Indels 138; Gaps 4;

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Qy        68 GTGAAGACGACATTGAGGCCGACCACGTAGGCTTCTATGGTACAACTGTTTATCAGTCTC 127
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Db       773 GTGAAGACGACATTGAGGCCGACCACGTAGGCGTCTATGGTACAACTGTATATCAGTCTC 832

Qy       128 CTGGAGACATTGGCCAGTACACACATGAATTTGATGGTGATGAGTTGTTCTATGTGGACT 187
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db       833 CTGGAGACATTGGCCAGTACACACATGAATTTGATGGTGATGAGTGGTTCTATGTGGACT 892

Qy       188 TGGATAAGAAGAAAACTGTCTGGAGGCTTCCTGAGTTTGGCCAATTGATACTCTTTGAGC 247
             |||||||||||| | ||| |||||| |||||||||||||||||||||||| | |||||| |
Db       893 TGGATAAGAAGGAGACTATCTGGATGCTTCCTGAGTTTGGCCAATTGACAAGCTTTGACC 952

Qy       248 CCCAAGGTGGACTGCAAAACATAGCTGCAGAAAAACACAACTTGGGAATCTTGACTAAGA 307
             |||||||||||||||||||||||||| ||| |||| ||| ||||||||||||||||||||
Db       953 CCCAAGGTGGACTGCAAAACATAGCTACAGGAAAATACACCTTGGGAATCTTGACTAAGA 1012

Qy       308 GGTCAAATTTCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGTTCCCCAAGTCCC 367
             ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1013 GGTCAAATTCCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGTTCCCCAAGTCCC 1072

Qy       368 CTGTGCTGCTGGGTCAGCCCAACACCCTTATCTGCTTTGTGGACAACATCTTCCCACCTG 427
             |||||||||||||||||||||||||||||||| |||||||||||||||||||||||| ||||
Db      1073 CTGTGCTGCTGGGTCAGCCCAACACCCTCATCTGCTTTGTGGACAACATCTTCCCTCCTG 1132

Qy       428 TGATCAACATCACATGGCTCAGAAATAGCAAGTCAGTCACAGACGGCGTTTATGAGACCA 487
             |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db      1133 TGATCAACATCACATGGCTCAGAAATAGTAAGTCAGTCACAGACGGCGTTTATGAGACCA 1192

Qy       488 GCTTCCTCGTCAACCGTGACCATTCCTTCCACAAGCTGTCTTATCTCACCTTCATCCCTT 547
             ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1193 GCTTCCTTGTCAACCGTGACCATTCCTTCCACAAGCTGTCTTATCTCACCTTCATCCCTT 1252

Qy       548 CTGATGATGACATTTATGACTGCAAGGTGGAGCACTGGGGCCTGGAGGAGCCGGTTCTGA 607
             |||| ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1253 CTGACGATGATATTTATGACTGCAAGGTGGAGCACTGGGGCCTGGAGGAGCCGGTTCTGA 1312

Qy       608 AACACTGGG---------------------------------------------------- 616
             |||||||||
Db      1313 AACACTGGGCTAGCGGAGGGGGCGGAAGCGGCGGAGGAAGCTTAGCCAAAACGACACCCC 1372

Qy       617 -AACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAA---------------------- 654
              | |      || |      ||| ||      |||| |  ||
Db      1373 CATCTGTCTATCCACTGGCCCCTGGATCTGCTGCCCAAACTAACTCCATGGTGACCCTGG 1432

Qy       655 ----ACTGGAGGTGGAGGATCCACTACAGCTCCATCAGCTCAGCTCGAAAAAGAGCTCCA 710
                 ||||     ||   ||   |   |||          | | || |||      | |||
Db      1433 GATGCCTGGTCAAGGGCTATTTCCCTGAGCCAGTGACAGTGACCTGGAACTCTGGATCCC 1492

Qy       711 GGCCCTGGAGAAGGAAAAT-----------------------------------------GCA 732
              | || |  |   | | |                                           |||
Db      1493 TGTCCAGCGGTGTGCACACCTTCCCAGCTGTCCTGCAGTCTGACCTCTACACTCTGAGCA 1552

Qy       733 CAGCTGGAATGGGAGTTGCAAGCACTGGAAAAGGAACTGGCTCAGGCAGCATCTGAGCCC 792
                | |  | |      | |||||  |      |      |      | ||| |   ||||
Db      1553 GCTCAGTGACTGTCCCCTCCAGCACCTGGCCCAGCGAGACCGTCACCTGCAACGTTGCCC 1612

Qy       793 AGAGGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCAG---------------- 835
             |  ||||  ||          ||  |   |      |||||||
Db      1613 ACCCGGCCAGCAGCACCAAGGTGGACAAGAAAATTGTGCCCAGGGATTGTGGTTGTAAGC 1672

Qy       836 ------CACCTAACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGG 889
                   |  ||   ||   |  | | |||| ||||||||||||||| ||||||  |||||
Db      1673 CTTGCATATGTACAGTCCCAGAAGTATCATCTGTCTTCATCTTCCCCCCAAAGCCCAAGG 1732

Qy       890 ATGTACTCATGATCTCCCTGAGCCCCATAGTCACATGTGTGGTGGTGGATGTGAGCGAGG 949
             |||| |||| ||  | |||| || | ||||| ||||| ||||| ||  | ||| |||
Db      1733 ATGTGCTCACCATTACTCTGACTCCTAAGGTCACGTGTGTTGTGGTAGACATCAGCAAGG 1792

Qy       950 ATGACCCAGATGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGA 1009
             |||| || || |||||| ||||||||||||||  |  | ||||| || ||||||||||||||
Db      1793 ATGATCCCGAGGTCCAGTTCAGCTGGTTTGTAGATGATGTGGAGGTGCACACAGCTCAGA 1852

Qy      1010 CACAAACCCATAGAGAGGATTACAACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCC 1069
             | ||| |||      ||| | | |||||| ||| ||||     |||||||  || ||||||
Db      1853 CGCAACCCCGGGAGGAGCAGTTCAACAGCACTTTCCGCTCAGTCAGTGAACTTCCCATCA 1912

Qy      1070 AGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAAGACCTCC 1129
             |||||||||||||  | | ||||||||||||||||||||| ||||||||    ||  |||
Db      1913 TGCACCAGGACTGGCTCAATGGCAAGGAGTTCAAATGCAGGGTCAACAGTGCAGCTTTCC 1972

Qy      1130 CAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTAT 1189
             | || |||||||||| |||||||||| ||| |||||||    |    | |||||||||||  |
Db      1973 CTGCCCCCATCGAGAAAACCATCTCCAAAACCAAAGGCAGACCGAAGGCTCCACAGGTGT 2032

Qy      1190 ATGTCTTGCCTCCACCAGAAGAAGAGATGACTAAGAAACAGGTCACTCTGACCTGCATGG 1249
             |   | | || || ||  | ||  ||||| | ||| |   | |||| ||||||||||||
Db      2033 ACACCATTCCACCTCCCAAGGAGCAGATGGCCAAGGATAAAGTCAGTCTGACCTGCATGA 2092

Qy      1250 TCACAGACTTCATGCCTGAAGACATTTACGTGGAGTGGACCAACAACGGGAAAACAGAGC 1309
             | ||||||||| | ||||||||||||    |||||||||      || ||| |   ||| |
Db      2093 TAACAGACTTCTTCCCTGAAGACATTACTGTGGAGTGGCAGTGGAATGGGCAGCCAGCGG 2152

Qy      1310 TAAACTACAAGAACACTGAACCAGTCCTGGACTCTGATGGTTCTTACTTCATGTACAGCA 1369
               |||||||||||||| | ||  || ||||| | ||||| ||||||||| | |||||||
Db      2153 AGAACTACAAGAACACTCAGCCCATCATGGACACAGATGGCTCTTACTTCGTCTACAGCA 2212

Qy      1370 AGCTGAGAGTGGAAAAGAAGAACTGGGTGGAAAGAAATAGCTACTCCTGTTCAGTGGTCC 1429
             |||| |  ||| | ||||  ||||||| || | |||||   | | |||| || ||| | |
Db      2213 AGCTCAATGTGCAGAAGAGCAACTGGGAGGCAGGAAATACTTTCACCTGCTCTGTGTTAC 2272

Qy      1430 ACGAGGGTCTGCACAATCACCACACGACTAAGAGCTTCTCCCGGACTCCGGGTAAA 1485
             | ||||| |||||||| ||||| ||     |||||| ||||||    |||| ||||||
Db      2273 ATGAGGGCCTGCACAACCACCATACTGAGAAGAGCCTCTCCCACTCTCCTGGTAAA 2328
```

RESULT 8
ADO07566
ID ADO07566 standard; DNA; 1045 BP.
XX
AC ADO07566;
XX
DT 15-JUL-2004 (first entry)
XX
DE Fusion protein WT-IL-15-mIgG2a coding sequence.
XX
KW immunosuppressive; antirheumatic; antiarthritic; antidiabetic;
KW neuroprotective; antipsoriatic; dermatological; antiinflammatory;
KW cytostatic; interleukin-15; immunoglobulin G; ds; gene.
XX
OS Synthetic.
OS Unidentified.
XX

FH	Key	Location/Qualifiers
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FT		/product= "WT-IL-15-mIgG2a"
FT		/transl_except

/note= "(pos: 34. .36, aa: Thr"
/partial
/note= "no start codon"

WO2004035622-A2.

29-APR-2004.

13-OCT-2003; 2003WO-CH000666.

14-OCT-2002; 2002EP-00022869.

(HOFF) HOFFMANN LA ROCHE & CO AG F.

Dreher I, Moll T;

WPI; 2004-357203/33.
P-PSDB; ADO07559.

New fusion protein of interleukin-15 and Fc fragment, useful for treating e.g. transplantation disorders, autoimmune diseases and tumors, also related nucleic acid.

Disclosure; Fig 5; 63pp; German.

The present invention relates to a fusion protein consisting of wild-type interleukin-15 (IL-15) and an immunoglobulin G (IgG) Fc fragment, other than a murine IgG2b Fc fragment. The fusion proteins and coding sequences are used to prevent or treat consequences of transplantation and/or autoimmune diseases, e.g. rheumatoid arthritis, diabetes, multiple sclerosis, psoriasis, neurodermatitis, ulcerative colitis, tumours and AIDS, etc., and tissues or organs that express the protein are useful for transplantation into humans or other mammals, as allo-, auto- or xeno-transplants. Also transgenic animals that express the fusion proteins are useful as source of cells, tissues and organs for transplantation or to screen for pharmaceuticals and/or to identify toxic substances. The present sequence is a polypeptide coding sequence used in the exemplification of the invention.

Sequence 1045 BP; 331 A; 238 C; 235 G; 241 T; 0 U; 0 Other;

ery Match 47.2%; Score 701.2; DB 12; Length 1045;
st Local Similarity 93.3%; Pred. No. 1.6e-178;
tches 733; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

```
Qy       700 AAAGAGCTCCAGGCCCTGGAGAAGGAAAATGCACAGCTGGAATGGGAGTTGCAAGCACTG 759
            |||||     |||  |||||| |  |||||     |       | | ||       | ||
Db       256 AAAGAATGTGAGGAACTGGAGGAAAAAAATATTAAAGAATTTTTGCAGAGTTTTGTACAT 315

Qy       760 GAAAAGGAACTGGCTCAGGCAGCATCTGAGCCCAGAGGGCCCACAATCAAGCCCTGTCCT 819
                 || ||      | || || ||||||||||||||||||||||||||||||||
Db       316 ATTGTCCAAATGTTCATCAACACTTCGGATCCCAGAGGGCCCACAATCAAGCCCTGTCCT 375

Qy       820 CCATGCAAATGCCCAGCACCTAACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCTCCA 879
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       376 CCATGCAAATGCCCAGCACCTAACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCTCCA 435

Qy       880 AAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCATAGTCACATGTGTGGTGGTGGAT 939
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       436 AAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCATAGTCACATGTGTGGTGGTGGAT 495

Qy       940 GTGAGCGAGGATGACCCAGATGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTACAC 999
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       496 GTGAGCGAGGATGACCCAGATGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTACAC 555

Qy      1000 ACAGCTCAGACACAAACCCATAGAGAGGATTACAACAGTACTCTCCGGGTGGTCAGTGCC 1059
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       556 ACAGCTCAGACACAAACCCATAGAGAGGATTACAACAGTACTCTCCGGGTGGTCAGTGCC 615

Qy      1060 CTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAAC 1119
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       616 CTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAAC 675

Qy      1120 AAAGACCTCCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGGTCAGTAAGAGCT 1179
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 AAAGACCTCCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGGTCAGTAAGAGCT 735

Qy      1180 CCACAGGTATATGTCTTGCCTCCACCAGAAGAAGAGATGACTAAGAAACAGGTCACTCTG 1239
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        736 CCACAGGTATATGTCTTGCCTCCACCAGAAGAAGAGATGACTAAGAAACAGGTCACTCTG 795

Qy      1240 ACCTGCATGGTCACAGACTTCATGCCTGAAGACATTTACGTGGAGTGGACCAACAACGGG 1299
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        796 ACCTGCATGGTCACAGACTTCATGCCTGAAGACATTTACGTGGAGTGGACCAACAACGGG 855

Qy      1300 AAAACAGAGCTAAACTACAAGAACACTGAACCAGTCCTGGACTCTGATGGTTCTTACTTC 1359
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        856 AAAACAGAGCTAAACTACAAGAACACTGAACCAGTCCTGGACTCTGATGGTTCTTACTTC 915

Qy      1360 ATGTACAGCAAGCTGAGAGTGGAAAAGAAGAACTGGGTGGAAAGAAATAGCTACTCCTGT 1419
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        916 ATGTACAGCAAGCTGAGAGTGGAAAAGAAGAACTGGGTGGAAAGAAATAGCTACTCCTGT 975

Qy      1420 TCAGTGGTCCACGAGGGTCTGCACAATCACCACACGACTAAGAGCTTCTCCCGGACTCCG 1479
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        976 TCAGTGGTCCACGAGGGTCTGCACAATCACCACACGACTAAGAGCTTCTCCCGGACTCCG 1035

Qy      1480 GGTAAA 1485
            ||||||
Db      1036 GGTAAA 1041
```

RESULT 9
ADO07578
ID ADO07578 standard; DNA; 1108 BP.
XX
AC ADO07578;
XX
DT 15-JUL-2004 (first entry)
XX
DE Fusion protein coding sequence fragment 149-Fc.
XX
KW immunosuppressive; antirheumatic; antiarthritic; antidiabetic;
KW neuroprotective; antipsoriatic; dermatological; antiinflammatory;
KW cytostatic; interleukin-15; immunoglobulin G; ds; gene; human.
XX
OS Synthetic.
OS Unidentified.
XX
PN WO2004035622-A2.
XX
PD 29-APR-2004.
XX
PF 13-OCT-2003; 2003WO-CH000666.
XX
PR 14-OCT-2002; 2002EP-00022869.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Dreher I, Moll T;
XX
DR WPI; 2004-357203/33.
XX
PT New fusion protein of interleukin-15 and Fc fragment, useful for treating
PT e.g. transplantation disorders, autoimmune diseases and tumors, also
PT related nucleic acid.
XX
PS Disclosure; Fig 11; 63pp; German.
XX
CC The present invention relates to a fusion protein consisting of wild-type
CC interleukin-15 (IL-15) and an immunoglobulin G (IgG) Fc fragment, other
CC than a murine IgG2b Fc fragment. The fusion proteins and coding sequences
CC are used to prevent or treat consequences of transplantation and/or
CC autoimmune diseases, e.g. rheumatoid arthritis, diabetes, multiple
CC sclerosis, psoriasis, neurodermatitis, ulcerative colitis, tumours and
CC AIDS, etc., and tissues or organs that express the protein are useful for

transplantation into humans or other mammals, as allo-, auto- or xeno-transplants. Also transgenic animals that express the fusion proteins are useful as source of cells, tissues and organs for transplantation or to screen for pharmaceuticals and/or to identify toxic substances. The present sequence is a coding sequence used in the exemplification of the invention.

Sequence 1108 BP; 343 A; 255 C; 253 G; 257 T; 0 U; 0 Other;

Query Match 47.2%; Score 701.2; DB 12; Length 1108;
Best Local Similarity 93.3%; Pred. No. 1.7e-178;
Matches 733; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

```
Qy        700 AAAGAGCTCCAGGCCCTGGAGAAGGAAAATGCACAGCTGGAATGGGAGTTGCAAGCACTG 759
              |||||     |||  ||||||  |  |||||     |       | |||       | ||
Db        319 AAAGAATGTGAGGAACTGGAGGAAAAAAATATTAAAGAATTTTTGGACAGTTTTGTACAT 378

Qy        760 GAAAAGGAACTGGCTCAGGCAGCATCTGAGCCCAGAGGGCCCACAATCAAGCCCTGTCCT 819
                  ||  ||          |  ||  || ||||||||||||||||||||||||||||||
Db        379 ATTGTCCAAATGTTCATCAACACTTCGGATCCCAGAGGGCCCACAATCAAGCCCTGTCCT 438

Qy        820 CCATGCAAATGCCCAGCACCTAACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCTCCA 879
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 CCATGCAAATGCCCAGCACCTAACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCTCCA 498

Qy        880 AAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCATAGTCACATGTGTGGTGGTGGAT 939
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 AAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCATAGTCACATGTGTGGTGGTGGAT 558

Qy        940 GTGAGCGAGGATGACCCAGATGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTACAC 999
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 GTGAGCGAGGATGACCCAGATGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTACAC 618

Qy       1000 ACAGCTCAGACACAAACCCATAGAGAGGATTACAACAGTACTCTCCGGGTGGTCAGTGCC 1059
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 ACAGCTCAGACACAAACCCATAGAGAGGATTACAACAGTACTCTCCGGGTGGTCAGTGCC 678

Qy       1060 CTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAAC 1119
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        679 CTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAAC 738

Qy       1120 AAAGACCTCCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGGTCAGTAAGAGCT 1179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 AAAGACCTCCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGGTCAGTAAGAGCT 798

Qy       1180 CCACAGGTATATGTCTTGCCTCCACCAGAAGAAGAGATGACTAAGAAACAGGTCACTCTG 1239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 CCACAGGTATATGTCTTGCCTCCACCAGAAGAAGAGATGACTAAGAAACAGGTCACTCTG 858

Qy       1240 ACCTGCATGGTCACAGACTTCATGCCTGAAGACATTTACGTGGAGTGGACCAACAACGGG 1299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 ACCTGCATGGTCACAGACTTCATGCCTGAAGACATTTACGTGGAGTGGACCAACAACGGG 918

Qy       1300 AAAACAGAGCTAAACTACAAGAACACTGAACCAGTCCTGGACTCTGATGGTTCTTACTTC 1359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 AAAACAGAGCTAAACTACAAGAACACTGAACCAGTCCTGGACTCTGATGGTTCTTACTTC 978

Qy       1360 ATGTACAGCAAGCTGAGAGTGGAAAAGAAGAACTGGGTGGAAAGAAATAGCTACTCCTGT 1419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        979 ATGTACAGCAAGCTGAGAGTGGAAAAGAAGAACTGGGTGGAAAGAAATAGCTACTCCTGT 1038

Qy       1420 TCAGTGGTCCACGAGGGTCTGCACAATCACCACACGACTAAGAGCTTCTCCCGGACTCCG 1479
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 TCAGTGGTCCACGAGGGTCTGCACAATCACCACACGACTAAGAGCTTCTCCCGGACTCCG 1098

Qy       1480 GGTAAA 1485
              ||||||
Db       1099 GGTAAA 1104
```

ULT 10
07577
ADO07577 standard; DNA; 1108 BP.

XX
AC ADO07577;
XX
DT 15-JUL-2004 (first entry)
XX
DE Fusion protein coding sequence fragment Igk8.
XX
KW immunosuppressive; antirheumatic; antiarthritic; antidiabetic;
KW neuroprotective; antipsoriatic; dermatological; antiinflammatory;
KW cytostatic; interleukin-15; immunoglobulin G; ds; gene.
XX
OS Synthetic.
OS Unidentified.
XX
PN WO2004035622-A2.
XX
PD 29-APR-2004.
XX
PF 13-OCT-2003; 2003WO-CH000666.
XX
PR 14-OCT-2002; 2002EP-00022869.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Dreher I, Moll T;
XX
DR WPI; 2004-357203/33.
XX
PT New fusion protein of interleukin-15 and Fc fragment, useful for treating
PT e.g. transplantation disorders, autoimmune diseases and tumors, also
PT related nucleic acid.
XX
PS Disclosure; Fig 10; 63pp; German.
XX
CC The present invention relates to a fusion protein consisting of wild-type
CC interleukin-15 (IL-15) and an immunoglobulin G (IgG) Fc fragment, other
CC than a murine IgG2b Fc fragment. The fusion proteins and coding sequences
CC are used to prevent or treat consequences of transplantation and/or
CC autoimmune diseases, e.g. rheumatoid arthritis, diabetes, multiple
CC sclerosis, psoriasis, neurodermatitis, ulcerative colitis, tumours and
CC AIDS, etc., and tissues or organs that express the protein are useful for
CC transplantation into humans or other mammals, as allo-, auto- or xeno-
CC transplants. Also transgenic animals that express the fusion proteins are
CC useful as source of cells, tissues and organs for transplantation or to
CC screen for pharmaceuticals and/or to identify toxic substances. The
CC present sequence is a coding sequence used in the exemplification of the
CC invention.
XX
SQ Sequence 1108 BP; 342 A; 255 C; 254 G; 257 T; 0 U; 0 Other;

Query Match 47.2%; Score 701.2; DB 12; Length 1108;
Best Local Similarity 93.3%; Pred. No. 1.7e-178;
Matches 733; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

Qy 700 AAAGAGCTCCAGGCCCTGGAGAAGGAAAATGCACAGCTGGAATGGGAGTTGCAAGCACTG 759
Db 319 AAAGAATGTGAGGAACTGGAGGAAAAAAATATTAAAGAATTTTTGGACAGTTTTGTACAT 378

Qy 760 GAAAAGGAACTGGCTCAGGCAGCATCTGAGCCCAGAGGGCCCACAATCAAGCCCTGTCCT 819
Db 379 ATTGTCGACATGTTCATCAACACTTCGGATCCCAGAGGGCCCACAATCAAGCCCTGTCCT 438

Qy 820 CCATGCAAATGCCCAGCACCTAACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCTCCA 879
Db 439 CCATGCAAATGCCCAGCACCTAACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCTCCA 498

Qy 880 AAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCATAGTCACATGTGTGGTGGTGGAT 939
Db 499 AAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCATAGTCACATGTGTGGTGGTGGAT 558

Qy 940 GTGAGCGAGGATGACCCAGATGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTACAC 999
Db 559 GTGAGCGAGGATGACCCAGATGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTACAC 618

```
1000 ACAGCTCAGACACAAACCCATAGAGAGGATTACAACAGTACTCTCCGGGTGGTCAGTGCC 1059
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 619 ACAGCTCAGACACAAACCCATAGAGAGGATTACAACAGTACTCTCCGGGTGGTCAGTGCC 678

1060 CTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAAC 1119
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 679 CTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAAC 738

1120 AAAGACCTCCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGGTCAGTAAGAGCT 1179
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 739 AAAGACCTCCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGGTCAGTAAGAGCT 798

1180 CCACAGGTATATGTCTTGCCTCCACCAGAAGAAGAGATGACTAAGAAACAGGTCACTCTG 1239
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 799 CCACAGGTATATGTCTTGCCTCCACCAGAAGAAGAGATGACTAAGAAACAGGTCACTCTG 858

1240 ACCTGCATGGTCACAGACTTCATGCCTGAAGACATTTACGTGGAGTGGACCAACAACGGG 1299
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 859 ACCTGCATGGTCACAGACTTCATGCCTGAAGACATTTACGTGGAGTGGACCAACAACGGG 918

1300 AAAACAGAGCTAAACTACAAGAACACTGAACCAGTCCTGGACTCTGATGGTTCTTACTTC 1359
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 919 AAAACAGAGCTAAACTACAAGAACACTGAACCAGTCCTGGACTCTGATGGTTCTTACTTC 978

1360 ATGTACAGCAAGCTGAGAGTGGAAAAGAAGAACTGGGTGGAAAGAAATAGCTACTCCTGT 1419
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 979 ATGTACAGCAAGCTGAGAGTGGAAAAGAAGAACTGGGTGGAAAGAAATAGCTACTCCTGT 1038

1420 TCAGTGGTCCACGAGGGTCTGCACAATCACCACACGACTAAGAGCTTCTCCCGGACTCCG 1479
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1039 TCAGTGGTCCACGAGGGTCTGCACAATCACCACACGACTAAGAGCTTCTCCCGGACTCCG 1098

1480 GGTAAA 1485
     ||||||
1099 GGTAAA 1104
```

LT 11
5694
ADL15694 standard; DNA; 990 BP.

ADL15694;

20-MAY-2004 (first entry)

Murine immunoglobulin heavy chain constant region DNA SeqID 68.

mouse; murine; antibody; gene; ds; beta-amyloid; A-beta;
amyloid beta A4 precursor protein; APP; presenilin;
lipoprotein receptor related protein; LRP; beta-amyloid 42; A-beta 42;
Alzheimer's disease; neuroprotective; nootropic.

Mus musculus.

WO2004018997-A2.

04-MAR-2004.

20-AUG-2003; 2003WO-US026173.

20-AUG-2002; 2002US-0405417P.
18-SEP-2002; 2002US-0411974P.

(NEUR-) NEUROGENETICS INC.

Kounnas M, Patrick A, Velicelebi G, Wagner S;

WPI; 2004-226902/21.
P-PSDB; ADL15695.

New polypeptide comprises a sequence of amino acids that is selectively reactive with beta-amyloid peptide 42 or at least one complementarity-determining region of antibody A387 or B436, useful for treating Alzheimer's disease.

XX

PS Disclosure; SEQ ID NO 68; 408pp; English.

XX

CC This invention relates to novel methods and compositions for detecting and modulating beta-amyloid (A-beta) peptide levels and the processing of amyloid beta A4 precursor protein (APP). Specifically, it refers to methods of assessing the presenilin activity of compounds using the lipoprotein receptor related protein (LRP), in order to identify presenilin proteins that can be used to affect the processing of APP. The present invention describes methods to identify agents that modulate presenilin activity and A-beta levels, in particular beta-amyloid 42 (A-beta 42), such that the agent is selectivly reactive with A-beta 42 and binds at least one complementarity determining region (CDR) of either antibody A387 or antibody B436. As such, the polypeptides, nucleic acids and antibodies are useful for treating Alzheimer's disease, accordingly the compositions exhibit neuroprotective and nootropic activities. This polynucleotide sequence is a murine antibody chain DNA fragment of the invention.

XX

SQ Sequence 990 BP; 274 A; 286 C; 235 G; 195 T; 0 U; 0 Other;

Query Match 47.2%; Score 700.6; DB 12; Length 990;
Best Local Similarity 100.0%; Pred. No. 2.3e-178;
Matches 700; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       786 TGAGCCCAGAGGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCAGCACCTAACCT 845
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       291 TGAGCCCAGAGGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCAGCACCTAACCT 350

Qy       846 CTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTC 905
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       351 CTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTC 410

Qy       906 CCTGAGCCCCATAGTCACATGTGTGGTGGTGGATGTGAGCGAGGATGACCCAGATGTCCA 965
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       411 CCTGAGCCCCATAGTCACATGTGTGGTGGTGGATGTGAGCGAGGATGACCCAGATGTCCA 470

Qy       966 GATCAGCTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAAACCCATAGAGA 1025
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       471 GATCAGCTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAAACCCATAGAGA 530

Qy      1026 GGATTACAACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGACTGGAT 1085
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       531 GGATTACAACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGACTGGAT 590

Qy      1086 GAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAAGACCTCCCAGCGCCCATCGAGAG 1145
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       591 GAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAAGACCTCCCAGCGCCCATCGAGAG 650

Qy      1146 AACCATCTCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACC 1205
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       651 AACCATCTCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACC 710

Qy      1206 AGAAGAAGAGATGACTAAGAAACAGGTCACTCTGACCTGCATGGTCACAGACTTCATGCC 1265
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       711 AGAAGAAGAGATGACTAAGAAACAGGTCACTCTGACCTGCATGGTCACAGACTTCATGCC 770

Qy      1266 TGAAGACATTTACGTGGAGTGGACCAACAACGGGAAAACAGAGCTAAACTACAAGAACAC 1325
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       771 TGAAGACATTTACGTGGAGTGGACCAACAACGGGAAAACAGAGCTAAACTACAAGAACAC 830

Qy      1326 TGAACCAGTCCTGGACTCTGATGGTTCTTACTTCATGTACAGCAAGCTGAGAGTGGAAAA 1385
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       831 TGAACCAGTCCTGGACTCTGATGGTTCTTACTTCATGTACAGCAAGCTGAGAGTGGAAAA 890

Qy      1386 GAAGAACTGGGTGGAAAGAAATAGCTACTCCTGTTCAGTGGTCCACGAGGGTCTGCACAA 1445
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       891 GAAGAACTGGGTGGAAAGAAATAGCTACTCCTGTTCAGTGGTCCACGAGGGTCTGCACAA 950

Qy      1446 TCACCACACGACTAAGAGCTTCTCCCGGACTCCGGGTAAA 1485
            ||||||||||||||||||||||||||||||||||||||||
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951 TCACCACACGACTAAGAGCTTCTCCCGGACTCCGGGTAAA 990

ULT 12
20762
AEC20762 standard; cDNA; 1401 BP.

AEC20762;

20-OCT-2005 (first entry)

M-CSF specific murine antibody RX1 heavy chain cDNA.

endocrine-gen.; antiarthritic; antibacterial; antiinflammatory; antirheumatic; antithyroid; bone metastases; calcium antagonist; cancer; cardiovascular-gen.; degeneration; eating-disorders-gen.; endocrine disease; endocrine-gen.; endocrine-gen.; gastrointestinal-gen.; gene; genetic disorder; heavy chain; hepatotropic; hypercalcemia; immune disorder; immunotherapy; inflammation; monoclonal antibody; mouth disease; musculoskeletal disease; neoplasm; nephrotropic; osteopathic; osteopetrosis; osteoporosis; pagets disease; periodontal disease; pharmaceutical; rheumatoid arthritis; ss.

Mus musculus.

WO2005068503-A2.

28-JUL-2005.

06-JAN-2005; 2005WO-US000546.

07-JAN-2004; 2004US-0535181P.
02-JUN-2004; 2004US-0576417P.

(CHIR) CHIRON CORP.
(XOMA) XOMA TECHNOLOGY LTD.

Liu C, Zimmerman DL, Harrowe GM, Koths K, Kavanaugh WM, Long L; Calderon-Cacia M, Horwitz AH;

WPI; 2005-597707/61.
P-PSDB; AEC20763.

Novel non-murine antibody that competes with monoclonal antibody RX1 for binding to macrophage colony stimulating factor, useful for treating hypogonadism, hypercalcemia, rickets, scurvy, homocystinuria, cancer, osteoporosis.

Claim 67; SEQ ID NO 1; 269pp; English.

The invention describes a non-murine antibody (I) that competes with monoclonal antibody RX1 for binding to macrophage colony stimulating factor (M-CSF) by more than 75%, where the monoclonal antibody RXI has the heavy chain and light chain amino acid sequences having a fully defined 447 amino acids (SEQ ID No. 2) and 214 amino acids (SEQ ID No. 4) sequences given in the specification, respectively. (I) is useful for preventing a subject afflicted with a disease that causes or contributes to osteolysis, where the antibody effectively reduces the severity of bone loss associated with the disease. The disease is chosen from metabolic bone diseases associated with relatively increased osteoclast activity, including endocrinopathies, hypercalcemia, deficiency states, chronic diseases, and hereditary diseases, cancer, osteoporosis, osteopetrosis, inflammation of bone associated with arthritis and rheumatoid arthritis, periodontal disease, fibrous dysplasia, and/or Paget's disease. (I) is useful for preventing or treating metastatic cancer. Antibodies of the invention are useful for preventing or reducing bone loss; osteolysis; metastatic cancer to bone and cancer. (I) is useful for manufacturing a medicament for preventing or reducing bone loss in a patient exhibiting osteolysis, manufacturing a medicament for treating a patient afflicted with a disease that causes or contributes to osteolysis, and metastatic cancer to bone in a patient suffering from metastatic cancer, for manufacturing a medicament for treating a patient having cancer. (I) in synergistic combination, is useful for preparing a medicament for treating a patient exhibiting osteolysis. This sequence encodes macrophage colony stimulating factor (M-CSF) specific murine antibody RX1 heavy chain.

XX
SQ Sequence 1401 BP; 369 A; 407 C; 327 G; 298 T; 0 U; 0 Other;

Query Match 47.2%; Score 700.6; DB 14; Length 1401;
Best Local Similarity 100.0%; Pred. No. 2.7e-178;
Matches 700; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       786 TGAGCCCAGAGGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCAGCACCTAACCT 845
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       702 TGAGCCCAGAGGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCAGCACCTAACCT 761

Qy       846 CTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTC 905
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       762 CTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTC 821

Qy       906 CCTGAGCCCCATAGTCACATGTGTGGTGGTGGATGTGAGCGAGGATGACCCAGATGTCCA 965
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       822 CCTGAGCCCCATAGTCACATGTGTGGTGGTGGATGTGAGCGAGGATGACCCAGATGTCCA 881

Qy       966 GATCAGCTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAAACCCATAGAGA 1025
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       882 GATCAGCTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAAACCCATAGAGA 941

Qy      1026 GGATTACAACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGACTGGAT 1085
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       942 GGATTACAACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGACTGGAT 1001

Qy      1086 GAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAAGACCTCCCAGCGCCCATCGAGAG 1145
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1002 GAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAAGACCTCCCAGCGCCCATCGAGAG 1061

Qy      1146 AACCATCTCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACC 1205
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1062 AACCATCTCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACC 1121

Qy      1206 AGAAGAAGAGATGACTAAGAAACAGGTCACTCTGACCTGCATGGTCACAGACTTCATGCC 1265
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1122 AGAAGAAGAGATGACTAAGAAACAGGTCACTCTGACCTGCATGGTCACAGACTTCATGCC 1181

Qy      1266 TGAAGACATTTACGTGGAGTGGACCAACAACGGGAAAACAGAGCTAAACTACAAGAACAC 1325
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1182 TGAAGACATTTACGTGGAGTGGACCAACAACGGGAAAACAGAGCTAAACTACAAGAACAC 1241

Qy      1326 TGAACCAGTCCTGGACTCTGATGGTTCTTACTTCATGTACAGCAAGCTGAGAGTGGAAAA 1385
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1242 TGAACCAGTCCTGGACTCTGATGGTTCTTACTTCATGTACAGCAAGCTGAGAGTGGAAAA 1301

Qy      1386 GAAGAACTGGGTGGAAAGAAATAGCTACTCCTGTTCAGTGGTCCACGAGGGTCTGCACAA 1445
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1302 GAAGAACTGGGTGGAAAGAAATAGCTACTCCTGTTCAGTGGTCCACGAGGGTCTGCACAA 1361

Qy      1446 TCACCACACGACTAAGAGCTTCTCCCGGACTCCGGGTAAA 1485
            |||||||||||||||||||||||||||||||||||||||||
Db      1362 TCACCACACGACTAAGAGCTTCTCCCGGACTCCGGGTAAA 1401
```

RESULT 13
AED19725
ID AED19725 standard; DNA; 1560 BP.
XX
AC AED19725;
XX
DT 15-DEC-2005 (first entry)
XX
DE Anti-PrP antibody heavy chain 44B1H DNA SEQ ID NO 5.
XX
KW cerebroprotective; cell therapy; gene therapy; drug delivery;
KW prion disease; 44B1H; ds; therapeutic; monoclonal antibody; heavy chain.
XX
OS Unidentified.

WO2005094846-A1.

13-OCT-2005.

30-MAR-2005; 2005WO-JP006189.

30-MAR-2004; 2004JP-00100649.

(RENO-) RENOMEDIX INST INC.

Fujinaga K, Shinagawa M, Niitsu Y, Hamada H, Horiuchi M; Honmou O, Umetani A;

WPI; 2005-725409/74.

Agent useful for treating prion disease or delivering a substance to a lesioned region of prion disease, comprises a mesenchymal cell.

Claim 4; SEQ ID NO 5; 34pp; Japanese.

The invention describes an agent (I) for treating prion disease or delivering a substance to the lesioned region of prion disease, comprising a mesenchymal cell. Also described are: a nucleic acid (II) having an anti-prion antibody gene comprising: an antibody heavy chain gene having SEQ ID No: 1, 3, 5, 30, 32 and 34, a nucleotide sequence consisting of a degenerate genetic code, which encodes a polypeptide same as that of the above nucleotide sequence, a nucleotide sequence, which is a mutant of the above sequences, or a nucleotide sequence that is complementary to the above sequences and that hybridizes under stringent conditions with the above sequences; and an antibody light chain gene having SEQ ID No: 2, 4, 6, 31, 33 and 35, a nucleotide sequence consisting of degenerate genetic code, which encodes a polypeptide same as that of the above nucleotide sequence, a nucleotide sequence, which is a mutant of the above sequences, or a nucleotide sequence that is complementary to the above sequences and that hybridizes under stringent conditions with the above sequences; a vector (III) comprising (II); an anti-prion chimeric antibody (IV) comprising variable region of antibody encoded by (II) and constant region of antibody of animal other than mouse; a nucleic acid that encodes (IV); preparing (M1) a cell having abnormal prion proliferation inhibition activity, comprising transducing a gene that provides abnormal prion proliferation inhibition activity to the cell; a cell (V) having abnormal prion proliferation inhibition activity, being obtainable by (M1) or by utilizing (II) or (III); a sustainable formulation (VI) for discharge of an anti-prion antibody utilized for treating prion disease; use of a mesenchymal cell for producing an agent for delivering a substance to the lesioned region of prion disease; and delivering a substance to the lesioned region of a prion disease, comprising utilizing mesenchymal cell. (I) Is useful for treating prion disease or delivering a substance to the lesioned region of prion disease. (II), (III) Or (M1) is useful for preparing a cell having abnormal prion proliferation inhibition activity. (I), (II), (III), (IV) Or (VI) is useful for treating prion disease. (I) Enables improvement of the symptoms of prion disease. This sequence an anti-PrP monoclonal antibody heavy chain. Note: This sequence does not appear in the printed specification but has been obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_squences.

Sequence 1560 BP; 413 A; 424 C; 388 G; 335 T; 0 U; 0 Other;

ery Match 47.2%; Score 700.6; DB 14; Length 1560;
st Local Similarity 100.0%; Pred. No. 2.8e-178;
tches 700; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
      786 TGAGCCCAGAGGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCAGCACCTAACCT 845
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      850 TGAGCCCAGAGGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCAGCACCTAACCT 909

      846 CTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTC 905
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      910 CTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTC 969

      906 CCTGAGCCCCATAGTCACATGTGTGGTGGTGGATGTGAGCGAGGATGACCCAGATGTCCA 965
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      970 CCTGAGCCCCATAGTCACATGTGTGGTGGTGGATGTGAGCGAGGATGACCCAGATGTCCA 1029

      966 GATCAGCTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAAACCCATAGAGA 1025
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     1030 GATCAGCTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAAACCCATAGAGA 1089

     1026 GGATTACAACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGACTGGAT 1085
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     1090 GGATTACAACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGACTGGAT 1149

     1086 GAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAAGACCTCCCAGCGCCCATCGAGAG 1145
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     1150 GAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAAGACCTCCCAGCGCCCATCGAGAG 1209

     1146 AACCATCTCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACC 1205
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     1210 AACCATCTCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACC 1269

     1206 AGAAGAAGAGATGACTAAGAAACAGGTCACTCTGACCTGCATGGTCACAGACTTCATGCC 1265
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     1270 AGAAGAAGAGATGACTAAGAAACAGGTCACTCTGACCTGCATGGTCACAGACTTCATGCC 1329

     1266 TGAAGACATTTACGTGGAGTGGACCAACAACGGGAAAACAGAGCTAAACTACAAGAACAC 1325
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     1330 TGAAGACATTTACGTGGAGTGGACCAACAACGGGAAAACAGAGCTAAACTACAAGAACAC 1389

     1326 TGAACCAGTCCTGGACTCTGATGGTTCTTACTTCATGTACAGCAAGCTGAGAGTGGAAAA 1385
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     1390 TGAACCAGTCCTGGACTCTGATGGTTCTTACTTCATGTACAGCAAGCTGAGAGTGGAAAA 1449

     1386 GAAGAACTGGGTGGAAAGAAATAGCTACTCCTGTTCAGTGGTCCACGAGGGTCTGCACAA 1445
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     1450 GAAGAACTGGGTGGAAAGAAATAGCTACTCCTGTTCAGTGGTCCACGAGGGTCTGCACAA 1509

     1446 TCACCACACGACTAAGAGCTTCTCCCGGACTCCGGGTAAA 1485
          ||||||||||||||||||||||||||||||||||||||||
     1510 TCACCACACGACTAAGAGCTTCTCCCGGACTCCGGGTAAA 1549
```

RESULT 14
ADV26108
ID ADV26108 standard; DNA; 1569 BP.
XX
AC ADV26108;
XX
DT 10-MAR-2005 (first entry)
XX
DE Mouse OKT3 VH gene.
XX
KW ds; gene; immunostimulant; immunogenicity; antibody.
XX
OS Mus sp.
XX
PN WO2004108158-A1.
XX
PD 16-DEC-2004.
XX
PF 28-MAY-2004; 2004WO-US017219.
XX
PR 02-JUN-2003; 2003US-0475155P.
XX
PA (ALEX-) ALEXION PHARM INC.
XX
PI Rother RP, Faas-Knight S, Wu D, Carr FJ, Hamilton A;
XX
DR WPI; 2005-031597/03.
DR P-PSDB; ADV26107.
XX
PT New de-immunized anti-CD3 antibody, useful for stimulating an immune
PT response against infections and for treating infections.
XX
PS Disclosure; Fig 1a; 75pp; English.

The invention relates to a de-immunized anti-CD3 antibody. The antibody, composition and methods are useful for stimulating an immune response against infections and for treating infections. The present sequence represents DNA encoding mouse OKT3 VH.

Sequence 1569 BP; 446 A; 443 C; 356 G; 324 T; 0 U; 0 Other;

Query Match 47.2%; Score 700.6; DB 14; Length 1569;
Best Local Similarity 100.0%; Pred. No. 2.8e-178;
Matches 700; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        786 TGAGCCCAGAGGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCAGCACCTAACCT 845
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        744 TGAGCCCAGAGGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCAGCACCTAACCT 803

Qy        846 CTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTC 905
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        804 CTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTC 863

Qy        906 CCTGAGCCCCATAGTCACATGTGTGGTGGTGGATGTGAGCGAGGATGACCCAGATGTCCA 965
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        864 CCTGAGCCCCATAGTCACATGTGTGGTGGTGGATGTGAGCGAGGATGACCCAGATGTCCA 923

Qy        966 GATCAGCTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAAACCCATAGAGA 1025
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        924 GATCAGCTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAAACCCATAGAGA 983

Qy       1026 GGATTACAACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGACTGGAT 1085
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        984 GGATTACAACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGACTGGAT 1043

Qy       1086 GAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAAGACCTCCCAGCGCCCATCGAGAG 1145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1044 GAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAAGACCTCCCAGCGCCCATCGAGAG 1103

Qy       1146 AACCATCTCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACC 1205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1104 AACCATCTCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACC 1163

Qy       1206 AGAAGAAGAGATGACTAAGAAACAGGTCACTCTGACCTGCATGGTCACAGACTTCATGCC 1265
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1164 AGAAGAAGAGATGACTAAGAAACAGGTCACTCTGACCTGCATGGTCACAGACTTCATGCC 1223

Qy       1266 TGAAGACATTTACGTGGAGTGGACCAACAACGGGAAAACAGAGCTAAACTACAAGAACAC 1325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1224 TGAAGACATTTACGTGGAGTGGACCAACAACGGGAAAACAGAGCTAAACTACAAGAACAC 1283

Qy       1326 TGAACCAGTCCTGGACTCTGATGGTTCTTACTTCATGTACAGCAAGCTGAGAGTGGAAAA 1385
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1284 TGAACCAGTCCTGGACTCTGATGGTTCTTACTTCATGTACAGCAAGCTGAGAGTGGAAAA 1343

Qy       1386 GAAGAACTGGGTGGAAAGAAATAGCTACTCCTGTTCAGTGGTCCACGAGGGTCTGCACAA 1445
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1344 GAAGAACTGGGTGGAAAGAAATAGCTACTCCTGTTCAGTGGTCCACGAGGGTCTGCACAA 1403

Qy       1446 TCACCACACGACTAAGAGCTTCTCCCGGACTCCGGGTAAA 1485
              ||||||||||||||||||||||||||||||||||||||||
Db        1404 TCACCACACGACTAAGAGCTTCTCCCGGACTCCGGGTAAA 1443
```

RESULT 15
AAW71834
ID ADW71834 standard; DNA; 1569 BP.
XX
AC ADW71834;
XX
DT 07-APR-2005 (first entry)
XX
DE Murine OKT3 heavy chain variable region DNA.
XX
KW fusion protein; IgG; antibody; antiinflammatory; antimicrobial-gen.; cytokine release syndrome; inflammation; infection; ds; gene.
XX
OS Mus sp.
OS Synthetic.
XX
PN WO2005007809-A2.
XX
PD 27-JAN-2005.
XX
PF 28-MAY-2004; 2004WO-US017005.
XX
PR 30-MAY-2003; 2003US-0475202P.
PR 19-APR-2004; 2004US-0563500P.
XX
PA (ALEX-) ALEXION PHARM INC.
XX
PI Rother RP, Faas-Knight S, Wu D, Squinto SP, Evans MJ;
XX
DR WPI; 2005-112860/12.
DR P-PSDB; ADW71833.
XX
PT Reducing antibody-mediated cell activation or inflammation events, useful
PT for preventing infections, comprises administering an antibody including
PT an engineered constant region.
XX
PS Disclosure; SEQ ID NO 18; 87pp; English.
XX
CC The invention relates to a novel fusion protein, comprising a non-Fc
CC component and an Fc region having a first portion derived from one or
CC more human IgG2 antibodies and a second portion derived from one or more
CC human IgG4 antibodies. The invention further comprises: a method for
CC reducing antibody-mediated cell activation or inflammation events,
CC comprising administering an antibody which binds to either a cell surface
CC molecule or a soluble molecule that binds to a cell surface molecule, the
CC antibody including an engineered heavy chain constant region having a
CC first portion derived from one or more human IgG2 antibodies and a second
CC portion derived from one or more human IgG4 antibodies; a method of
CC increasing the half life of a non-Fc component, increasing the avidity of
CC a non-Fc component for a molecule to which the non-Fc component binds,
CC forming a dimer of a non-Fc component, reducing or eliminating Fc
CC receptor binding and complement activation associated with a Fc fusion
CC protein, or improving expression of a non-Fc component in mammalian cells
CC ; a nucleic acid encoding a fusion protein; an expression vector
CC containing the nucleic acid; a host cell transfected with an expression
CC vector; and a composition comprising the fusion protein and a
CC pharmaceutical carrier. The fusion protein has antiinflammatory and
CC antimicrobial activities. The antibody and fusion protein are useful in
CC preventing or reducing cytokine release or the severity of cytokine
CC release syndrome, and in reducing antibody-mediated cell activation or
CC inflammation events. The antibodies, fusion proteins and nucleic acids,
CC composition, methods are useful for preventing infections. This
CC polynucleotide sequence represents the murine OKT3 heavy chain variable
CC region DNA relating to the novel fusion protein of the invention.
XX
SQ Sequence 1569 BP; 446 A; 443 C; 356 G; 324 T; 0 U; 0 Other;

Query Match 47.2%; Score 700.6; DB 14; Length 1569;
Best Local Similarity 100.0%; Pred. No. 2.8e-178;
Matches 700; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 786 TGAGCCCAGAGGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCAGCACCTAACCT 845
Db 744 TGAGCCCAGAGGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCAGCACCTAACCT 803

Qy 846 CTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTC 905
Db 804 CTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTC 863

Qy 906 CCTGAGCCCCATAGTCACATGTGTGGTGGTGGATGTGAGCGAGGATGACCCAGATGTCCA 965
Db 864 CCTGAGCCCCATAGTCACATGTGTGGTGGTGGATGTGAGCGAGGATGACCCAGATGTCCA 923

Qy 966 GATCAGCTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAAACCCATAGAGA 1025

```
 924 GATCAGCTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAAACCCATAGAGA 983

1026 GGATTACAACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGACTGGAT 1085
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 984 GGATTACAACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGACTGGAT 1043

1086 GAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAAGACCTCCCAGCGCCCATCGAGAG 1145
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1044 GAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAAGACCTCCCAGCGCCCATCGAGAG 1103

1146 AACCATCTCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACC 1205
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1104 AACCATCTCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACC 1163

1206 AGAAGAAGAGATGACTAAGAAACAGGTCACTCTGACCTGCATGGTCACAGACTTCATGCC 1265
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1164 AGAAGAAGAGATGACTAAGAAACAGGTCACTCTGACCTGCATGGTCACAGACTTCATGCC 1223

1266 TGAAGACATTTACGTGGAGTGGACCAACAACGGGAAAACAGAGCTAAACTACAAGAACAC 1325
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1224 TGAAGACATTTACGTGGAGTGGACCAACAACGGGAAAACAGAGCTAAACTACAAGAACAC 1283

1326 TGAACCAGTCCTGGACTCTGATGGTTCTTACTTCATGTACAGCAAGCTGAGAGTGGAAAA 1385
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1284 TGAACCAGTCCTGGACTCTGATGGTTCTTACTTCATGTACAGCAAGCTGAGAGTGGAAAA 1343

1386 GAAGAACTGGGTGGAAAGAAATAGCTACTCCTGTTCAGTGGTCCACGAGGGTCTGCACAA 1445
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1344 GAAGAACTGGGTGGAAAGAAATAGCTACTCCTGTTCAGTGGTCCACGAGGGTCTGCACAA 1403

1446 TCACCACACGACTAAGAGCTTCTCCCGGACTCCGGGTAAA 1485
     ||||||||||||||||||||||||||||||||||||||||
1404 TCACCACACGACTAAGAGCTTCTCCCGGACTCCGGGTAAA 1443
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time : 1032.58 secs

GenCore version 5.1.8

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on: May 31, 2006, 23:41:05 ; Search time 657.424 Seconds
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10085.747 Million cell updates/sec

le: US-10-048-116B-5
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ring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

rched: 5244920 seqs, 3486124231 residues

al number of hits satisfying chosen parameters: 10489840

imum DB seq length: 0
imum DB seq length: 2000000000

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Maximum Match 100%
Listing first 45 summaries

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3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	921	96.8	921	5	AAF55099	Aaf55099 DNA encod
2	709.2	74.6	893	2	AAT04262	Aat04262 Hybrid IA
3	665.2	69.9	945	12	ADQ31225	Adq31225 I-Ab(beta
4	648	68.1	1013	2	AAT04269	Aat04269 Hybrid IA
5	628.6	66.1	915	12	ADQ31228	Adq31228 I-Ab(beta
6	607.8	63.9	1382	2	AAT86989	Aat86989 SCE1 sing
7	607.8	63.9	1382	8	ACA60744	Aca60744 Mouse MHC
8	607.8	63.9	1385	2	AAT86987	Aat86987 SSC1 sing
9	607.8	63.9	1385	8	ACA60742	Aca60742 Mouse MHC
10	607.8	63.9	1508	2	AAT86988	Aat86988 SCT1 sing
11	607.8	63.9	1508	2	AAX89069	Aax89069 Single ch
12	607.8	63.9	1508	8	ACA60743	Aca60743 Mouse MHC
13	606.2	63.7	1382	2	AAT17588	Aat17588 Vector SC
14	606.2	63.7	1385	2	AAT17586	Aat17586 Vector SS
15	606.2	63.7	1508	2	AAT17587	Aat17587 Vector SC
16	598.6	62.9	4724	2	AAV12068	Aav12068 Murine IA
17	561.8	59.1	798	12	ADJ75986	Adj75986 Marker ge
18	561.8	59.1	798	14	ADX26090	Adx26090 Novel cel
19	549.8	57.8	1085	4	ABI99040	Abi99040 Murine pC
20	542	57.0	702	2	AAQ03170	Aaq03170 Sequence
21	542	57.0	702	2	AAT06286	Aat06286 I-Ab-beta
22	542	57.0	702	2	AAQ56920	Aaq56920 Mouse I-A
23	535.6	56.3	702	2	AAQ35055	Aaq35055 IAB beta
24	525.4	55.2	1698	4	ABI99038	Abi99038 Murine pC
25	502.6	52.8	1243	6	ABN84048	Abn84048 Single ch
26	499.4	52.5	1662	4	ABI99039	Abi99039 Murine pC
27	497.2	52.3	1686	4	ABI99031	Abi99031 MBP 1-14
28	497.2	52.3	1701	4	ABI99028	Abi99028 IAS MBP 1
29	497.2	52.3	2059	4	ABI99032	Abi99032 MBP 1-14
30	497.2	52.3	2346	4	ABI99027	Abi99027 IAS MBP 1
31	496	52.2	1680	4	ABI99021	Abi99021 I-As MBP.
32	496	52.2	1707	4	ABI99030	Abi99030 IAS MBP 9
33	496	52.2	2053	4	ABI99029	Abi99029 IAS MBP 9
34	496	52.2	2343	4	ABI99033	Abi99033 MBP 90-10
35	433.6	45.6	562	6	ABK63510	Abk63510 Rat seque
36	433.6	45.6	562	10	ADB57995	Adb57995 Toxicity-
37	433.6	45.6	562	10	ABT41775	Abt41775 Toxicity
38	433.6	45.6	562	11	ADW21868	Adw21868 Rat hepat
39	433.6	45.6	562	13	ADV40851	Adv40851 Rat cardi
40	433.6	45.6	562	14	ADX25826	Adx25826 Novel cel
41	414.8	43.6	1869	13	ADQ38634	Adq38634 Human SNP
42	414.8	43.6	1892	13	ADQ38637	Adq38637 Human SNP
43	410.8	43.2	1171	6	ABK84087	Abk84087 Human cDN
44	410.8	43.2	1199	8	ABX63009	Abx63009 Human cDN
45	407.6	42.9	1192	10	AAD63150	Aad63150 Human maj

ALIGNMENTS

RESULT 1
AAF55099
ID AAF55099 standard; DNA; 921 BP.
XX
AC AAF55099;
XX
DT 15-MAY-2001 (first entry)
XX
DE DNA encoding a fusion protein comprising a beta chain of MHC.
XX
KW Recombinant protein; alpha chain; beta chain; MHC; immunoglobulin;
KW major histocompatibility complex; Fc region; antigen; T lymphocyte;
KW immunostimulant; vaccine; infection; tumour; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1. .921
FT /*tag= a
XX
PN WO200109194-A1.
XX
PD 08-FEB-2001.
XX
PF 28-JUL-2000; 2000WO-FR002193.
XX
PR 29-JUL-1999; 99FR-00009862.
XX
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
PI Glaichenhaus N, Malherbe L;
XX
DR WPI; 2001-182944/18.
DR P-PSDB; AAB67481.
XX
PT New soluble recombinant protein, useful e.g. as immunostimulant,
PT comprises dimeric major histocompatibility complex molecule fused to
PT immunoglobulin Fc region.
XX
PS Example 1; Page 34-35; 43pp; French.
XX

The specification describes soluble recombinant proteins that comprise at least a dimer formed from the alpha and beta-chains of MHC (major histocompatibility complex) Class I and II molecules in which at least one chain has, attached to its C-terminus, at least part of the Fc region of an immunoglobulin. The recombinant proteins, when linked to an antigenic peptide, are used to count and/or purify antigen-reactive T lymphocytes and to characterize their phenotype, e.g. in preclinical evaluation of vaccines. They are also used as immunostimulants, particularly for vaccine development (against infections and tumours), to count and determine phenotype of autoreactive T cells in subjects with, or at risk of developing, autoimmune diseases, e.g. for staging or evaluating treatments, and (to purify and/or enrich Ag-reactive T cells from cell cultures or patient samples, for use in subsequent curative or preventative cellular therapy. The present sequence encodes a recombinant protein of the invention, comprising a beta chain of MHC molecules

Sequence 921 BP; 214 A; 265 C; 286 G; 156 T; 0 U; 0 Other;

ery Match 96.8%; Score 921; DB 5; Length 921;
st Local Similarity 100.0%; Pred. No. 8.4e-205;
tches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         21 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 60

Qy         81 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120

Qy        141 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 180

Qy        201 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 240

Qy        261 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 300

Qy        321 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 360

Qy        381 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 420

Qy        441 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 480

Qy        501 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 540

Qy        561 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 600

Qy        621 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 660

Qy        681 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 720

Qy        741 AGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCCGAGTCTGCCCGGAGCAAG 800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCCGAGTCTGCCCGGAGCAAG 780

Qy        801 GGAGGTGGAGGATCCACTACAGCTCCATCAGCTCAGTTGAAAAAGAAATTGCAAGCACTG 860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGAGGTGGAGGATCCACTACAGCTCCATCAGCTCAGTTGAAAAAGAAATTGCAAGCACTG 840

Qy        861 AAGAAAAAGAACGCTCAGCTGAAGTGGAAACTTCAAGCCCTCAAGAAGAAACTCGCCCAG 920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAAAAAGAACGCTCAGCTGAAGTGGAAACTTCAAGCCCTCAAGAAGAAACTCGCCCAG 900

Qy        921 CATCATCATCATCATCATTGA 941
              ||||||||||||||||||||||
Db        901 CATCATCATCATCATCATTGA 921
```

RESULT 2
AAT04262
ID AAT04262 standard; DNA; 893 BP.
XX
AC AAT04262;
XX
DT 16-APR-1996 (first entry)
XX
DE Hybrid IA beta chain gene.
XX
KW Polymerase chain reaction; PCR; primer; amplify;
KW major histocompatability complex; MHC; T-cell receptor; TCR;
KW autoimmune disease; immunodeficiency disease; immune response;
KW immunoproliferation disease; graft-host rejection; therapy; ss.
XX
OS Synthetic.
XX

FH	Key	Location/Qualifiers
FT	primer_bind	1. .16
FT		/*tag= a
FT		/note= "probable primer binding site (primer #233)"
FT	primer_bind	complement(45. .74)
FT		/*tag= b
FT		/note= "binding site for primer #261 (see AAT04260)"
FT	CDS	61. .828
FT		/*tag= c
FT		/product= "hybrid IA beta chain"
FT	sig_peptide	61. .141
FT		/*tag= d
FT		/note= "leader region"
FT	primer_bind	complement(119. .172)
FT		/*tag= e
FT		/note= "binding site for primer #331 (see AAT04261)"
FT	primer_bind	complement(158. .212)
FT		/*tag= f
FT		/note= "primer #332 binding site"
FT	primer_bind	complement(199. .250)
FT		/*tag= g
FT		/note= "primer #333 (see AAT04263) binding site"
FT	misc_feature	371. .389
FT		/*tag= h
FT		/note= "probable primer binding site (primer #270)"
FT	mat_peptide	511. .825
FT		/*tag= i
FT		/product= "IA beta chain beta 2 region"
FT	primer_bind	521. .550
FT		/*tag= j
FT		/note= "probable primer binding site (primer #271)"
FT	primer_bind	532. .554
FT		/*tag= k
FT		/note= "probable primer binding site (primer #272)"
FT	primer_bind	808. .836
FT		/*tag= l
FT		/note= "probable primer binding site (primer #259)"
FT	primer_bind	877. .893
FT		/*tag= m
FT		/note= "probable primer binding site (primer #232)"

XX
PN WO9523814-A1.

08-SEP-1995.

03-MAR-1995; 95WO-US002689.

04-MAR-1994; 94US-00207481.

(NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.

Kappler JW, Marrack P;

WPI; 1995-320543/41.
P-PSDB; AAR82533.

Peptide-MHC complex comprising antigenic peptide, linker and MHC segment - useful as reagents for the treatment of diseases including auto-immune diseases, immuno-stimulatory diseases or graft-host rejection.

Example 1; Page 53; 94pp; English.

This sequence represents a hybrid IA beta chain gene, containing the chicken ovalbumin peptide (cOVA). This sequence was used in the construction of a hybrid IA alpha beta dimer. The encoded protein (pIAd-OVA) was found to be more stable than the IA alpha beta dimer. The stability was decreased by the addition of a MHC groove specific binding peptide (e.g. see AAR82527, AAR82528 and AAR82531), compared to an increase seen on the addition of a MHC binding peptide to IE k/d-MCC. These complexes may be used to regulate an immune response. The complexes are capable of being recognised by a TCR alone or in combination with additional MHC proteins. These complexes are useful for therapeutic purposes and experimental purposes. They can also be used as reagents for the treatment of diseases including autoimmune diseases, immunodeficiency diseases, immunoproliferation diseases, and graft-host rejection

Sequence 893 BP; 204 A; 239 C; 275 G; 175 T; 0 U; 0 Other;

ıery Match 74.6%; Score 709.2; DB 2; Length 893;
ɜst Local Similarity 94.7%; Pred. No. 2.1e-155;
ıtches 761; Conservative 0; Mismatches 28; Indels 15; Gaps 2;

```
Qy          8 GGAATTCTTAGAGATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGT 67
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         48 GGAATTCTTAGAGATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGT 107

Qy         68 GCTGATGGTGCTGAGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTC 127
              ||||||||||||||||||||||||||||||||||||||||||||||      || || | |
Db        108 GCTGATGGTGCTGAGCAGCCCCGGGACTGAGGGCGGAAACTCC-----GTACATGCTGCC 162

Qy        128 GCTGGAGCACCCGATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCC 187
              || |   | ||   | || | |           ||||||||||||||||||||||
Db        163 CATGCTGAGATCAATGAGGCTGGCAG----------AGGAGGTGGGGGCTCACTAGTGCC 212

Qy        188 CCGAGGCTCTGGAGGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTG 247
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 CCGAGGCTCTGGAGGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTG 272

Qy        248 CTACTACACCAACGGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGA 307
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 CTACTACACCAACGGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGA 332

Qy        308 GGAGTACGTGCGCTACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCG 367
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        333 GGAGTACGTGCGCTACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCG 392

Qy        368 GCCAGACGCCGAGTACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGT 427
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 GCCAGACGCCGAGTACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGT 452

Qy        428 GGACACGGCGTGCAGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCT 487
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 GGACACGGCGTGCAGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCT 512

Qy        488 TGAACAGCCCAATGTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACAC 547
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        513 TGAACAGCCCAATGTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACAC 572

Qy        548 TCTGGTCTGTTCGGTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAA 607
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        573 TCTGGTCTGTTCGGTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAA 632

Qy        608 TGGCCAGGAGGAGACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGAC 667
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 TGGCCAGGAGGAGACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGAC 692

Qy        668 CTTCCAGGTCCTGGTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCA 727
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 CTTCCAGGTCCTGGTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCA 752

Qy        728 TGTGGAGCATCCCAGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCCGAGTC 787
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 TGTGGAGCATCCCAGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCCGAGTC 812

Qy        788 TGCCCGGAGCAAGGGAGGTGGAGG 811
              |||||||||||||  ||   | ||
Db        813 TGCCCGGAGCAAGTAAGCATGCGG 836
```

RESULT 3
ADQ31225
ID ADQ31225 standard; cDNA; 945 BP.
XX
AC ADQ31225;
XX
DT 07-OCT-2004 (first entry)
XX
DE I-Ab(beta)-Cholera toxin B subunit-leucine zipper (LZ)-BirA fusion cDNA.
XX
KW class II major histocompatibility complex; MHC; CD4+ T-cell detection;
KW flow cytometry; mucous membrane invasive antigen;
KW I-Ab(beta)-cholera toxin B subunit-leucine zipper-BirA fusion; CTB; ss;
KW gene.
XX
OS Vibrio cholerae.
OS Unidentified.
XX
FH Key Location/Qualifiers
FT CDS 1. .945
FT /*tag= a
FT /product= "I-Ab(beta)-Cholera toxin B subunit (CTB)-
FT leucine zipper (LZ)-BirA fusion cDNA"
XX
PN JP2004196789-A.
XX
PD 15-JUL-2004.
XX
PF 03-DEC-2003; 2003JP-00404367.
XX
PR 03-DEC-2002; 2002JP-00351818.
XX
PA (SENT-) SENTAN KAGAKU GIJUTSU INCUBATION CENT KK.
XX
DR WPI; 2004-546819/53.
DR P-PSDB; ADQ31224.
XX
PT Peptide-Class II major histocompatibility complex (MHC) composite, useful
PT for detecting antigen specific CD4+ T-cell, comprises antigen peptide
PT containing epitope of mucous membrane invasive protein, and extracellular
PT region of MHC.
XX
PS Example 1; SEQ ID NO 10; 30pp; Japanese.
XX
CC The invention relates to a novel class II major histocompatibility
CC complex (MHC) antigenic peptide composite comprising a peptide containing
CC the T-cell antigenic determinant of a mucous membrane invasive protein
CC and the extracellular region of a class II MHC molecule or at least part
CC of the extracellular region of the class II MHC molecule having an amino

acid sequence comprising one or more deletions, substitutions or additions. The molecule of the invention may be useful for detecting an antigen-specific CD4+ T-cell by flow cytometry and for presenting a microorganism-derived mucous membrane invasive protein as an antigen. The method of the invention enables efficient detection of antigen-specific activation of CD4+ T-cells in the mucous membrane. The current sequence is that of the class II major histocompatibility complex-related I-Ab(alpha)-Cholera toxin B subunit (CTB)-leucine zipper (LZ)-BirA fusion cDNA of the invention.

Sequence 945 BP; 230 A; 256 C; 294 G; 165 T; 0 U; 0 Other;

ery Match 69.9%; Score 665.2; DB 12; Length 945;
st Local Similarity 86.6%; Pred. No. 3.8e-145;
tches 759; Conservative 0; Mismatches 108; Indels 9; Gaps 2;

```
Qy      63 GTGGTGCTGATGGTGCTGAGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCG 122
           |||   |||||||||||||||  |||   | ||  ||  ||| |||||  |   |
Db      49 GTGACACTGATGGTGCTGAGCTCCCCACTGGCTTTGGCTGGAGACTCCTGCGTGTGGAAC 108

Qy     123 CCGTCGCTGGAGCACCCGATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTA 182
           |  |  |||| |||||| ||    | |||    | ||||||||| || ||
Db     109 AATAAGACGCCGCACGCGATCGCGGCCATCAGCATGGCGAACGGAGGTGGTGGGTCCGGT 168

Qy     183 GTGCCCCGAGGCTCTGGAGGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGC 242
           |      || |  |||||||||||| || ||||||||||||||  |||||||| ||||
Db     169 GGAGGGGGAAG---TGGAGGTGGAGGGTCTGAAAGGCATTTCGTGTACCAGTTCATGGGC 225

Qy     243 GAGTGCTACTACACCAACGGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAAC 302
           |||||||| ||||||||||||||||||||||    |||||||||||||||||||||||
Db     226 GAGTGCTACTTCACCAACGGGACGCAGCGCATACGATATGTGACCAGATACATCTACAAC 285

Qy     303 CGGGAGGAGTACGTGCGCTACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTG 362
           |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db     286 CGGGAGGAGTACGTGCGCTACGACAGCGACGTGGGCGAGCACCGCGCGGTGACCGAGCTG 345

Qy     363 GGGCGGCCAGACGCCGAGTACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCC 422
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     346 GGGCGGCCAGACGCCGAGTACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCC 405

Qy     423 GAGGTGGACACGGCGTGCAGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGG 482
           ||| |||||||| |||||||||||||||||||||||||||||||  ||||||||||||||
Db     406 GAGCTGGACACGGTGTGCAGACACAACTACGAGGGGCCGGAGACCCACACCTCCCTGCGG 465

Qy     483 CGGCTTGAACAGCCCAATGTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCAC 542
           |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db     466 CGGCTTGAACAGCCCAATGTCGTCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCAC 525

Qy     543 AACACTCTGGTCTGTTCGGTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTC 602
           |||||||||||||| || ||||||||||||||||||||||||||||||||||||||||||
Db     526 AACACTCTGGTCTGCTCAGTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTC 585

Qy     603 AGGAATGGCCAGGAGGAGACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGAC 662
           ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db     586 CGGAATGGCCAGGAGGAGACGGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGAC 645

Qy     663 TGGACCTTCCAGGTCCTGGTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACC 722
           |||||||||||||||||||||||||||||||||||||  | ||||||||||||||||
Db     646 TGGACCTTCCAGGTCCTGGTCATGCTGGAGATGACCCCTCGGCGGGGAGAGGTCTACACC 705

Qy     723 TGCCATGTGGAGCATCCCAGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCC 782
           || || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     706 TGTCACGTGGAGCATCCCAGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCG 765

Qy     783 GAGTCTGCCCGGAGCAAGGGAGGTGGAGGATCCACTACAGCTCCATCAGCTCAGTTGAAA 842
           | | ||       ||      | ||||||||||||||||||||||||||||||||||||
Db     766 TCAGCAGACC------TGGTTCCGCGCGGATCCACTACAGCTCCATCAGCTCAGTTGAAA 819

Qy     843 AAGAAATTGCAAGCACTGAAGAAAAAGAACGCTCAGCTGAAGTGGAAACTTCAAGCCCTC 902
           |||||| |||| ||||| ||||||||||||||||||||||||||||||||||||||||||
Db     820 AAGAAACTGCAGGCACTTAAGAAAAAGAACGCTCAGCTGAAGTGGAAACTTCAAGCCCTC 879

Qy     903 AAGAAGAAACTCGCCCAGCATCATCATCATCATCAT 938
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           ||||||||||||||||||  ||||||  ||   ||
Db     880 AAGAAGAAACTCGCCCAGCTGCATCATATTCTGGAT 915
```

RESULT 4
AAT04269
ID AAT04269 standard; DNA; 1013 BP.
XX
AC AAT04269;
XX
DT 16-APR-1996 (first entry)
XX
DE Hybrid IA beta chain gene.
XX
KW Major histocompatability complex; MHC; T-cell receptor; TCR;
KW autoimmune disease; immunodeficiency disease; immune response;
KW immunoproliferation disease; graft-host rejection; therapy; B cell;
KW M12.C3; pM12-IAb-Ea; ss.
XX
OS Synthetic.
XX

FH	Key	Location/Qualifiers
FT	primer_bind	1. .18
FT		/*tag= a
FT		/note= "probable primer binding site (primer #76)"
FT	primer_bind	complement(40. .74)
FT		/*tag= b
FT		/note= "binding site for primer #362 (see AAT04270)"
FT	CDS	63. .959
FT		/*tag= c
FT		/product= "hybrid IA beta chain"
FT	sig_peptide	63. .143
FT		/*tag= d
FT		/note= "leader region"
FT	primer_bind	complement(140. .191)
FT		/*tag= e
FT		/note= "binding site for primer #363 (see AAT04271)"
FT	primer_bind	complement(177. .226)
FT		/*tag= f
FT		/note= "primer #364 binding site"
FT	primer_bind	complement(212. .266)
FT		/*tag= g
FT		/note= "primer #365 (see AAT04272) binding site"
FT	primer_bind	385. .403
FT		/*tag= h
FT		/note= "probable primer binding site (primer #270)"
FT	mat_peptide	531. .959
FT		/*tag= i
FT		/product= "IA beta chain beta 2 region"
FT	primer_bind	535. .564
FT		/*tag= j
FT		/note= "probable primer binding site (primer #271)"
FT	primer_bind	544. .568
FT		/*tag= k
FT		/note= "probable primer binding site (primer #272)"
FT	primer_bind	823. .850
FT		/*tag= l
FT		/note= "probable primer binding site (primer #259)"
FT	primer_bind	942. .976
FT		/*tag= m
FT		/note= "probable primer binding site (primer #366)"
FT	primer_bind	1000. .1013
FT		/*tag= n
FT		/note= "probable primer binding site (primer #59)"

XX
PN WO9523814-A1.
XX
PD 08-SEP-1995.
XX
PF 03-MAR-1995; 95WO-US002689.
XX
PR 04-MAR-1994; 94US-00207481.
XX

(NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.

Kappler JW, Marrack P;

WPI; 1995-320543/41.
P-PSDB; AAR82538.

Peptide-MHC complex comprising antigenic peptide, linker and MHC segment - useful as reagents for the treatment of diseases including auto-immune diseases, immuno-stimulatory diseases or graft-host rejection.

Example 2; Page 65; 94pp; English.

This sequence represents a hybrid IA beta chain gene. This sequence contains a fragment of the IE alpha chain (residues 56-73), as well as a linker and cleavage site. This sequence was transfected into a B cell line (M12.C3) using plasmid pM12-IAb-Ea. It was found that the encoded sequence was expressed in these cells. Complexes such as this may be used to regulate an immune response. The complexes are capable of being recognised by a TCR alone or in combination with additional MHC proteins. These complexes are useful for therapeutic purposes and experimental purposes. They can also be used as reagents for the treatment of diseases including autoimmune diseases, immunodeficiency diseases, immunoproliferation diseases, and graft-host rejection

Sequence 1013 BP; 220 A; 272 C; 327 G; 192 T; 0 U; 2 Other;

ıery Match 68.1%; Score 648; DB 2; Length 1013;
ɜst Local Similarity 89.3%; Pred. No. 4e-141;
ıtches 709; Conservative 1; Mismatches 81; Indels 3; Gaps 1;

```
Qy        7 GGGAATTCTTAGAGATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGG 66
            |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       49 GGGAATTCTTAGAGATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCGGCTGCTGTGGTGG 108

Qy       67 TGCTGATGGTGCTGAGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGT 126
            |||| |||||||||||||||| |||||||||||||| ||||||         ||    |
Db      109 TGCTCATGGTGCTGAGCAGCCCAGGGACTGAGGGCGGAGACTCCGAAGCTAGCTTTGAGG 168

Qy      127 CGCTGGAGCACCCGATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGC 186
            | | ||     | |  |     |  | | |  |  ||  |||||||| || ||    |
Db      169 CTCAGGGTGCACTGGCCAACATTGCTGTCGACAAGGCTGGAGGTGGTGGATC---CGGTG 225

Qy      187 CCCGAGGCTCTGGAGGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGT 246
              | ||   |||||||||||| || ||||||||||||||  ||||||||  ||||||||
Db      226 GAGGGGGAAGTGGAGGTGGAGGGTCTGAAAGGCATTTCGTGTACCAGTTCATGGGCGAGT 285

Qy      247 GCTACTACACCAACGGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGG 306
            |||||| |||||||||||||||||||||||    |||||||||||||||||||||||||||
Db      286 GCTACTTCACCAACGGGACGCAGCGCATACGATATGTGACCAGATACATCTACAACCGGG 345

Qy      307 AGGAGTACGTGCGCTACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGC 366
            |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db      346 AGGAGTACGTGCGCTACGACAGCGACGTGGGCGAGCACCGCGCGGTGACCGAGCTGGGGC 405

Qy      367 GGCCAGACGCCGAGTACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGG 426
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      406 GGCCAGACGCCGAGTACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGG 465

Qy      427 TGGACACGGCGTGCAGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGC 486
            ||||||||| ||||||||||||||||||||||||||||||  ||||||||||||||||||
Db      466 TGGACACGGTGTGCAGACACAACTACGAGGGGCCGGAGACCCACACCTCCCTGCGGCGGC 525

Qy      487 TTGAACAGCCCAATGTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACA 546
            |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db      526 TTGAACAGCCCAATGTCGTCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACA 585

Qy      547 CTCTGGTCTGTTCGGTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGA 606
            |||||||||| || |||||||||||||||||||||||||||||||||||||||||||||||
Db      586 CTCTGGTCTGCTCAGTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCCGGA 645

Qy      607 ATGGCCAGGAGGAGACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGA 666
            |||||||||||||||| |||||| ||||||||||||||||||||||||||||||||||||
```

```
Db      646 ATGGCCAGGAGGAGACGGTGGGGCTCTCATCCACACAGCTTATTAGGAATGGGGACTGGA 705

Qy      667 CCTTCCAGGTCCTGGTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCC 726
            |||||||||||||||||||||||||||||||||||||||||  | ||||||||||||:|||| |
Db      706 CCTTCCAGGTCCTGGTCATGCTGGAGATGACCCCTCGGCGGGGAGAGGTCTAYACCTGTC 765

Qy      727 ATGTGGAGCATCCCAGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCCGAGT 786
            | |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db      766 ACGTGGAGCATCCCAGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCTGAGT 825

Qy      787 CTGCCCGGAGCAAG 800
            ||||| ||||||||
Db      826 CTGCCTGGAGCAAG 839
```

RESULT 5
ADQ31228
ID ADQ31228 standard; cDNA; 915 BP.
XX
AC ADQ31228;
XX
DT 07-OCT-2004 (first entry)
XX
DE I-Ab(beta)-E. coli heat-labile toxin B subunit-LZ-BirA fusion cDNA.
XX
KW class II major histocompatibility complex; MHC; CD4+ T-cell detection;
KW flow cytometry; mucous membrane invasive antigen;
KW I-Ab(beta)-heat-labile toxin B subunit-leucine zipper-BirA fusion; LTB;
KW ss; gene.
XX
OS Escherichia coli.
OS Unidentified.
XX
FH Key Location/Qualifiers
FT CDS 1. .915
FT /*tag= a
FT /product= "I-Ab(beta)-Escherichia coli heat-labile toxin
FT B subunit (LTB)-leucine zipper (LZ)-BirA fusion protein"
XX
PN JP2004196789-A.
XX
PD 15-JUL-2004.
XX
PF 03-DEC-2003; 2003JP-00404367.
XX
PR 03-DEC-2002; 2002JP-00351818.
XX
PA (SENT-) SENTAN KAGAKU GIJUTSU INCUBATION CENT KK.
XX
DR WPI; 2004-546819/53.
DR P-PSDB; ADQ31227.
XX
PT Peptide-Class II major histocompatibility complex (MHC) composite, useful
PT for detecting antigen specific CD4+ T-cell, comprises antigen peptide
PT containing epitope of mucous membrane invasive protein, and extracellular
PT region of MHC.
XX
PS Example 3; SEQ ID NO 13; 30pp; Japanese.
XX
CC The invention relates to a novel class II major histocompatibility
CC complex (MHC) antigenic peptide composite comprising a peptide containing
CC the T-cell antigenic determinant of a mucous membrane invasive protein
CC and the extracellular region of a class II MHC molecule or at least part
CC of the extracellular region of the class II MHC molecule having an amino
CC acid sequence comprising one or more deletions, substitutions or
CC additions. The molecule of the invention may be useful for detecting an
CC antigen-specific CD4+ T-cell by flow cytometry and for presenting a
CC microorganism-derived mucous membrane invasive protein as an antigen. The
CC method of the invention enables efficient detection of antigen-specific
CC activation of CD4+ T-cells in the mucous membrane. The current sequence
CC is that of the class II major histocompatibility complex-related I-
CC Ab(alpha)-Escherichia coli heat-labile toxin B subunit (LTB)-leucine
CC zipper (LZ)-BirA fusion cDNA of the invention.

```
 Sequence 915 BP; 228 A; 242 C; 271 G; 174 T; 0 U; 0 Other;

ery Match             66.1%;  Score 628.6;  DB 12;  Length 915;
st Local Similarity   91.9%;  Pred. No. 1.3e-136;
tches  677;  Conservative    0;  Mismatches   54;  Indels    6;  Gaps    1;

    202 GTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAACG 261
        | || ||    ||||||||||||||  |||||||| ||||||||||||||| ||||||||
    155 GAGGTGGTAGTGAAAGGCATTTCGTGTACCAGTTCATGGGCGAGTGCTACTTCACCAACG 214

    262 GGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGCT 321
        ||||||||||||||    ||||||||||||||||||||||||||||||||||||||||
    215 GGACGCAGCGCATACGATATGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGCT 274

    322 ACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAGT 381
        |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
    275 ACGACAGCGACGTGGGCGAGCACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAGT 334

    382 ACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGCA 441
        |||||||||||||||||||||||||||||||||||||||| |||||||| |||||||||
    335 ACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGCTGGACACGGTGTGCA 394

    442 GACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAATG 501
        ||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
    395 GACACAACTACGAGGGGCCGGAGACCCACACCTCCCTGCGGCGGCTTGAACAGCCCAATG 454

    502 TCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCGG 561
        ||| |||||||||||||||||||||||||||||||||||||||||||||||||||| || |
    455 TCGTCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGCTCAG 514

    562 TGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAGA 621
        |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
    515 TGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCCGGAATGGCCAGGAGGAGA 574

    622 CAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTGG 681
        | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    575 CGGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTGG 634

    682 TCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCCA 741
        |||||||||||||||||||  | |||||||||||||||||| || ||||||||||||||
    635 TCATGCTGGAGATGACCCCTCGGCGGGGAGAGGTCTACACCTGTCACGTGGAGCATCCCA 694

    742 GCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCCGAGTCTGCCCGGAGCAAGG 801
        |||||||||||||||||||||||||||||||||||||||| | | ||       ||
    695 GCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCGTCAGCAGACC------TGG 748

    802 GAGGTGGAGGATCCACTACAGCTCCATCAGCTCAGTTGAAAAAGAAATTGCAAGCACTGA 861
            | |||||||||||||||||||||||||||||||||||||| |||| ||||| |
    749 TTCCGCGCGGATCCACTACAGCTCCATCAGCTCAGTTGAAAAAGAAACTGCAGGCACTTA 808

    862 AGAAAAAGAACGCTCAGCTGAAGTGGAAACTTCAAGCCCTCAAGAAGAAACTCGCCCAGC 921
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    809 AGAAAAAGAACGCTCAGCTGAAGTGGAAACTTCAAGCCCTCAAGAAGAAACTCGCCCAGC 868

    922 ATCATCATCATCATCAT 938
        ||||||  ||   ||
    869 TGCATCATATTCTGGAT 885


LT 6
6989
 AAT86989 standard; DNA; 1382 BP.

 AAT86989;

 27-MAR-1998  (first entry)

 SCE1 single chain gene.

 Construction; major histocompatibility complex; MHC; fusion complex;
 SCE1 single chain gene; ss.

OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             6. .1382
FT                   /*tag=  a
XX
PN   WO9728191-A1.
XX
PD   07-AUG-1997.
XX
PF   30-JAN-1997;   97WO-US001617.
XX
PR   31-JAN-1996;   96US-00596387.
XX
PA   (DADE-) DADE INT INC.
XX
PI   Rhode PR,  Jiao J,  Burkhardt M,  Wong HC;
XX
DR   WPI; 1997-402555/37.
DR   P-PSDB; AAW29214.
XX
PT   Single chain major histocompatibility complex comprising linked alpha and
PT   beta chains - useful for suppressing an immune response to an auto:immune
PT   disease, e.g. multiple sclerosis, rheumatoid arthritis, diabetes
PT   mellitus, etc.
XX
PS   Example 17; Page 140-141; 217pp; English.
XX
CC   The present sequence was used in the construction of major
CC   histocompatibility complex (MHC) fusion complexes
XX
SQ   Sequence 1382 BP; 320 A; 373 C; 405 G; 284 T; 0 U; 0 Other;

  Query Match             63.9%;  Score 607.8;  DB 2;  Length 1382;
  Best Local Similarity   89.6%;  Pred. No. 1e-131;
  Matches  673;  Conservative    0;  Mismatches   57;  Indels   21;  Gaps    1;

Qy         21 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         81 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 140
              ||||||||  ||||                  |||        || | ||      |
Db         66 AGCAGCCCAAGGAC--------------------CTTAAGTATCTCTCAGGCTGTTCAC 104

Qy        141 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 200
                |  | | | |  || | ||| | |       || |  | || ||   |||
Db        105 GCTGCTCACGCTGAAATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGCGGCGGA 164

Qy        201 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 260
              || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy        261 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        321 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        381 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        441 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        501 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524
```

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      561 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

      621 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

      681 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

      741 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 771
          ||||||||||||||||||||||||||||||
      705 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 735
```

JLT 7
;0744
ACA60744 standard; DNA; 1382 BP.

ACA60744;

16-JUN-2003 (first entry)

Mouse MHC I-Ad/Ova 323-339 synthetic gene SCE1.

MHC; major histocompatibility complex; gene therapy; fusion complex; peptide-binding groove; T cell modulation; class II MHC; vaccine; autoimmune disorder; multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes mellitus; myasthenia gravis; immunogen; chronic allergy; mouse; ds; I-Ad; gene.

Mus sp.
Synthetic.

US2002198144-A1.

26-DEC-2002.

06-JUL-2001; 2001US-00900379.

29-JUL-1994; 94US-00283302.
01-FEB-1995; 95US-00382454.
17-JAN-1997; 97US-00776084.

(DADE-) DADE INT INC.

Wong HC, Rhode PR, Weidanz JA, Grammer S, Edwards AC;
Chavaillaz P, Jiao JJJ;

WPI; 2003-341126/32.
P-PSDB; ABU72108.

Novel major histocompatibility complex fusion complex having presenting peptide covalently linked to MHC molecule containing peptide-binding groove, used for suppressing immune response in multiple sclerosis, allergies.

Example 17; Fig 29; 126pp; English.

The invention relates to a major histocompatibility complex (MHC) fusion complex (I) comprising an MHC molecule that contains a peptide-binding groove, and a presenting peptide covalently (e.g. an antigenic peptide) linked to the MHC molecule, where (I) is capable of modulating the activity of a T cell. Also included are a DNA construct coding for the complex, where the MHC molecule is a class II MHC (e.g. mouse I-Ad or I-As, or human HLA-DR1 (human leukocyte antigen-DR1)), a multivalent MHC fusion complex comprising two or more linked complexes, identifying a peptide that can modulate the activity of T cells (involving introducing into host cells cloning vectors that each contain the fusion complex DNA, culturing the host cells under conditions suitable for expression of the MHC fusion complex, and selecting host cells that express MHC fusion

CC complex that modulate the activity of T cells), a single recombinant
CC expression vector comprising DNA that codes for the alpha and beta chains
CC of the fusion complex MHC protein, a single recombinant expression vector
CC comprising DNA that codes for a T cell costimulatory factor and the alpha
CC and beta chains of the MHC fusion complex. The DNA constructs can contain
CC heterologous leader peptide sequences and Kozak sequence for efficient
CC expression of the fusion complex. Also included are inducing an immune
CC response in a mammal (including vaccinating a mammal against a targeted
CC disorder, by administering DNA sequence comprising a fusion complex, or
CC DNA sequence coding for a fusion complex which is a single chain fusion
CC molecule) and suppressing an immune response in a mammal by administering
CC to the mammal a DNA sequence comprising an expression vector, encoding a
CC full length MHC molecule that contains a transmembrane domain, and a
CC presenting peptide that is a T cell receptor (TCR) antagonist or partial
CC agonist and is covalently linked to the MHC protein, or DNA sequence
CC coding for the fusion complex which is a single chain fusion molecule.
CC The methods are useful for identifying a peptide that can modulate the
CC activity of T cells, inducing an immune response in a mammal (including
CC vaccinating a mammal against a targeted disorder) and for suppressing an
CC immune response in a mammal. The disorders include an autoimmune disorder
CC such as multiple sclerosis, insulin-dependent diabetes mellitus,
CC rheumatoid arthritis, myasthenia gravis or chronic allergies. The present
CC sequence encodes a mouse MHC class II I-Ad fusion complex of the
CC invention
XX
SQ Sequence 1382 BP; 320 A; 373 C; 405 G; 284 T; 0 U; 0 Other;

Query Match 63.9%; Score 607.8; DB 8; Length 1382;
Best Local Similarity 89.6%; Pred. No. 1e-131;
Matches 673; Conservative 0; Mismatches 57; Indels 21; Gaps 1;

```
Qy         21 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         81 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 140
              ||||||||  ||||                     |||       || | ||     |
Db         66 AGCAGCCCAAGGAC--------------------CTTAAGTATCTCTCAGGCTGTTCAC 104

Qy        141 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 200
              |    | | | |   || |  ||| | |       || |  | || ||   |||
Db        105 GCTGCTCACGCTGAAATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGCGGCGGA 164

Qy        201 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 260
              || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy        261 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        321 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        381 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        441 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        501 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        561 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        621 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
      585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

      681 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

      741 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 771
          ||||||||||||||||||||||||||||||
      705 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 735


LT 8
6987
 AAT86987 standard; DNA; 1385 BP.

 AAT86987;

 27-MAR-1998  (first entry)

 SSC1 single chain gene.

 Construction; major histocompatibility complex; MHC; fusion complex;
 SSC1 single chain gene; ss.

 Synthetic.

 Key             Location/Qualifiers
 CDS             6. .1385
                 /*tag=  a

 WO9728191-A1.

 07-AUG-1997.

 30-JAN-1997;   97WO-US001617.

 31-JAN-1996;   96US-00596387.

 (DADE-) DADE INT INC.

 Rhode PR,  Jiao J,  Burkhardt M,  Wong HC;

 WPI; 1997-402555/37.
 P-PSDB; AAW29212.

 Single chain major histocompatibility complex comprising linked alpha and
 beta chains - useful for suppressing an immune response to an auto:immune
 disease, e.g. multiple sclerosis, rheumatoid arthritis, diabetes
 mellitus, etc.

 Example 17; Page 135-137; 217pp; English.

 The present sequence was used in the construction of major
 histocompatibility complex (MHC) fusion complexes

 Sequence 1385 BP; 316 A; 383 C; 399 G; 287 T; 0 U; 0 Other;

ery Match             63.9%;  Score 607.8;  DB 2;  Length 1385;
st Local Similarity   89.6%;  Pred. No. 1e-131;
tches  673;  Conservative    0;  Mismatches   57;  Indels   21;  Gaps    1;

       21 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

       81 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 140
          ||||||||  ||||                    |||      || | ||    |
       66 AGCAGCCCAAGGAC--------------------CTTAAGTATCTCTCAGGCTGTTCAC 104

      141 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 200
          |      | |  | |   || |  ||| | |       || |  | || ||   |||
      105 GCTGCTCACGCTGAAATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGCGGCGGA 164

Qy        201 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 260
              || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy        261 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        321 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        381 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        441 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        501 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        561 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        621 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        681 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        741 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 771
              ||||||||||||||||||||||||||||||
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 735


RESULT 9
ACA60742
ID   ACA60742 standard; DNA; 1385 BP.
XX
AC   ACA60742;
XX
DT   16-JUN-2003  (first entry)
XX
DE   Mouse MHC I-Ad/Ova 323-339 synthetic gene SSC1.
XX
KW   MHC; major histocompatibility complex; gene therapy; fusion complex;
KW   peptide-binding groove; T cell modulation; class II MHC; vaccine;
KW   autoimmune disorder; multiple sclerosis; rheumatoid arthritis;
KW   insulin-dependent diabetes mellitus; myasthenia gravis; immunogen;
KW   chronic allergy; mouse; ds; I-Ad; gene.
XX
OS   Mus sp.
OS   Synthetic.
XX
PN   US2002198144-A1.
XX
PD   26-DEC-2002.
XX
PF   06-JUL-2001; 2001US-00900379.
XX
PR   29-JUL-1994;   94US-00283302.
PR   01-FEB-1995;   95US-00382454.
PR   17-JAN-1997;   97US-00776084.
XX
PA   (DADE-) DADE INT INC.
XX
PI   Wong HC,  Rhode PR,  Weidanz JA,  Grammer S,  Edwards AC;
```

Chavaillaz P, Jiao JJJ;

WPI; 2003-341126/32.
P-PSDB; ABU72106.

Novel major histocompatibility complex fusion complex having presenting peptide covalently linked to MHC molecule containing peptide-binding groove, used for suppressing immune response in multiple sclerosis, allergies.

Example 17; Fig 27; 126pp; English.

The invention relates to a major histocompatibility complex (MHC) fusion complex (I) comprising an MHC molecule that contains a peptide-binding groove, and a presenting peptide covalently (e.g. an antigenic peptide) linked to the MHC molecule, where (I) is capable of modulating the activity of a T cell. Also included are a DNA construct coding for the complex, where the MHC molecule is a class II MHC (e.g. mouse I-Ad or I-As, or human HLA-DR1 (human leukocyte antigen-DR1)), a multivalent MHC fusion complex comprising two or more linked complexes, identifying a peptide that can modulate the activity of T cells (involving introducing into host cells cloning vectors that each contain the fusion complex DNA, culturing the host cells under conditions suitable for expression of the MHC fusion complex, and selecting host cells that express MHC fusion complex that modulate the activity of T cells), a single recombinant expression vector comprising DNA that codes for the alpha and beta chains of the fusion complex MHC protein, a single recombinant expression vector comprising DNA that codes for a T cell costimulatory factor and the alpha and beta chains of the MHC fusion complex. The DNA constructs can contain heterologous leader peptide sequences and Kozak sequence for efficient expression of the fusion complex. Also included are inducing an immune response in a mammal (including vaccinating a mammal against a targeted disorder, by administering DNA sequence comprising a fusion complex, or DNA sequence coding for a fusion complex which is a single chain fusion molecule) and suppressing an immune response in a mammal by administering to the mammal a DNA sequence comprising an expression vector, encoding a full length MHC molecule that contains a transmembrane domain, and a presenting peptide that is a T cell receptor (TCR) antagonist or partial agonist and is covalently linked to the MHC protein, or DNA sequence coding for the fusion complex which is a single chain fusion molecule. The methods are useful for identifying a peptide that can modulate the activity of T cells, inducing an immune response in a mammal (including vaccinating a mammal against a targeted disorder) and for suppressing an immune response in a mammal. The disorders include an autoimmune disorder such as multiple sclerosis, insulin-dependent diabetes mellitus, rheumatoid arthritis, myasthenia gravis or chronic allergies. The present sequence encodes a mouse MHC class II I-Ad fusion complex of the invention

Sequence 1385 BP; 316 A; 383 C; 399 G; 287 T; 0 U; 0 Other;

```
ıery Match            63.9%;  Score 607.8;  DB 8;  Length 1385;
ɜst Local Similarity  89.6%;  Pred. No. 1e-131;
ıtches  673;  Conservative    0;  Mismatches   57;  Indels   21;  Gaps    1;

        21 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

        81 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 140
           ||||||||  ||||                        |||       || | ||     |
        66 AGCAGCCCAAGGAC--------------------CTTAAGTATCTCTCAGGCTGTTCAC 104

       141 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 200
           |     | |  | |  . || |  ||| | |       || |  | || ||   |||
       105 GCTGCTCACGCTGAAATCAACGAAGCTGGTCGTGCTAGCGGAGGGGCGGAAGCGGCGGA 164

       201 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 260
           || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
       165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

       261 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db     225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy     321 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy     381 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy     441 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy     501 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy     561 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy     621 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy     681 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy     741 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 771
           |||||||||||||||||||||||||||||||
Db     705 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 735
```

RESULT 10
AAT86988
ID AAT86988 standard; DNA; 1508 BP.
XX
AC AAT86988;
XX
DT 27-MAR-1998 (first entry)
XX
DE SCT1 single chain gene.
XX
KW Construction; major histocompatibility complex; MHC; fusion complex;
KW SCT1 single chain gene; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 6. .1508
FT /*tag= a
XX
PN WO9728191-A1.
XX
PD 07-AUG-1997.
XX
PF 30-JAN-1997; 97WO-US001617.
XX
PR 31-JAN-1996; 96US-00596387.
XX
PA (DADE-) DADE INT INC.
XX
PI Rhode PR, Jiao J, Burkhardt M, Wong HC;
XX
DR WPI; 1997-402555/37.
DR P-PSDB; AAW29213.
XX
PT Single chain major histocompatibility complex comprising linked alpha and
PT beta chains - useful for suppressing an immune response to an auto:immune
PT disease, e.g. multiple sclerosis, rheumatoid arthritis, diabetes
PT mellitus, etc.

Example 17; Page 137-139; 217pp; English.

The present sequence was used in the construction of major histocompatibility complex (MHC) fusion complexes

Sequence 1508 BP; 337 A; 413 C; 441 G; 317 T; 0 U; 0 Other;

ery Match 63.9%; Score 607.8; DB 2; Length 1508;
st Local Similarity 89.6%; Pred. No. 1.1e-131;
tches 673; Conservative 0; Mismatches 57; Indels 21; Gaps 1;

```
       21 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

       81 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 140
          ||||||||  ||||                    |||        || | ||     |
       66 AGCAGCCCAAGGAC--------------------CTTAAGTATCTCTCAGGCTGTTCAC 104

      141 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 200
          |      | |  | |   || |  ||| | |       || |  | || ||   |||
      105 GCTGCTCACGCTGAAATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGCGGCGGA 164

      201 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 260
          || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

      261 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

      321 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

      381 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

      441 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

      501 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

      561 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

      621 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

      681 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

      741 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 771
          ||||||||||||||||||||||||||||||
      705 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 735
```

LT 11
9069
AAX89069 standard; DNA; 1508 BP.

AAX89069;

14-SEP-1999 (first entry)

DE Single chain IAd/OVA 323-229 MHC fusion protein encoding DNA.
XX
KW Major histocompatibility complex; MHC; single chain MHC; sc-MHC; Ig;
KW peptide binding groove; immunoglobulin; T cell receptor; immune response;
KW immune-related disorder; antigenic peptide; fusion protein; ss.
XX
OS Synthetic.
XX
PN WO9921572-A1.
XX
PD 06-MAY-1999.
XX
PF 13-OCT-1998; 98WO-US021520.
XX
PR 29-OCT-1997; 97US-00960190.
XX
PA (SUNO-) SUNOL MOLECULAR CORP.
XX
PI Rhode PR, Acevedo J, Burkhardt M, Jiao J, Wong HC;
XX
DR WPI; 1999-418411/35.
DR P-PSDB; AAY27111.
XX
PT Single chain major histocompatibility complex class I complexes.
XX
PS Example 1; Fig 1; 148pp; English.
XX
CC The invention relates to new single chain major histocompatibility
CC complex (sc-MHC) class II complexes that comprise a peptide binding
CC groove, and a modified class II beta 2 chain or covalently linked
CC immunoglobulin (Ig) light chain constant (C1) region. The MHC complexes
CC are useful for detection and analysis of peptide ligands, pathogenic T-
CC cells, for functional, cellular and molecular assays. They can be used to
CC identify and isolate T cell receptor and/or MHC agonists and antagonists.
CC They can be used in vivo to compete with pathogenic antigen presenting
CC cells involved in immune-related disorders. They can also be used to
CC raise antibodies and to screen immune cells. It is also use in a method
CC of suppressing an immune response in mammals. The sc-MHC complexes
CC comprising modified class II beta 2 chains and/or Ig-C1 regions are
CC soluble and provide enhanced yield. These MHC complexes also can contain
CC single antigenic peptides readily isolated from expressing cells in
CC significant quantities. The polyspecific MHC complexes also provide a
CC means to detect cells expressing multiple target structures with a single
CC complex. The present sequence represents a DNA encoding a single chain
CC IAd/OVA 323-229 MHC fusion protein
XX
SQ Sequence 1508 BP; 337 A; 413 C; 441 G; 317 T; 0 U; 0 Other;

Query Match 63.9%; Score 607.8; DB 2; Length 1508;
Best Local Similarity 89.6%; Pred. No. 1.1e-131;
Matches 673; Conservative 0; Mismatches 57; Indels 21; Gaps 1;

```
Qy         21 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         81 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 140
              ||||||||  ||||                    |||        || | ||     |
Db         66 AGCAGCCCAAGGAC--------------------CTTAAGTATCTCTCAGGCTGTTCAC 104

Qy        141 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 200
                 |      | |  | |   || |  ||| | |       || |  | || ||   |||
Db        105 GCTGCTCACGCTGAAATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGCGGCGGA 164

Qy        201 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 260
              || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy        261 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        321 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 380
```

```
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
285  TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

381  TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 440
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
345  TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

441  AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 500
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
405  AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

501  GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 560
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
465  GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

561  GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 620
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
525  GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

621  ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 680
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
585  ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

681  GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 740
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
645  GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

741  AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 771
     |||||||||||||||||||||||||||||||
705  AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 735
```

'LT 12
;0743
ACA60743 standard; DNA; 1508 BP.

ACA60743;

16-JUN-2003 (first entry)

Mouse MHC I-Ad/Ova 323-339 synthetic gene SCT1.

MHC; major histocompatibility complex; gene therapy; fusion complex; peptide-binding groove; T cell modulation; class II MHC; vaccine; autoimmune disorder; multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes mellitus; myasthenia gravis; immunogen; chronic allergy; mouse; ds; I-Ad; gene.

Mus sp.
Synthetic.

US2002198144-A1.

26-DEC-2002.

06-JUL-2001; 2001US-00900379.

29-JUL-1994; 94US-00283302.
01-FEB-1995; 95US-00382454.
17-JAN-1997; 97US-00776084.

(DADE-) DADE INT INC.

Wong HC, Rhode PR, Weidanz JA, Grammer S, Edwards AC;
Chavaillaz P, Jiao JJJ;

WPI; 2003-341126/32.
P-PSDB; ABU72107.

Novel major histocompatibility complex fusion complex having presenting peptide covalently linked to MHC molecule containing peptide-binding groove, used for suppressing immune response in multiple sclerosis, allergies.

XX
PS Example 17; Fig 28; 126pp; English.
XX
CC The invention relates to a major histocompatibility complex (MHC) fusion
CC complex (I) comprising an MHC molecule that contains a peptide-binding
CC groove, and a presenting peptide covalently (e.g. an antigenic peptide)
CC linked to the MHC molecule, where (I) is capable of modulating the
CC activity of a T cell. Also included are a DNA construct coding for the
CC complex, where the MHC molecule is a class II MHC (e.g. mouse I-Ad or I-
CC As, or human HLA-DR1 (human leukocyte antigen-DR1)), a multivalent MHC
CC fusion complex comprising two or more linked complexes, identifying a
CC peptide that can modulate the activity of T cells (involving introducing
CC into host cells cloning vectors that each contain the fusion complex DNA,
CC culturing the host cells under conditions suitable for expression of the
CC MHC fusion complex, and selecting host cells that express MHC fusion
CC complex that modulate the activity of T cells), a single recombinant
CC expression vector comprising DNA that codes for the alpha and beta chains
CC of the fusion complex MHC protein, a single recombinant expression vector
CC comprising DNA that codes for a T cell costimulatory factor and the alpha
CC and beta chains of the MHC fusion complex. The DNA constructs can contain
CC heterologous leader peptide sequences and Kozak sequence for efficient
CC expression of the fusion complex. Also included are inducing an immune
CC response in a mammal (including vaccinating a mammal against a targeted
CC disorder, by administering DNA sequence comprising a fusion complex, or
CC DNA sequence coding for a fusion complex which is a single chain fusion
CC molecule) and suppressing an immune response in a mammal by administering
CC to the mammal a DNA sequence comprising an expression vector, encoding a
CC full length MHC molecule that contains a transmembrane domain, and a
CC presenting peptide that is a T cell receptor (TCR) antagonist or partial
CC agonist and is covalently linked to the MHC protein, or DNA sequence
CC coding for the fusion complex which is a single chain fusion molecule.
CC The methods are useful for identifying a peptide that can modulate the
CC activity of T cells, inducing an immune response in a mammal (including
CC vaccinating a mammal against a targeted disorder) and for suppressing an
CC immune response in a mammal. The disorders include an autoimmune disorder
CC such as multiple sclerosis, insulin-dependent diabetes mellitus,
CC rheumatoid arthritis, myasthenia gravis or chronic allergies. The present
CC sequence encodes a mouse MHC class II I-Ad fusion complex of the
CC invention
XX
SQ Sequence 1508 BP; 337 A; 413 C; 441 G; 317 T; 0 U; 0 Other;

Query Match 63.9%; Score 607.8; DB 8; Length 1508;
Best Local Similarity 89.6%; Pred. No. 1.1e-131;
Matches 673; Conservative 0; Mismatches 57; Indels 21; Gaps 1;

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LT 13
7588
AAT17588 standard; DNA; 1382 BP.

AAT17588;

26-SEP-1996 (first entry)

Vector SCE1-derived single chain gene encoding MHC fusion complex.

MHC; major histocompatibility complex; PCR; polymerase chain reaction; T cell activity modulator; antagonist; immune disorder; allergy; multiple sclerosis; insulin-dependent diabetes mellitus; rheumatoid arthritis; myasthenia gravis; ds.

Synthetic.

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PN WO9604314-A1.
XX
PD 15-FEB-1996.
XX
PF 31-JUL-1995; 95WO-US009816.
XX
PR 29-JUL-1994; 94US-00283302.
PR 01-FEB-1995; 95US-00382454.
XX
PA (DADE-) DADE INT INC.
XX
PI Wong HC, Rhode PR, Weidanz JA, Grammer S, Edwards AC;
PI Chavaillaz P, Jiao J;
XX
DR WPI; 1996-129343/13.
DR P-PSDB; AAR98907.
XX
PT Major histocompatability complex fusion complex for modulating T cell
PT activity - used in the treatment of immune disorders, e.g. multiple
PT sclerosis, IDDM and rheumatoid arthritis.
XX
PS Example 17; Fig 29; 210pp; English.
XX
CC AAT17588 encodes a murine MHC fusion complex capable of modulating T cell
CC activity encoded by the vector SCE1. The MHC fusion complex comprises at
CC least one MHC molecule containing a peptide-binding groove and a
CC presenting peptide covalently linked to the MHC molecule and opt. a
CC transmembrane domain. DNA encoding a MHC fusion complex may be cloned
CC into a host cell to express the complex. The transformed cells may then
CC be used to identify peptides that modulate, pref. antagonise, T cell
CC activity. DNA encoding a MHC fusion complex or a single chain fusion
CC molecule may be used to vaccinate a mammal against a targeted disorder.
CC The fusion complexes may be used to suppress an immune response in an
CC animal suffering from an immune disorder e.g. multiple sclerosis, insulin
CC -dependent diabetes mellitus, rheumatoid arthritis, myasthenia gravis or
CC chronic allergies. The complexes may also be used in the treatment of
CC livestock and pets such as cats and dogs. The MHC fusion complexes can be
CC produced such that they contain a single antigenic peptide including one
CC of known structure, additionally a wide range of peptides can be
CC presented for T cell interaction
XX
SQ Sequence 1382 BP; 320 A; 374 C; 404 G; 284 T; 0 U; 0 Other;

Query Match 63.7%; Score 606.2; DB 2; Length 1382;
Best Local Similarity 89.5%; Pred. No. 2.4e-131;
Matches 672; Conservative 0; Mismatches 58; Indels 21; Gaps 1;

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Qy         81 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 140
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      741 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 771
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      705 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 735


JLT 14
17586
  AAT17586 standard; DNA; 1385 BP.

  AAT17586;

  26-SEP-1996  (first entry)

  Vector SSC1-derived single chain gene encoding MHC fusion complex.

  MHC; major histocompatibility complex; PCR; polymerase chain reaction;
  T cell activity modulator; antagonist; immune disorder; allergy;
  multiple sclerosis; insulin-dependent diabetes mellitus;
  rheumatoid arthritis; myasthenia gravis; ds.

  Synthetic.

  Key             Location/Qualifiers
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                  /note= "murine MHC class II I-Ad gene beta chain leader
                  sequence"
  misc_feature    87. .137
                  /*tag= c
                  /label= OVA_323-339
                  /note= "chicken ovalbumin residues 323-339"
  misc_feature    138. .167
                  /*tag= d
                  /note= "10 residue linker peptide"
  misc_feature    168. .452
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                  /note= "murine MHC class II I-Ad gene beta-1 domain"
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                  /*tag= f
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FT                /note= "murine MHC class II I-Ad gene beta-2 domain"
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PN  WO9604314-A1.
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PD  15-FEB-1996.
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PF  31-JUL-1995;  95WO-US009816.
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PR  29-JUL-1994;  94US-00283302.
PR  01-FEB-1995;  95US-00382454.
XX
PA  (DADE-) DADE INT INC.
XX
PI  Wong HC,  Rhode PR,  Weidanz JA,  Grammer S,  Edwards AC;
PI  Chavaillaz P,  Jiao J;
XX
DR  WPI; 1996-129343/13.
DR  P-PSDB; AAR98905.
XX
PT  Major histocompatability complex fusion complex for modulating T cell
PT  activity - used in the treatment of immune disorders, e.g. multiple
PT  sclerosis, IDDM and rheumatoid arthritis.
XX
PS  Example 17; Fig 27; 210pp; English.
XX
CC  AAT17586 encodes a murine MHC fusion complex capable of modulating T cell
CC  activity encoded by the vector SSC1. The MHC fusion complex comprises at
CC  least one MHC molecule containing a peptide-binding groove and a
CC  presenting peptide covalently linked to the MHC molecule and opt. a
CC  transmembrane domain. DNA encoding a MHC fusion complex may be cloned
CC  into a host cell to express the complex. The transformed cells may then
CC  be used to identify peptides that modulate, pref. antagonise, T cell
CC  activity. DNA encoding a MHC fusion complex or a single chain fusion
CC  molecule may be used to vaccinate a mammal against a targeted disorder.
CC  The fusion complexes may be used to suppress an immune response in an
CC  animal suffering from an immune disorder e.g. multiple sclerosis, insulin
CC  -dependent diabetes mellitus, rheumatoid arthritis, myasthenia gravis or
CC  chronic allergies. The complexes may also be used in the treatment of
CC  livestock and pets such as cats and dogs. The MHC fusion complexes can be
CC  produced such that they contain a single antigenic peptide including one
CC  of known structure, additionally a wide range of peptides can be
CC  presented for T cell interaction
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SQ  Sequence 1385 BP; 316 A; 384 C; 398 G; 287 T; 0 U; 0 Other;

  Query Match             63.7%;  Score 606.2;  DB 2;  Length 1385;
  Best Local Similarity   89.5%;  Pred. No. 2.4e-131;
  Matches  672;  Conservative    0;  Mismatches   58;  Indels   21;  Gaps    1;

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Qy         81 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 140
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Db         66 AGCAGCCCAAGGAC--------------------CTTAAGTATCTCTCAGGCTGTTCAC 104

Qy        141 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 200
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225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

321 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 380
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345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

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561 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 620
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705 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 735
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LT 15
7587
AAT17587 standard; DNA; 1508 BP.

AAT17587;

26-SEP-1996 (first entry)

Vector SCT1-derived single chain gene encoding MHC fusion complex.

MHC; major histocompatibility complex; PCR; polymerase chain reaction; T cell activity modulator; antagonist; immune disorder; allergy; multiple sclerosis; insulin-dependent diabetes mellitus; rheumatoid arthritis; myasthenia gravis; ds.

Synthetic.

Key	Location/Qualifiers
CDS	6. .1508
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sig_peptide	6. .86
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	/note= "murine MHC class II I-Ad gene beta chain leader sequence"
misc_feature	87. .137
	/*tag= c
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	/note= "chicken ovalbumin residues 323-339"
misc_feature	138. .167
	/*tag= d
	/note= "10 residue linker peptide"
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	/*tag= e
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	/note= "murine MHC class II I-Ad gene beta-1 domain"
misc_feature	453. .734
	/*tag= f
	/label= I-Ad_beta2
	/note= "murine MHC class II I-Ad gene beta-2 domain"
misc_feature	735. .806
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PN WO9604314-A1.
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PD 15-FEB-1996.
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PF 31-JUL-1995; 95WO-US009816.
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PR 29-JUL-1994; 94US-00283302.
PR 01-FEB-1995; 95US-00382454.
XX
PA (DADE-) DADE INT INC.
XX
PI Wong HC, Rhode PR, Weidanz JA, Grammer S, Edwards AC;
PI Chavaillaz P, Jiao J;
XX
DR WPI; 1996-129343/13.
DR P-PSDB; AAR98906.
XX
PT Major histocompatability complex fusion complex for modulating T cell
PT activity - used in the treatment of immune disorders, e.g. multiple
PT sclerosis, IDDM and rheumatoid arthritis.
XX
PS Example 17; Fig 28; 210pp; English.
XX
CC AAT17587 encodes a murine MHC fusion complex capable of modulating T cell
CC activity encoded by the vector SCT1. The MHC fusion complex comprises at
CC least one MHC molecule containing a peptide-binding groove and a
CC presenting peptide covalently linked to the MHC molecule and opt. a
CC transmembrane domain. DNA encoding a MHC fusion complex may be cloned
CC into a host cell to express the complex. The transformed cells may then
CC be used to identify peptides that modulate, pref. antagonise, T cell
CC activity. DNA encoding a MHC fusion complex or a single chain fusion
CC molecule may be used to vaccinate a mammal against a targeted disorder.
CC The fusion complexes may be used to suppress an immune response in an
CC animal suffering from an immune disorder e.g. multiple sclerosis, insulin
CC -dependent diabetes mellitus, rheumatoid arthritis, myasthenia gravis or
CC chronic allergies. The complexes may also be used in the treatment of
CC livestock and pets such as cats and dogs. The MHC fusion complexes can be
CC produced such that they contain a single antigenic peptide including one
CC of known structure, additionally a wide range of peptides can be
CC presented for T cell interaction
XX
SQ Sequence 1508 BP; 337 A; 414 C; 440 G; 317 T; 0 U; 0 Other;

Query Match 63.7%; Score 606.2; DB 2; Length 1508;
Best Local Similarity 89.5%; Pred. No. 2.5e-131;

```
itches  672;  Conservative    0;  Mismatches   58;  Indels   21;  Gaps    1;

        21 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

        81 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 140
           ||||||||  ||||                  |||         || | ||      |
        66 AGCAGCCCAAGGAC--------------------CTTAAGTATCTCTCAGGCTGTTCAC 104

       141 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 200
           |       | |  | |   || |  ||| | |        || |  | || ||   |||
       105 GCTGCTCACGCTGAAATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGCGGCGGA 164

       201 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 260
           || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
       165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

       261 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

       321 TACGACAGCGACGTGGGCGAGTACCGCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 380
           |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
       285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTCGGGCGGCCAGACGCCGAG 344

       381 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

       441 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

       501 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

       561 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

       621 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

       681 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

       741 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 771
           ||||||||||||||||||||||||||||||
       705 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 735

ch completed: June  1, 2006, 00:09:27
 time : 661.424 secs
```

GenCore version 5.1.8

rotein - nucleic search, using frame_plus_p2n model

on: May 31, 2006, 23:04:55 ; Search time 714 Seconds
(without alignments)
4482.160 Million cell updates/sec

le: US-10-048-116B-6
ect score: 1620
ence: 1 MALQIPSLLLSAAVVVLMVL.....LKWKLQALKKKLAQHHHHHH 306

ring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

rched: 5244920 seqs, 3486124231 residues

al number of hits satisfying chosen parameters: 10489840

mum DB seq length: 0
mum DB seq length: 2000000000

-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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TS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
ALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
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N_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
APOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

base : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

lt o.	Score	% Query Match	Length	DB	ID	Description
1	1620	100.0	921	5	AAF55099	Aaf55099 DNA encod
2	1255.5	77.5	893	2	AAT04262	Aat04262 Hybrid IA
3	1235	76.2	945	12	ADQ31225	Adq31225 I-Ab(beta
4	1219	75.2	915	12	ADQ31228	Adq31228 I-Ab(beta
5	1161.5	71.7	4724	2	AAV12068	Aav12068 Murine IA
6	1151	71.0	1013	2	AAT04269	Aat04269 Hybrid IA
7	1145	70.7	1382	2	AAT17588	Aat17588 Vector SC
8	1145	70.7	1382	2	AAT86989	Aat86989 SCE1 sing
9	1145	70.7	1382	8	ACA60744	Aca60744 Mouse MHC
10	1145	70.7	1385	2	AAT17586	Aat17586 Vector SS
11	1145	70.7	1385	2	AAT86987	Aat86987 SSC1 sing
12	1145	70.7	1385	8	ACA60742	Aca60742 Mouse MHC
13	1145	70.7	1508	2	AAT17587	Aat17587 Vector SC
14	1145	70.7	1508	2	AAT86988	Aat86988 SCT1 sing
15	1145	70.7	1508	2	AAX89069	Aax89069 Single ch
16	1145	70.7	1508	8	ACA60743	Aca60743 Mouse MHC
17	1096.5	67.7	798	12	ADJ75986	Adj75986 Marker ge
18	1096.5	67.7	798	14	ADX26090	Adx26090 Novel cel
19	1093	67.5	1085	4	ABI99040	Abi99040 Murine pC
20	1049.5	64.8	1698	4	ABI99038	Abi99038 Murine pC
21	1044.5	64.5	1662	4	ABI99039	Abi99039 Murine pC
22	979.5	60.5	702	2	AAQ03170	Aaq03170 Sequence
23	979.5	60.5	702	2	AAT06286	Aat06286 I-Ab-beta
24	979.5	60.5	702	2	AAQ56920	Aaq56920 Mouse I-A
25	972	60.0	1243	6	ABN84048	Abn84048 Single ch
26	963.5	59.5	702	2	AAQ35055	Aaq35055 IAB beta
27	957	59.1	1686	4	ABI99031	Abi99031 MBP 1-14
28	957	59.1	1701	4	ABI99028	Abi99028 IAS MBP 1
29	957	59.1	2059	4	ABI99032	Abi99032 MBP 1-14
30	957	59.1	2346	4	ABI99027	Abi99027 IAS MBP 1
31	952	58.8	1707	4	ABI99030	Abi99030 IAS MBP 9
32	949	58.6	1680	4	ABI99021	Abi99021 I-As MBP.
33	949	58.6	2053	4	ABI99029	Abi99029 IAS MBP 9
34	949	58.6	2343	4	ABI99033	Abi99033 MBP 90-10
35	871	53.8	1344	2	AAT60705	Aat60705 cDNA enco
36	854.5	52.7	1323	2	AAT60700	Aat60700 cDNA enco
37	844.5	52.1	861	14	AEC64482	Aec64482 DRB1-biot
38	839.5	51.8	1192	10	AAD63150	Aad63150 Human maj
39	839.5	51.8	1192	10	AAD62751	Aad62751 Human maj
40	839.5	51.8	1192	11	ADP88246	Adp88246 Lung canc
41	839.5	51.8	1192	13	ADR24869	Adr24869 Breast ca
42	833.5	51.5	941	12	ADO40822	Ado40822 DNA encod
43	829	51.2	562	6	ABK63510	Abk63510 Rat seque
44	829	51.2	562	10	ADB57995	Adb57995 Toxicity-
45	829	51.2	562	10	ABT41775	Abt41775 Toxicity

ALIGNMENTS

RESULT 1
AAF55099
ID AAF55099 standard; DNA; 921 BP.
XX
AC AAF55099;
XX
DT 15-MAY-2001 (first entry)
XX
DE DNA encoding a fusion protein comprising a beta chain of MHC.
XX
KW Recombinant protein; alpha chain; beta chain; MHC; immunoglobulin;
KW major histocompatibility complex; Fc region; antigen; T lymphocyte;
KW immunostimulant; vaccine; infection; tumour; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1. .921
FT /*tag= a
XX
PN WO200109194-A1.
XX
PD 08-FEB-2001.
XX
PF 28-JUL-2000; 2000WO-FR002193.
XX
PR 29-JUL-1999; 99FR-00009862.

(CNRS) CNRS CENT NAT RECH SCI.

Glaichenhaus N, Malherbe L;

WPI; 2001-182944/18.
P-PSDB; AAB67481.

New soluble recombinant protein, useful e.g. as immunostimulant, comprises dimeric major histocompatibility complex molecule fused to immunoglobulin Fc region.

Example 1; Page 34-35; 43pp; French.

The specification describes soluble recombinant proteins that comprise at least a dimer formed from the alpha and beta-chains of MHC (major histocompatibility complex) Class I and II molecules in which at least one chain has, attached to its C-terminus, at least part of the Fc region of an immunoglobulin. The recombinant proteins, when linked to an antigenic peptide, are used to count and/or purify antigen-reactive T lymphocytes and to characterize their phenotype, e.g. in preclinical evaluation of vaccines. They are also used as immunostimulants, particularly for vaccine development (against infections and tumours), to count and determine phenotype of autoreactive T cells in subjects with, or at risk of developing, autoimmune diseases, e.g. for staging or evaluating treatments, and (to purify and/or enrich Ag-reactive T cells from cell cultures or patient samples, for use in subsequent curative or preventative cellular therapy. The present sequence encodes a recombinant protein of the invention, comprising a beta chain of MHC molecules

Sequence 921 BP; 214 A; 265 C; 286 G; 156 T; 0 U; 0 Other;

nment Scores:

. No.:	6.68e-144	Length:	921
e:	1620.00	Matches:	306
ent Similarity:	100.0%	Conservative:	0
Local Similarity:	100.0%	Mismatches:	0
y Match:	100.0%	Indels:	0
	5	Gaps:	0

)-048-116B-6 (1-306) x AAF55099 (1-921)

```
        1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        1 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 60

       21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       61 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120

       41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      121 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 180

       61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      181 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 240

       81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      241 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 300

      101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      301 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 360

      121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      361 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 420

      141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      421 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 480

Qy      161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 540

Qy      181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 600

Qy      201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 660

Qy      221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 720

Qy      241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 AGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCCGAGTCTGCCCGGAGCAAG 780

Qy      261 GlyGlyGlyGlySerThrThrAlaProSerAlaGlnLeuLysLysLysLeuGlnAlaLeu 280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 GGAGGTGGAGGATCCACTACAGCTCCATCAGCTCAGTTGAAAAAGAAATTGCAAGCACTG 840

Qy      281 LysLysLysAsnAlaGlnLeuLysTrpLysLeuGlnAlaLeuLysLysLysLeuAlaGln 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 AAGAAAAAGAACGCTCAGCTGAAGTGGAAACTTCAAGCCCTCAAGAAGAAACTCGCCCAG 900

Qy      301 HisHisHisHisHisHis 306
            ||||||||||||||||||
Db      901 CATCATCATCATCATCAT 918
```

RESULT 2
AAT04262
ID AAT04262 standard; DNA; 893 BP.
XX
AC AAT04262;
XX
DT 16-APR-1996 (first entry)
XX
DE Hybrid IA beta chain gene.
XX
KW Polymerase chain reaction; PCR; primer; amplify;
KW major histocompatability complex; MHC; T-cell receptor; TCR;
KW autoimmune disease; immunodeficiency disease; immune response;
KW immunoproliferation disease; graft-host rejection; therapy; ss.
XX
OS Synthetic.
XX

FH	Key	Location/Qualifiers
FT	primer_bind	1. .16
FT		/*tag= a
FT		/note= "probable primer binding site (primer #233)"
FT	primer_bind	complement(45. .74)
FT		/*tag= b
FT		/note= "binding site for primer #261 (see AAT04260)"
FT	CDS	61. .828
FT		/*tag= c
FT		/product= "hybrid IA beta chain"
FT	sig_peptide	61. .141
FT		/*tag= d
FT		/note= "leader region"
FT	primer_bind	complement(119. .172)
FT		/*tag= e
FT		/note= "binding site for primer #331 (see AAT04261)"
FT	primer_bind	complement(158. .212)
FT		/*tag= f
FT		/note= "primer #332 binding site"
FT	primer_bind	complement(199. .250)
FT		/*tag= g
FT		/note= "primer #333 (see AAT04263) binding site"
FT	misc_feature	371. .389

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                /*tag=  h
                /note= "probable primer binding site (primer #270)"
mat_peptide     511. .825
                /*tag=  i
                /product= "IA beta chain beta 2 region"
primer_bind     521. .550
                /*tag=  j
                /note= "probable primer binding site (primer #271)"
primer_bind     532. .554
                /*tag=  k
                /note= "probable primer binding site (primer #272)"
primer_bind     808. .836
                /*tag=  l
                /note= "probable primer binding site (primer #259)"
primer_bind     877. .893
                /*tag=  m
                /note= "probable primer binding site (primer #232)"

WO9523814-A1.

08-SEP-1995.

03-MAR-1995;   95WO-US002689.

04-MAR-1994;   94US-00207481.

(NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.

Kappler JW,  Marrack P;

WPI; 1995-320543/41.
P-PSDB; AAR82533.

Peptide-MHC complex comprising antigenic peptide, linker and MHC segment
- useful as reagents for the treatment of diseases including auto-immune
diseases, immuno-stimulatory diseases or graft-host rejection.

Example 1; Page 53; 94pp; English.

This sequence represents a hybrid IA beta chain gene, containing the
chicken ovalbumin peptide (cOVA). This sequence was used in the
construction of a hybrid IA alpha beta dimer. The encoded protein (pIAd-
OVA) was found to be more stable than the IA alpha beta dimer. The
stability was decreased by the addition of a MHC groove specific binding
peptide (e.g. see AAR82527, AAR82528 and AAR82531), compared to an
increase seen on the addition of a MHC binding peptide to IE k/d-MCC.
These complexes may be used to regulate an immune response. The complexes
are capable of being recognised by a TCR alone or in combination with
additional MHC proteins. These complexes are useful for therapeutic
purposes and experimental purposes. They can also be used as reagents for
the treatment of diseases including autoimmune diseases, immunodeficiency
diseases, immunoproliferation diseases, and graft-host rejection

Sequence 893 BP; 204 A; 239 C; 275 G; 175 T; 0 U; 0 Other;

;nment Scores:
i. No.:              2.39e-109      Length:        893
:e:                  1255.50        Matches:       242
:ent Similarity:     95.4%          Conservative:  6
: Local Similarity:  93.1%          Mismatches:    7
:y Match:            77.5%          Indels:        5
                     2              Gaps:          1

!0-048-116B-6 (1-306) x AAT04262 (1-893)

          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         61 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 120

         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
            ||||||||||||||||||||||||||||||:::     :::   :::
        121 AGCAGCCCCGGGACTGAGGGCGGAAACTCCGTACATGCTGCCCATGCT------------ 168

Qy          41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
                     ::::::   :::  ||||||||||||||||||||||||||||||||||||||||||
Db         169 ---GAGATCAATGAGGCTGGCAGAGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 225

Qy          61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         226 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 285

Qy          81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         286 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 345

Qy         101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         346 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 405

Qy         121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         406 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 465

Qy         141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         466 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 525

Qy         161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         526 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 585

Qy         181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         586 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 645

Qy         201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         646 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 705

Qy         221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         706 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 765

Qy         241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         766 AGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCCGAGTCTGCCCGGAGCAAG 825

RESULT 3
ADQ31225
ID   ADQ31225 standard; cDNA; 945 BP.
XX
AC   ADQ31225;
XX
DT   07-OCT-2004  (first entry)
XX
DE   I-Ab(beta)-Cholera toxin B subunit-leucine zipper (LZ)-BirA fusion cDNA.
XX
KW   class II major histocompatibility complex; MHC; CD4+ T-cell detection;
KW   flow cytometry; mucous membrane invasive antigen;
KW   I-Ab(beta)-cholera toxin B subunit-leucine zipper-BirA fusion; CTB; ss;
KW   gene.
XX
OS   Vibrio cholerae.
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .945
FT                   /*tag=  a
FT                   /product= "I-Ab(beta)-Cholera toxin B subunit (CTB)-
FT                   leucine zipper (LZ)-BirA fusion cDNA"
XX
PN   JP2004196789-A.
XX
PD   15-JUL-2004.
XX
PF   03-DEC-2003; 2003JP-00404367.
```

03-DEC-2002; 2002JP-00351818.

(SENT-) SENTAN KAGAKU GIJUTSU INCUBATION CENT KK.

WPI; 2004-546819/53.
P-PSDB; ADQ31224.

Peptide-Class II major histocompatibility complex (MHC) composite, useful for detecting antigen specific CD4+ T-cell, comprises antigen peptide containing epitope of mucous membrane invasive protein, and extracellular region of MHC.

Example 1; SEQ ID NO 10; 30pp; Japanese.

The invention relates to a novel class II major histocompatibility complex (MHC) antigenic peptide composite comprising a peptide containing the T-cell antigenic determinant of a mucous membrane invasive protein and the extracellular region of a class II MHC molecule or at least part of the extracellular region of the class II MHC molecule having an amino acid sequence comprising one or more deletions, substitutions or additions. The molecule of the invention may be useful for detecting an antigen-specific CD4+ T-cell by flow cytometry and for presenting a microorganism-derived mucous membrane invasive protein as an antigen. The method of the invention enables efficient detection of antigen-specific activation of CD4+ T-cells in the mucous membrane. The current sequence is that of the class II major histocompatibility complex-related I-Ab(alpha)-Cholera toxin B subunit (CTB)-leucine zipper (LZ)-BirA fusion cDNA of the invention.

Sequence 945 BP; 230 A; 256 C; 294 G; 165 T; 0 U; 0 Other;

nment Scores:
. No.: 2.27e-107 Length: 945
e: 1235.00 Matches: 244
ent Similarity: 84.9% Conservative: 14
Local Similarity: 80.3% Mismatches: 42
y Match: 76.2% Indels: 4
12 Gaps: 3

)-048-116B-6 (1-306) x ADQ31225 (1-945)

```
  1 MetAlaLeuGlnIlePro---SerLeuLeuLeuSerAlaAlaValValValLeuMetVal 19
    :::   |||::::::|||           ::::::        |||   |||||||||
  4 GTGTGTCTGAAGCTCCCTGGAGGTTCCTACATGGCAAAGCTGACAGTGACACTGATGGTG 63

 20 LeuSerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHis 39
    ||||||||||||          |||:::|||     ::::::          |||
 64 CTGAGCTCCCCACTGGCTTTGGCTGGAGACTCCTGCGTGTGGAACAATAAGACGCCGCAC 123

 40 ProIleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySer 59
      |||          :::|||||||||||||||                  ||||||
124 GCGATCGCGGCCATCAGCATGGCGAACGGAGGTGGTGGGTCC---GGTGGAGGGGGAAGT 180

 60 GlyGlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThr 79
    ||||||||||||||||||||||||||||||   ||||||   ||||||||||||:::|||
181 GGAGGTGGAGGGTCTGAAAGGCATTTCGTGTACCAGTTCATGGGCGAGTGCTACTTCACC 240

 80 AsnGlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrVal 99
    ||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
241 AACGGGACGCAGCGCATACGATATGTGACCAGATACATCTACAACCGGGAGGAGTACGTG 300

100 ArgTyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAla 119
    ||||||||||||||||||||||:::||||||||||||||||||||||||||||||||||
301 CGCTACGACAGCGACGTGGGCGAGCACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCC 360

120 GluTyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAla 139
    ||||||||||||||||||||||||||||||||||||||||||:::||||||
361 GAGTACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGCTGGACACGGTG 420

140 CysArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnPro 159
    ||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
421 TGCAGACACAACTACGAGGGGCCGGAGACCCACACCTCCCTGCGGCGGCTTGAACAGCCC 480
```

```
Qy  160 AsnValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCys 179
            ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 AATGTCGTCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGC 540

Qy  180 SerValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGlu 199
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 TCAGTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCCGGAATGGCCAGGAG 600

Qy  200 GluThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnVal 219
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 GAGACGGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTC 660

Qy  220 LeuValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHis 239
        ||||||||||||||||||||||||   :::||||||||||||||||||||||||||||||
Db  661 CTGGTCATGCTGGAGATGACCCCTCGGCGGGGAGAGGTCTACACCTGTCACGTGGAGCAT 720

Qy  240 ProSerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSer 259
        ||||||||||||||||||||||||||||||||||||||||||   :::
Db  721 CCCAGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCGTCAGCA------GAC 774

Qy  260 LysGlyGlyGlyGlySerThrThrAlaProSerAlaGlnLeuLysLysLysLeuGlnAla 279
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  775 CTGGTTCCGCGCGGATCCACTACAGCTCCATCAGCTCAGTTGAAAAAGAAACTGCAGGCA 834

Qy  280 LeuLysLysLysAsnAlaGlnLeuLysTrpLysLeuGlnAlaLeuLysLysLysLeuAla 299
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  835 CTTAAGAAAAAGAACGCTCAGCTGAAGTGGAAACTTCAAGCCCTCAAGAAGAAACTCGCC 894

Qy  300 GlnHisHisHis 303
            |||   ||||||
Db  895 CAGCTGCATCAT 906
```

RESULT 4
ADQ31228
ID ADQ31228 standard; cDNA; 915 BP.
XX
AC ADQ31228;
XX
DT 07-OCT-2004 (first entry)
XX
DE I-Ab(beta)-E. coli heat-labile toxin B subunit-LZ-BirA fusion cDNA.
XX
KW class II major histocompatibility complex; MHC; CD4+ T-cell detection;
KW flow cytometry; mucous membrane invasive antigen;
KW I-Ab(beta)-heat-labile toxin B subunit-leucine zipper-BirA fusion; LTB;
KW ss; gene.
XX
OS Escherichia coli.
OS Unidentified.
XX
FH Key Location/Qualifiers
FT CDS 1. .915
FT /*tag= a
FT /product= "I-Ab(beta)-Escherichia coli heat-labile toxin
FT B subunit (LTB)-leucine zipper (LZ)-BirA fusion protein"
XX
PN JP2004196789-A.
XX
PD 15-JUL-2004.
XX
PF 03-DEC-2003; 2003JP-00404367.
XX
PR 03-DEC-2002; 2002JP-00351818.
XX
PA (SENT-) SENTAN KAGAKU GIJUTSU INCUBATION CENT KK.
XX
DR WPI; 2004-546819/53.
DR P-PSDB; ADQ31227.
XX
PT Peptide-Class II major histocompatibility complex (MHC) composite, useful
PT for detecting antigen specific CD4+ T-cell, comprises antigen peptide
PT containing epitope of mucous membrane invasive protein, and extracellular

region of MHC.

Example 3; SEQ ID NO 13; 30pp; Japanese.

The invention relates to a novel class II major histocompatibility complex (MHC) antigenic peptide composite comprising a peptide containing the T-cell antigenic determinant of a mucous membrane invasive protein and the extracellular region of a class II MHC molecule or at least part of the extracellular region of the class II MHC molecule having an amino acid sequence comprising one or more deletions, substitutions or additions. The molecule of the invention may be useful for detecting an antigen-specific CD4+ T-cell by flow cytometry and for presenting a microorganism-derived mucous membrane invasive protein as an antigen. The method of the invention enables efficient detection of antigen-specific activation of CD4+ T-cells in the mucous membrane. The current sequence is that of the class II major histocompatibility complex-related I-Ab(alpha)-Escherichia coli heat-labile toxin B subunit (LTB)-leucine zipper (LZ)-BirA fusion cDNA of the invention.

Sequence 915 BP; 228 A; 242 C; 271 G; 174 T; 0 U; 0 Other;

nment Scores:

i. No.:	7.14e-106	Length:	915
e:	1219.00	Matches:	242
ent Similarity:	84.9%	Conservative:	16
: Local Similarity:	79.6%	Mismatches:	32
y Match:	75.2%	Indels:	14
	12	Gaps:	5

.0-048-116B-6 (1-306) x ADQ31228 (1-915)

```
        1 MetAlaLeuGlnIlePro---SerLeuLeuLeuSerAlaAlaValValValLeuMetVal 19
          :::   |||:::::|||         ::::::       |||   |||||||||
        4 GTGTGTCTGAAGCTCCCTGGAGGTTCCTACATGGCAAAGCTGACAGTGACACTGATGGTG 63

       20 LeuSerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHis 39
          ||||||||||||          |||:::|||
       64 CTGAGCTCCCCACTGGCTTTGGCTGGAGACTCC---------------GGTAAAAGAGAA 108

       40 ProIleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySer 59
             :::::::::      ::::::   ||||||||||||||||||||||||
      109 ATGGTTATCATT------ACATTTAAGGGTGGTGGTGGTTCTTTAGTTCCTAGA------ 156

       60 GlyGlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThr 79
             ||||||||||||||||||||||||   ||||||   ||||||||||||:::|||
      157 ------GGTGGTAGTGAAAGGCATTTCGTGTACCAGTTCATGGGCGAGTGCTACTTCACC 210

       80 AsnGlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrVal 99
          ||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
      211 AACGGGACGCAGCGCATACGATATGTGACCAGATACATCTACAACCGGGAGGAGTACGTG 270

      100 ArgTyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAla 119
          ||||||||||||||||||||||||:::||||||||||||||||||||||||||||||||
      271 CGCTACGACAGCGACGTGGGCGAGCACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCC 330

      120 GluTyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAla 139
          ||||||||||||||||||||||||||||||||||||||||||||:::||||||
      331 GAGTACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGCTGGACACGGTG 390

      140 CysArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnPro 159
          ||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
      391 TGCAGACACAACTACGAGGGGCCGGAGACCCACACCTCCCTGCGGCGGCTTGAACAGCCC 450

      160 AsnValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCys 179
          ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
      451 AATGTCGTCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGC 510

      180 SerValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGlu 199
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      511 TCAGTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCCGGAATGGCCAGGAG 570

      200 GluThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnVal 219
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db      571 GAGACGGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTC 630

Qy      220 LeuValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHis 239
            ||||||||||||||||||||||||   :::||||||||||||||||||||||||||||
Db      631 CTGGTCATGCTGGAGATGACCCCTCGGCGGGGAGAGGTCTACACCTGTCACGTGGAGCAT 690

Qy      240 ProSerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSer 259
            ||||||||||||||||||||||||||||||||||||||||||||||||||||   :::
Db      691 CCCAGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCGTCAGCA------GAC 744

Qy      260 LysGlyGlyGlyGlySerThrThrAlaProSerAlaGlnLeuLysLysLysLeuGlnAla 279
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      745 CTGGTTCCGCGCGGATCCACTACAGCTCCATCAGCTCAGTTGAAAAAGAAACTGCAGGCA 804

Qy      280 LeuLysLysLysAsnAlaGlnLeuLysTrpLysLeuGlnAlaLeuLysLysLysLeuAla 299
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      805 CTTAAGAAAAAGAACGCTCAGCTGAAGTGGAAACTTCAAGCCCTCAAGAAGAAACTCGCC 864

Qy      300 GlnHisHisHis 303
            |||   ||||||
Db      865 CAGCTGCATCAT 876
```

RESULT 5
AAV12068
ID AAV12068 standard; cDNA; 4724 BP.
XX
AC AAV12068;
XX
DT 08-JUN-1998 (first entry)
XX
DE Murine IAd beta chain cDNA.
XX
KW Major histocompatibility class II antigen; MHC class II; T cell;
KW T lymphocyte; Th1; Th2; activation; CD4+; antigen presenting cell; APC;
KW autoimmune disease; diabetes; multiple sclerosis; autoimmune thyroiditis;
KW systemic lupus erythromatosus; myasthenia gravis; Crohn's disease;
KW inflammatory bowel disease; allergy; asthma; contact sensitivity;
KW immunotherapy; therapy; IAd beta chain; mouse; ds; circular; cyclic.
XX
OS Mus musculus.
XX
PN WO9746256-A1.
XX
PD 11-DEC-1997.
XX
PF 22-MAY-1997; 97WO-US008697.
XX
PR 23-MAY-1996; 96US-0018175P.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Webb SR, Winqvist O, Karlsson L, Jackson MR, Peterson PA;
XX
DR WPI; 1998-041895/04.
XX
PT Synthetic antigen presenting cell for activating CD4+ T cells - useful to
PT treat autoimmune disease, e.g. diabetes, multiple sclerosis, Crohn's
PT disease and inflammatory bowel disease, or allergy, e.g. asthma and
PT contact sensitivity.
XX
PS Example 2; Page 94-96; 141pp; English.
XX
CC This nucleotide sequence comprises a PCR product obtained by
CC amplification of mouse splenocyte cDNA using primers (see AAV12065 and
CC AAV12066) designed for the amplification of IAd beta chain full-length
CC cDNA. IAd alpha chain cDNA (see AAV12067) has been similarly obtained.
CC The IAd sequences were cloned into metallothionein promoter (see
CC AAV12062)-driven vector pRmHa-3 prior to sequencing. Major
CC histocompatibility complex (MHC) class II IAd heterodimers were expressed
CC at the cell surface of transfected Drosophila Schneider 2 (ATCC CRL
CC 10974) cells. The invention relates to the preparation and use of
CC synthetic antigen presenting matrices, in particular antigen presenting
CC cells such as insect cells that have been transfected to produce MHC

antigen presenting molecules with one or more accessory molecules. The matrices are used to activate naive CD4+ T cells and to shift the ongoing activation state into a preferred differentiated population of Th1 or Th2 cells. Applications include the treatment of autoimmune disease, e.g. diabetes, multiple sclerosis, autoimmune thyroiditis, systemic lupus erythematosus, myasthenia gravis, Crohn's disease and inflammatory bowel disease, or an allergy, e.g. asthma and contact sensitivity

Sequence 4724 BP; 1196 A; 1194 C; 1200 G; 1134 T; 0 U; 0 Other;

ıment Scores:

. No.:	1.85e-99	Length:	4724
ɜ:	1161.50	Matches:	228
ɜnt Similarity:	85.8%	Conservative:	1
Local Similarity:	85.4%	Mismatches:	1
/ Match:	71.7%	Indels:	37
	2	Gaps:	2

)-048-116B-6 (1-306) x AAV12068 (1-4724)

```
        1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      451 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 510

       21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
          ||||||||||||||||||||||||||
      511 AGCAGCCCAGGGACTGAGGGCGGAAAC------------------------------ 537

       41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60

      537 ------------------------------------------------------------ 537

       61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||
      538 ---------TCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 588

       81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      589 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 648

      101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      649 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 708

      121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      709 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 768

      141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      769 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 828

      161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
          :::||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      829 ATCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 888

      181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      889 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 948

      201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      949 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 1008

      221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     1009 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 1068

      241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     1069 AGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCCGAGTCTGCCCGGAGCAAG 1128

      261 ---------GlyGlyGlyGly 264
```

```
                    |||   ||||||
Db       1129 ATGTTGAGCGGCATCGGGGGC 1149
```

RESULT 6
AAT04269
ID AAT04269 standard; DNA; 1013 BP.
XX
AC AAT04269;
XX
DT 16-APR-1996 (first entry)
XX
DE Hybrid IA beta chain gene.
XX
KW Major histocompatability complex; MHC; T-cell receptor; TCR;
KW autoimmune disease; immunodeficiency disease; immune response;
KW immunoproliferation disease; graft-host rejection; therapy; B cell;
KW M12.C3; pM12-IAb-Ea; ss.
XX
OS Synthetic.
XX

FH	Key	Location/Qualifiers
FT	primer_bind	1. .18
FT		/*tag= a
FT		/note= "probable primer binding site (primer #76)"
FT	primer_bind	complement(40. .74)
FT		/*tag= b
FT		/note= "binding site for primer #362 (see AAT04270)"
FT	CDS	63. .959
FT		/*tag= c
FT		/product= "hybrid IA beta chain"
FT	sig_peptide	63. .143
FT		/*tag= d
FT		/note= "leader region"
FT	primer_bind	complement(140. .191)
FT		/*tag= e
FT		/note= "binding site for primer #363 (see AAT04271)"
FT	primer_bind	complement(177. .226)
FT		/*tag= f
FT		/note= "primer #364 binding site"
FT	primer_bind	complement(212. .266)
FT		/*tag= g
FT		/note= "primer #365 (see AAT04272) binding site"
FT	primer_bind	385. .403
FT		/*tag= h
FT		/note= "probable primer binding site (primer #270)"
FT	mat_peptide	531. .959
FT		/*tag= i
FT		/product= "IA beta chain beta 2 region"
FT	primer_bind	535. .564
FT		/*tag= j
FT		/note= "probable primer binding site (primer #271)"
FT	primer_bind	544. .568
FT		/*tag= k
FT		/note= "probable primer binding site (primer #272)"
FT	primer_bind	823. .850
FT		/*tag= l
FT		/note= "probable primer binding site (primer #259)"
FT	primer_bind	942. .976
FT		/*tag= m
FT		/note= "probable primer binding site (primer #366)"
FT	primer_bind	1000. .1013
FT		/*tag= n
FT		/note= "probable primer binding site (primer #59)"

XX
PN WO9523814-A1.
XX
PD 08-SEP-1995.
XX
PF 03-MAR-1995; 95WO-US002689.
XX
PR 04-MAR-1994; 94US-00207481.
XX
PA (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.

Kappler JW, Marrack P;

WPI; 1995-320543/41.
P-PSDB; AAR82538.

Peptide-MHC complex comprising antigenic peptide, linker and MHC segment - useful as reagents for the treatment of diseases including auto-immune diseases, immuno-stimulatory diseases or graft-host rejection.

Example 2; Page 65; 94pp; English.

This sequence represents a hybrid IA beta chain gene. This sequence contains a fragment of the IE alpha chain (residues 56-73), as well as a linker and cleavage site. This sequence was transfected into a B cell line (M12.C3) using plasmid pM12-IAb-Ea. It was found that the encoded sequence was expressed in these cells. Complexes such as this may be used to regulate an immune response. The complexes are capable of being recognised by a TCR alone or in combination with additional MHC proteins. These complexes are useful for therapeutic purposes and experimental purposes. They can also be used as reagents for the treatment of diseases including autoimmune diseases, immunodeficiency diseases, immunoproliferation diseases, and graft-host rejection

Sequence 1013 BP; 220 A; 272 C; 327 G; 192 T; 0 U; 2 Other;

nment Scores:

i. No.:	2.31e-99	Length:	1013
e:	1151.00	Matches:	230
ent Similarity:	86.8%	Conservative:	6
: Local Similarity:	84.6%	Mismatches:	22
y Match:	71.0%	Indels:	14
	2	Gaps:	4

0-048-116B-6 (1-306) x AAT04269 (1-1013)

```
Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCGGCTGCTGTGGTGGTGCTCATGGTGCTG 122

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              ||||||||||||||||||||||:::|||           |||   |||
Db        123 AGCAGCCCAGGGACTGAGGGCGGAGACTCC---------GAAGCTAGCTTTGAGGCTCAG 173

Qy         41 ---------------IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuVal 55
                           |||   |||      :::     ||||||   |||
Db        174 GGTGCACTGGCCAACATTGCTGTCGACAAGGCTGGAGGTGGTGGATCCGGTGGA------ 227

Qy         56 ProArgGlySerGlyGlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGlu 75
              ||||||||||||||||||||||||||||||||    ||||||  ||||||
Db        228 ---GGGGGAAGTGGAGGTGGAGGGTCTGAAAGGCATTTCGTGTACCAGTTCATGGGCGAG 284

Qy         76 CysTyrTyrThrAsnGlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArg 95
              ||||||:::|||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        285 TGCTACTTCACCAACGGGACGCAGCGCATACGATATGTGACCAGATACATCTACAACCGG 344

Qy         96 GluGluTyrValArgTyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGly 115
              ||||||||||||||||||||||||||||||||:::||||||||||||||||||||||||
Db        345 GAGGAGTACGTGCGCTACGACAGCGACGTGGGCGAGCACCGCGCGGTGACCGAGCTGGGG 404

Qy        116 ArgProAspAlaGluTyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGlu 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 CGGCCAGACGCCGAGTACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAG 464

Qy        136 ValAspThrAlaCysArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArg 155
              |||||||||  ||||||||||||||||||||||||||||||  ||||||||||||||||
Db        465 GTGGACACGGTGTGCAGACACAACTACGAGGGGCCGGAGACCCACACCTCCCTGCGGCGG 524

Qy        156 LeuGluGlnProAsnValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsn 175
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db        525 CTTGAACAGCCCAATGTCGTCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAAC 584

Qy        176 ThrLeuValCysSerValThrAspPheTyrProAlaLysIleLysValArgTrpPheArg 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACTCTGGTCTGCTCAGTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCCGG 644

Qy        196 AsnGlyGlnGluGluThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrp 215
              ||||||||||||||||||||||||||:::||||||||||||||||||||||||||||||||
Db        645 AATGGCCAGGAGGAGACGGTGGGGCTCTCATCCACACAGCTTATTAGGAATGGGGACTGG 704

Qy        216 ThrPheGlnValLeuValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCys 235
              ||||||||||||||||||||||||||||||||||||    :::||||||||||||||||||
Db        705 ACCTTCCAGGTCCTGGTCATGCTGGAGATGACCCCTCGGCGGGGAGAGGTCTAYACCTGT 764

Qy        236 HisValGluHisProSerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGlu 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        765 CACGTGGAGCATCCCAGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCTGAG 824

Qy        256 SerAlaArgSerLys---------GlyGlyGlyGly 264
              ||||||   ||||||         |||   ||||||
Db        825 TCTGCCTGGAGCAAGATGTTGAGCGGCATCGGGGGC 860
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RESULT 7
AAT17588
ID AAT17588 standard; DNA; 1382 BP.
XX
AC AAT17588;
XX
DT 26-SEP-1996 (first entry)
XX
DE Vector SCE1-derived single chain gene encoding MHC fusion complex.
XX
KW MHC; major histocompatibility complex; PCR; polymerase chain reaction;
KW T cell activity modulator; antagonist; immune disorder; allergy;
KW multiple sclerosis; insulin-dependent diabetes mellitus;
KW rheumatoid arthritis; myasthenia gravis; ds.
XX
OS Synthetic.
XX

FH	Key	Location/Qualifiers
FT	CDS	6. .1382
FT		/*tag= a
FT	sig_peptide	6. .86
FT		/*tag= b
FT		/label= I-Ad_beta_chain_leader
FT		/note= "murine MHC class II I-Ad gene beta chain leader sequence"
FT	misc_feature	87. .137
FT		/*tag= c
FT		/label= OVA_323-339
FT		/note= "chicken ovalbumin residues 323-339"
FT	misc_feature	138. .167
FT		/*tag= d
FT		/note= "10 residue linker peptide"
FT	misc_feature	168. .452
FT		/*tag= e
FT		/label= I-Ad_beta1
FT		/note= "murine MHC class II I-Ad gene beta-1 domain"
FT	misc_feature	453. .734
FT		/*tag= f
FT		/label= I-Ad_beta2
FT		/note= "murine MHC class II I-Ad gene beta-2 domain"
FT	misc_feature	735. .806
FT		/*tag= g
FT		/note= "24 residue peptide linker"
FT	misc_feature	807. .1067
FT		/*tag= h
FT		/label= I-Ad_alpha1
FT		/note= "murine MHC class II I-Ad gene alpha-2 domain"
FT	misc_feature	1068. .1352
FT		/*tag= i
FT		/label= I-Ad_alpha2
FT		/note= "murine MHC class II I-Ad gene alpha-2 domain"
FT	misc_feature	1353. .1379
FT		/*tag= j
FT		/note= "EE tag"

WO9604314-A1.

15-FEB-1996.

31-JUL-1995; 95WO-US009816.

29-JUL-1994; 94US-00283302.
01-FEB-1995; 95US-00382454.

(DADE-) DADE INT INC.

Wong HC, Rhode PR, Weidanz JA, Grammer S, Edwards AC;
Chavaillaz P, Jiao J;

WPI; 1996-129343/13.
P-PSDB; AAR98907.

Major histocompatability complex fusion complex for modulating T cell activity - used in the treatment of immune disorders, e.g. multiple sclerosis, IDDM and rheumatoid arthritis.

Example 17; Fig 29; 210pp; English.

AAT17588 encodes a murine MHC fusion complex capable of modulating T cell activity encoded by the vector SCE1. The MHC fusion complex comprises at least one MHC molecule containing a peptide-binding groove and a presenting peptide covalently linked to the MHC molecule and opt. a transmembrane domain. DNA encoding a MHC fusion complex may be cloned into a host cell to express the complex. The transformed cells may then be used to identify peptides that modulate, pref. antagonise, T cell activity. DNA encoding a MHC fusion complex or a single chain fusion molecule may be used to vaccinate a mammal against a targeted disorder. The fusion complexes may be used to suppress an immune response in an animal suffering from an immune disorder e.g. multiple sclerosis, insulin -dependent diabetes mellitus, rheumatoid arthritis, myasthenia gravis or chronic allergies. The complexes may also be used in the treatment of livestock and pets such as cats and dogs. The MHC fusion complexes can be produced such that they contain a single antigenic peptide including one of known structure, additionally a wide range of peptides can be presented for T cell interaction

Sequence 1382 BP; 320 A; 374 C; 404 G; 284 T; 0 U; 0 Other;

ıment Scores:

. No.:	1.3e-98	Length:	1382
e:	1145.00	Matches:	227
ent Similarity:	87.2%	Conservative:	4
Local Similarity:	85.7%	Mismatches:	24
y Match:	70.7%	Indels:	10
	2	Gaps:	3

)-048-116B-6 (1-306) x AAT17588 (1-1382)

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        1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

       21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
          |||||||||   |||         :::           :::         |||
       66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

       41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
          |||     :::|||       ||||||||||||||                  |||
      120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC--------------GGCGGA 164

       61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
          ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
      165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

       81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy      101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTCGGGCGGCCAGACGCCGAG 344

Qy      121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy      141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy      161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy      181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy      201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy      221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy      241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
            ||||||||||||||||||||||||||||||||           :::
Db      705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy      261 GlyGlyGlyGlySer 265
            |||||||||||||||
Db      756 GGCGGTGGTGGTTCC 770
```

RESULT 8
AAT86989
ID AAT86989 standard; DNA; 1382 BP.
XX
AC AAT86989;
XX
DT 27-MAR-1998 (first entry)
XX
DE SCE1 single chain gene.
XX
KW Construction; major histocompatibility complex; MHC; fusion complex;
KW SCE1 single chain gene; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 6. .1382
FT /*tag= a
XX
PN WO9728191-A1.
XX
PD 07-AUG-1997.
XX
PF 30-JAN-1997; 97WO-US001617.
XX
PR 31-JAN-1996; 96US-00596387.
XX
PA (DADE-) DADE INT INC.
XX
PI Rhode PR, Jiao J, Burkhardt M, Wong HC;
XX
DR WPI; 1997-402555/37.
DR P-PSDB; AAW29214.
XX
PT Single chain major histocompatibility complex comprising linked alpha and
PT beta chains - useful for suppressing an immune response to an auto:immune

disease, e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, etc.

Example 17; Page 140-141; 217pp; English.

The present sequence was used in the construction of major histocompatibility complex (MHC) fusion complexes

Sequence 1382 BP; 320 A; 373 C; 405 G; 284 T; 0 U; 0 Other;

nment Scores:

l. No.:	1.3e-98	Length:	1382
e:	1145.00	Matches:	227
ent Similarity:	87.2%	Conservative:	4
Local Similarity:	85.7%	Mismatches:	24
y Match:	70.7%	Indels:	10
	2	Gaps:	3

.0-048-116B-6 (1-306) x AAT86989 (1-1382)

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        1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
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        6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

       21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
          |||||||||   |||         :::           :::         |||
       66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

       41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
          |||     :::|||       ||||||||||||||                  |||
      120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC--------------GGCGGA 164

       61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
          |||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||
      165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

       81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

      101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

      121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

      141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

      161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

      181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

      201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

      221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

      241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
          ||||||||||||||||||||||||||||||||  :::
      705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

      261 GlyGlyGlyGlySer 265
```

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                  ||||||||||||||||
Db        756 GGCGGTGGTGGTTCC 770
```

RESULT 9
ACA60744
ID ACA60744 standard; DNA; 1382 BP.
XX
AC ACA60744;
XX
DT 16-JUN-2003 (first entry)
XX
DE Mouse MHC I-Ad/Ova 323-339 synthetic gene SCE1.
XX
KW MHC; major histocompatibility complex; gene therapy; fusion complex;
KW peptide-binding groove; T cell modulation; class II MHC; vaccine;
KW autoimmune disorder; multiple sclerosis; rheumatoid arthritis;
KW insulin-dependent diabetes mellitus; myasthenia gravis; immunogen;
KW chronic allergy; mouse; ds; I-Ad; gene.
XX
OS Mus sp.
OS Synthetic.
XX
PN US2002198144-A1.
XX
PD 26-DEC-2002.
XX
PF 06-JUL-2001; 2001US-00900379.
XX
PR 29-JUL-1994; 94US-00283302.
PR 01-FEB-1995; 95US-00382454.
PR 17-JAN-1997; 97US-00776084.
XX
PA (DADE-) DADE INT INC.
XX
PI Wong HC, Rhode PR, Weidanz JA, Grammer S, Edwards AC;
PI Chavaillaz P, Jiao JJJ;
XX
DR WPI; 2003-341126/32.
DR P-PSDB; ABU72108.
XX
PT Novel major histocompatibility complex fusion complex having presenting
PT peptide covalently linked to MHC molecule containing peptide-binding
PT groove, used for suppressing immune response in multiple sclerosis,
PT allergies.
XX
PS Example 17; Fig 29; 126pp; English.
XX
CC The invention relates to a major histocompatibility complex (MHC) fusion
CC complex (I) comprising an MHC molecule that contains a peptide-binding
CC groove, and a presenting peptide covalently (e.g. an antigenic peptide)
CC linked to the MHC molecule, where (I) is capable of modulating the
CC activity of a T cell. Also included are a DNA construct coding for the
CC complex, where the MHC molecule is a class II MHC (e.g. mouse I-Ad or I-
CC As, or human HLA-DR1 (human leukocyte antigen-DR1)), a multivalent MHC
CC fusion complex comprising two or more linked complexes, identifying a
CC peptide that can modulate the activity of T cells (involving introducing
CC into host cells cloning vectors that each contain the fusion complex DNA,
CC culturing the host cells under conditions suitable for expression of the
CC MHC fusion complex, and selecting host cells that express MHC fusion
CC complex that modulate the activity of T cells), a single recombinant
CC expression vector comprising DNA that codes for the alpha and beta chains
CC of the fusion complex MHC protein, a single recombinant expression vector
CC comprising DNA that codes for a T cell costimulatory factor and the alpha
CC and beta chains of the MHC fusion complex. The DNA constructs can contain
CC heterologous leader peptide sequences and Kozak sequence for efficient
CC expression of the fusion complex. Also included are inducing an immune
CC response in a mammal (including vaccinating a mammal against a targeted
CC disorder, by administering DNA sequence comprising a fusion complex, or
CC DNA sequence coding for a fusion complex which is a single chain fusion
CC molecule) and suppressing an immune response in a mammal by administering
CC to the mammal a DNA sequence comprising an expression vector, encoding a
CC full length MHC molecule that contains a transmembrane domain, and a
CC presenting peptide that is a T cell receptor (TCR) antagonist or partial

agonist and is covalently linked to the MHC protein, or DNA sequence coding for the fusion complex which is a single chain fusion molecule. The methods are useful for identifying a peptide that can modulate the activity of T cells, inducing an immune response in a mammal (including vaccinating a mammal against a targeted disorder) and for suppressing an immune response in a mammal. The disorders include an autoimmune disorder such as multiple sclerosis, insulin-dependent diabetes mellitus, rheumatoid arthritis, myasthenia gravis or chronic allergies. The present sequence encodes a mouse MHC class II I-Ad fusion complex of the invention

Sequence 1382 BP; 320 A; 373 C; 405 G; 284 T; 0 U; 0 Other;

ıment Scores:

. No.:	1.3e-98	Length:	1382
ɜ:	1145.00	Matches:	227
ɜnt Similarity:	87.2%	Conservative:	4
Local Similarity:	85.7%	Mismatches:	24
ɣ Match:	70.7%	Indels:	10
	8	Gaps:	3

)-048-116B-6 (1-306) x ACA60744 (1-1382)

```
        1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
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        6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

       21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
          |||||||||   |||         :::           :::         |||
       66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

       41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
          |||      :::|||          |||||||||||||||                 |||
      120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC--------------GGCGGA 164

       61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
          ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
      165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

       81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

      101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

      121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

      141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

      161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

      181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

      201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

      221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

      241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
          ||||||||||||||||||||||||||||||  :::
```

```
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy        261 GlyGlyGlyGlySer 265
              |||||||||||||||
Db        756 GGCGGTGGTGGTTCC 770
```

RESULT 10
AAT17586
ID AAT17586 standard; DNA; 1385 BP.
XX
AC AAT17586;
XX
DT 26-SEP-1996 (first entry)
XX
DE Vector SSC1-derived single chain gene encoding MHC fusion complex.
XX
KW MHC; major histocompatibility complex; PCR; polymerase chain reaction;
KW T cell activity modulator; antagonist; immune disorder; allergy;
KW multiple sclerosis; insulin-dependent diabetes mellitus;
KW rheumatoid arthritis; myasthenia gravis; ds.
XX
OS Synthetic.
XX

FH	Key	Location/Qualifiers
FT	CDS	6. .1385
FT		/*tag= a
FT	sig_peptide	6. .86
FT		/*tag= b
FT		/label= I-Ad_beta_chain_leader
FT		/note= "murine MHC class II I-Ad gene beta chain leader sequence"
FT	misc_feature	87. .137
FT		/*tag= c
FT		/label= OVA_323-339
FT		/note= "chicken ovalbumin residues 323-339"
FT	misc_feature	138. .167
FT		/*tag= d
FT		/note= "10 residue linker peptide"
FT	misc_feature	168. .452
FT		/*tag= e
FT		/label= I-Ad_beta1
FT		/note= "murine MHC class II I-Ad gene beta-1 domain"
FT	misc_feature	453. .734
FT		/*tag= f
FT		/label= I-Ad_beta2
FT		/note= "murine MHC class II I-Ad gene beta-2 domain"
FT	misc_feature	735. .806
FT		/*tag= g
FT		/note= "24 residue peptide linker"
FT	misc_feature	807. .1067
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FT		/label= I-Ad_alpha1
FT		/note= "murine MHC class II I-Ad gene alpha-2 domain"
FT	misc_feature	1068. .1352
FT		/*tag= i
FT		/label= I-Ad_alpha2
FT		/note= "murine MHC class II I-Ad gene alpha-2 domain"
FT	misc_feature	1353. .1382
FT		/*tag= j
FT		/note= "6xHis tag"

XX
PN WO9604314-A1.
XX
PD 15-FEB-1996.
XX
PF 31-JUL-1995; 95WO-US009816.
XX
PR 29-JUL-1994; 94US-00283302.
PR 01-FEB-1995; 95US-00382454.
XX
PA (DADE-) DADE INT INC.
XX
PI Wong HC, Rhode PR, Weidanz JA, Grammer S, Edwards AC;

Chavaillaz P, Jiao J;

WPI; 1996-129343/13.
P-PSDB; AAR98905.

Major histocompatability complex fusion complex for modulating T cell activity - used in the treatment of immune disorders, e.g. multiple sclerosis, IDDM and rheumatoid arthritis.

Example 17; Fig 27; 210pp; English.

AAT17586 encodes a murine MHC fusion complex capable of modulating T cell activity encoded by the vector SSC1. The MHC fusion complex comprises at least one MHC molecule containing a peptide-binding groove and a presenting peptide covalently linked to the MHC molecule and opt. a transmembrane domain. DNA encoding a MHC fusion complex may be cloned into a host cell to express the complex. The transformed cells may then be used to identify peptides that modulate, pref. antagonise, T cell activity. DNA encoding a MHC fusion complex or a single chain fusion molecule may be used to vaccinate a mammal against a targeted disorder. The fusion complexes may be used to suppress an immune response in an animal suffering from an immune disorder e.g. multiple sclerosis, insulin -dependent diabetes mellitus, rheumatoid arthritis, myasthenia gravis or chronic allergies. The complexes may also be used in the treatment of livestock and pets such as cats and dogs. The MHC fusion complexes can be produced such that they contain a single antigenic peptide including one of known structure, additionally a wide range of peptides can be presented for T cell interaction

Sequence 1385 BP; 316 A; 384 C; 398 G; 287 T; 0 U; 0 Other;

ɣnment Scores:
i. No.: 1.3e-98 Length: 1385
:e: 1145.00 Matches: 227
:ent Similarity: 87.2% Conservative: 4
: Local Similarity: 85.7% Mismatches: 24
:y Match: 70.7% Indels: 10
2 Gaps: 3

:0-048-116B-6 (1-306) x AAT17586 (1-1385)

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  1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
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  6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

 21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
    |||||||||   |||          :::          :::          |||
 66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

 41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
    |||      :::|||         ||||||||||||||                   |||
120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC---------------GGCGGA 164

 61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
    |||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

 81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTCGGGCGGCCAGACGCCGAG 344

121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464
```

```
Qy      161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy      181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy      201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy      221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy      241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
            ||||||||||||||||||||||||||||||||           :::
Db      705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy      261 GlyGlyGlyGlySer 265
            |||||||||||||||
Db      756 GGCGGTGGTGGTTCC 770

RESULT 11
AAT86987
ID   AAT86987 standard; DNA; 1385 BP.
XX
AC   AAT86987;
XX
DT   27-MAR-1998  (first entry)
XX
DE   SSC1 single chain gene.
XX
KW   Construction; major histocompatibility complex; MHC; fusion complex;
KW   SSC1 single chain gene; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             6. .1385
FT                   /*tag= a
XX
PN   WO9728191-A1.
XX
PD   07-AUG-1997.
XX
PF   30-JAN-1997;   97WO-US001617.
XX
PR   31-JAN-1996;   96US-00596387.
XX
PA   (DADE-) DADE INT INC.
XX
PI   Rhode PR, Jiao J, Burkhardt M, Wong HC;
XX
DR   WPI; 1997-402555/37.
DR   P-PSDB; AAW29212.
XX
PT   Single chain major histocompatibility complex comprising linked alpha and
PT   beta chains - useful for suppressing an immune response to an auto:immune
PT   disease, e.g. multiple sclerosis, rheumatoid arthritis, diabetes
PT   mellitus, etc.
XX
PS   Example 17; Page 135-137; 217pp; English.
XX
CC   The present sequence was used in the construction of major
CC   histocompatibility complex (MHC) fusion complexes
XX
SQ   Sequence 1385 BP; 316 A; 383 C; 399 G; 287 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.3e-98 Length: 1385
Score: 1145.00 Matches: 227
```

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ent Similarity:     87.2%          Conservative:  4
 Local Similarity:  85.7%          Mismatches:    24
y Match:            70.7%          Indels:        10
                    2              Gaps:          3

0-048-116B-6 (1-306) x AAT86987 (1-1385)

        1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

       21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
          |||||||||   |||         :::         :::         |||
       66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

       41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
          |||      :::|||          ||||||||||||||                  |||
      120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC---------------GGCGGA 164

       61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
          ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
      165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

       81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

      101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

      121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

      141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

      161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

      181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

      201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

      221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

      241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
          ||||||||||||||||||||||||||||||||         :::
      705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

      261 GlyGlyGlyGlySer 265
          |||||||||||||||
      756 GGCGGTGGTGGTTCC 770

LT 12
0742
ACA60742 standard; DNA; 1385 BP.

ACA60742;

16-JUN-2003  (first entry)

Mouse MHC I-Ad/Ova 323-339 synthetic gene SSC1.
```

```
KW   MHC; major histocompatibility complex; gene therapy; fusion complex;
KW   peptide-binding groove; T cell modulation; class II MHC; vaccine;
KW   autoimmune disorder; multiple sclerosis; rheumatoid arthritis;
KW   insulin-dependent diabetes mellitus; myasthenia gravis; immunogen;
KW   chronic allergy; mouse; ds; I-Ad; gene.
XX
OS   Mus sp.
OS   Synthetic.
XX
PN   US2002198144-A1.
XX
PD   26-DEC-2002.
XX
PF   06-JUL-2001; 2001US-00900379.
XX
PR   29-JUL-1994;   94US-00283302.
PR   01-FEB-1995;   95US-00382454.
PR   17-JAN-1997;   97US-00776084.
XX
PA   (DADE-) DADE INT INC.
XX
PI   Wong HC,  Rhode PR,  Weidanz JA,  Grammer S,  Edwards AC;
PI   Chavaillaz P,  Jiao JJJ;
XX
DR   WPI; 2003-341126/32.
DR   P-PSDB; ABU72106.
XX
PT   Novel major histocompatibility complex fusion complex having presenting
PT   peptide covalently linked to MHC molecule containing peptide-binding
PT   groove, used for suppressing immune response in multiple sclerosis,
PT   allergies.
XX
PS   Example 17; Fig 27; 126pp; English.
XX
CC   The invention relates to a major histocompatibility complex (MHC) fusion
CC   complex (I) comprising an MHC molecule that contains a peptide-binding
CC   groove, and a presenting peptide covalently (e.g. an antigenic peptide)
CC   linked to the MHC molecule, where (I) is capable of modulating the
CC   activity of a T cell. Also included are a DNA construct coding for the
CC   complex, where the MHC molecule is a class II MHC (e.g. mouse I-Ad or I-
CC   As, or human HLA-DR1 (human leukocyte antigen-DR1)), a multivalent MHC
CC   fusion complex comprising two or more linked complexes, identifying a
CC   peptide that can modulate the activity of T cells (involving introducing
CC   into host cells cloning vectors that each contain the fusion complex DNA,
CC   culturing the host cells under conditions suitable for expression of the
CC   MHC fusion complex, and selecting host cells that express MHC fusion
CC   complex that modulate the activity of T cells), a single recombinant
CC   expression vector comprising DNA that codes for the alpha and beta chains
CC   of the fusion complex MHC protein, a single recombinant expression vector
CC   comprising DNA that codes for a T cell costimulatory factor and the alpha
CC   and beta chains of the MHC fusion complex. The DNA constructs can contain
CC   heterologous leader peptide sequences and Kozak sequence for efficient
CC   expression of the fusion complex. Also included are inducing an immune
CC   response in a mammal (including vaccinating a mammal against a targeted
CC   disorder, by administering DNA sequence comprising a fusion complex, or
CC   DNA sequence coding for a fusion complex which is a single chain fusion
CC   molecule) and suppressing an immune response in a mammal by administering
CC   to the mammal a DNA sequence comprising an expression vector, encoding a
CC   full length MHC molecule that contains a transmembrane domain, and a
CC   presenting peptide that is a T cell receptor (TCR) antagonist or partial
CC   agonist and is covalently linked to the MHC protein, or DNA sequence
CC   coding for the fusion complex which is a single chain fusion molecule.
CC   The methods are useful for identifying a peptide that can modulate the
CC   activity of T cells, inducing an immune response in a mammal (including
CC   vaccinating a mammal against a targeted disorder) and for suppressing an
CC   immune response in a mammal. The disorders include an autoimmune disorder
CC   such as multiple sclerosis, insulin-dependent diabetes mellitus,
CC   rheumatoid arthritis, myasthenia gravis or chronic allergies. The present
CC   sequence encodes a mouse MHC class II I-Ad fusion complex of the
CC   invention
XX
SQ   Sequence 1385 BP; 316 A; 383 C; 399 G; 287 T; 0 U; 0 Other;
```

```
;nment Scores:
i. No.:              1.3e-98        Length:          1385
:e:                  1145.00        Matches:         227
:ent Similarity:     87.2%          Conservative:    4
: Local Similarity:  85.7%          Mismatches:      24
:y Match:            70.7%          Indels:          10
                     8              Gaps:            3

!0-048-116B-6 (1-306) x ACA60742 (1-1385)

          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
            |||||||||   |||         :::         :::         |||
         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
            |||      :::|||           ||||||||||||||                |||
        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC--------------GGCGGA 164

         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
            ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
            ||||||||||||||||||||||||||||||||         :::
        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

        261 GlyGlyGlyGlySer 265
            |||||||||||||||
        756 GGCGGTGGTGGTTCC 770

JLT 13
.7587
  AAT17587 standard; DNA; 1508 BP.

  AAT17587;

  26-SEP-1996  (first entry)
```

```
XX
DE   Vector SCT1-derived single chain gene encoding MHC fusion complex.
XX
KW   MHC; major histocompatibility complex; PCR; polymerase chain reaction;
KW   T cell activity modulator; antagonist; immune disorder; allergy;
KW   multiple sclerosis; insulin-dependent diabetes mellitus;
KW   rheumatoid arthritis; myasthenia gravis; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             6. .1508
FT                   /*tag= a
FT   sig_peptide     6. .86
FT                   /*tag= b
FT                   /label= I-Ad_beta_chain_leader
FT                   /note= "murine MHC class II I-Ad gene beta chain leader
FT                   sequence"
FT   misc_feature    87. .137
FT                   /*tag= c
FT                   /label= OVA_323-339
FT                   /note= "chicken ovalbumin residues 323-339"
FT   misc_feature    138. .167
FT                   /*tag= d
FT                   /note= "10 residue linker peptide"
FT   misc_feature    168. .452
FT                   /*tag= e
FT                   /label= I-Ad_beta1
FT                   /note= "murine MHC class II I-Ad gene beta-1 domain"
FT   misc_feature    453. .734
FT                   /*tag= f
FT                   /label= I-Ad_beta2
FT                   /note= "murine MHC class II I-Ad gene beta-2 domain"
FT   misc_feature    735. .806
FT                   /*tag= g
FT                   /note= "24 residue peptide linker"
FT   misc_feature    807. .1067
FT                   /*tag= h
FT                   /label= I-Ad_alpha1
FT                   /note= "murine MHC class II I-Ad gene alpha-2 domain"
FT   misc_feature    1068. .1352
FT                   /*tag= i
FT                   /label= I-Ad_alpha2
FT                   /note= "murine MHC class II I-Ad gene alpha-2 domain"
FT   misc_feature    1353. .1505
FT                   /*tag= j
FT                   /label= I-Ad_alpha-TM
FT                   /note= "murine MHC class II I-Ad gene alpha-transmembrane
FT                   domain"
XX
PN   WO9604314-A1.
XX
PD   15-FEB-1996.
XX
PF   31-JUL-1995;   95WO-US009816.
XX
PR   29-JUL-1994;   94US-00283302.
PR   01-FEB-1995;   95US-00382454.
XX
PA   (DADE-) DADE INT INC.
XX
PI   Wong HC,  Rhode PR,  Weidanz JA,  Grammer S,  Edwards AC;
PI   Chavaillaz P,  Jiao J;
XX
DR   WPI; 1996-129343/13.
DR   P-PSDB; AAR98906.
XX
PT   Major histocompatability complex fusion complex for modulating T cell
PT   activity - used in the treatment of immune disorders, e.g. multiple
PT   sclerosis, IDDM and rheumatoid arthritis.
XX
PS   Example 17; Fig 28; 210pp; English.
XX
```

AAT17587 encodes a murine MHC fusion complex capable of modulating T cell activity encoded by the vector SCT1. The MHC fusion complex comprises at least one MHC molecule containing a peptide-binding groove and a presenting peptide covalently linked to the MHC molecule and opt. a transmembrane domain. DNA encoding a MHC fusion complex may be cloned into a host cell to express the complex. The transformed cells may then be used to identify peptides that modulate, pref. antagonise, T cell activity. DNA encoding a MHC fusion complex or a single chain fusion molecule may be used to vaccinate a mammal against a targeted disorder. The fusion complexes may be used to suppress an immune response in an animal suffering from an immune disorder e.g. multiple sclerosis, insulin -dependent diabetes mellitus, rheumatoid arthritis, myasthenia gravis or chronic allergies. The complexes may also be used in the treatment of livestock and pets such as cats and dogs. The MHC fusion complexes can be produced such that they contain a single antigenic peptide including one of known structure, additionally a wide range of peptides can be presented for T cell interaction

Sequence 1508 BP; 337 A; 414 C; 440 G; 317 T; 0 U; 0 Other;

ıment Scores:
. No.: 1.46e-98 Length: 1508
ɜ: 1145.00 Matches: 227
ɜnt Similarity: 87.2% Conservative: 4
Local Similarity: 85.7% Mismatches: 24
/ Match: 70.7% Indels: 10
2 Gaps: 3

)-048-116B-6 (1-306) x AAT17587 (1-1508)

```
Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              |||||||||   |||          :::          :::          |||
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              |||      :::|||       |||||||||||||||                  |||
Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC--------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
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Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
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Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTCGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
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Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
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Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy        261 GlyGlyGlyGlySer 265
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RESULT 14
AAT86988
ID AAT86988 standard; DNA; 1508 BP.
XX
AC AAT86988;
XX
DT 27-MAR-1998 (first entry)
XX
DE SCT1 single chain gene.
XX
KW Construction; major histocompatibility complex; MHC; fusion complex;
KW SCT1 single chain gene; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 6. .1508
FT /*tag= a
XX
PN WO9728191-A1.
XX
PD 07-AUG-1997.
XX
PF 30-JAN-1997; 97WO-US001617.
XX
PR 31-JAN-1996; 96US-00596387.
XX
PA (DADE-) DADE INT INC.
XX
PI Rhode PR, Jiao J, Burkhardt M, Wong HC;
XX
DR WPI; 1997-402555/37.
DR P-PSDB; AAW29213.
XX
PT Single chain major histocompatibility complex comprising linked alpha and
PT beta chains - useful for suppressing an immune response to an auto:immune
PT disease, e.g. multiple sclerosis, rheumatoid arthritis, diabetes
PT mellitus, etc.
XX
PS Example 17; Page 137-139; 217pp; English.
XX
CC The present sequence was used in the construction of major
CC histocompatibility complex (MHC) fusion complexes
XX
SQ Sequence 1508 BP; 337 A; 413 C; 441 G; 317 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.46e-98 Length: 1508
Score: 1145.00 Matches: 227
Percent Similarity: 87.2% Conservative: 4
Best Local Similarity: 85.7% Mismatches: 24
Query Match: 70.7% Indels: 10
DB: 2 Gaps: 3

US-10-048-116B-6 (1-306) x AAT86988 (1-1508)

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Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65
```

```
 21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
    ||||||||  |||      :::          :::          |||
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 41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
    |||      :::|||         ||||||||||||||                  |||
120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC--------------GGCGGA 164

 61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
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165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

 81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
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225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
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285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
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345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
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585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
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645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
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705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

261 GlyGlyGlyGlySer 265
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756 GGCGGTGGTGGTTCC 770
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JLT 15
!9069
AAX89069 standard; DNA; 1508 BP.

AAX89069;

14-SEP-1999 (first entry)

Single chain IAd/OVA 323-229 MHC fusion protein encoding DNA.

Major histocompatibility complex; MHC; single chain MHC; sc-MHC; Ig; peptide binding groove; immunoglobulin; T cell receptor; immune response; immune-related disorder; antigenic peptide; fusion protein; ss.

Synthetic.

WO9921572-A1.

06-MAY-1999.

13-OCT-1998; 98WO-US021520.

XX
PR 29-OCT-1997; 97US-00960190.
XX
PA (SUNO-) SUNOL MOLECULAR CORP.
XX
PI Rhode PR, Acevedo J, Burkhardt M, Jiao J, Wong HC;
XX
DR WPI; 1999-418411/35.
DR P-PSDB; AAY27111.
XX
PT Single chain major histocompatibility complex class I complexes.
XX
PS Example 1; Fig 1; 148pp; English.
XX
CC The invention relates to new single chain major histocompatibility
CC complex (sc-MHC) class II complexes that comprise a peptide binding
CC groove, and a modified class II beta 2 chain or covalently linked
CC immunoglobulin (Ig) light chain constant (C1) region. The MHC complexes
CC are useful for detection and analysis of peptide ligands, pathogenic T-
CC cells, for functional, cellular and molecular assays. They can be used to
CC identify and isolate T cell receptor and/or MHC agonists and antagonists.
CC They can be used in vivo to compete with pathogenic antigen presenting
CC cells involved in immune-related disorders. They can also be used to
CC raise antibodies and to screen immune cells. It is also use in a method
CC of suppressing an immune response in mammals. The sc-MHC complexes
CC comprising modified class II beta 2 chains and/or Ig-C1 regions are
CC soluble and provide enhanced yield. These MHC complexes also can contain
CC single antigenic peptides readily isolated from expressing cells in
CC significant quantities. The polyspecific MHC complexes also provide a
CC means to detect cells expressing multiple target structures with a single
CC complex. The present sequence represents a DNA encoding a single chain
CC IAd/OVA 323-229 MHC fusion protein
XX
SQ Sequence 1508 BP; 337 A; 413 C; 441 G; 317 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.46e-98	Length:	1508
Score:	1145.00	Matches:	227
Percent Similarity:	87.2%	Conservative:	4
Best Local Similarity:	85.7%	Mismatches:	24
Query Match:	70.7%	Indels:	10
DB:	2	Gaps:	3

US-10-048-116B-6 (1-306) x AAX89069 (1-1508)

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Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              ||||||||  |||      :::          :::          |||
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              |||      :::|||         ||||||||||||||                  |||
Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC--------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404
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141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
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405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
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585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
    ||||||||||||||||||||||||||||||||          :::
705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

261 GlyGlyGlyGlySer 265
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756 GGCGGTGGTGGTTCC 770
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GenCore version 5.1.8

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:al number of hits satisfying chosen parameters: 12732272

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	1100	73.5	1110	6	BC043925	BC043925 Mus muscu
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ALIGNMENTS

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ACCESSION   AX081280
VERSION     AX081280.1  GI:13170129
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SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Glaichenhaus,N. and Malherbe,L.
  TITLE     Recombinant proteins and molecular complexes derived therefrom,
            analogous to molecules involved in immune responses
  JOURNAL   Patent: WO 0109194-A 1 08-FEB-2001;
            CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
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                ETSFLVNRDHSFHKLSYLTFIPSDDDIYDCKVEHWGLEEPVLKHWEPEIPAPMSELTE
                TGGGGSTTAPSAQLEKELQALEKENAQLEWELQALEKELAQAASEPRGPTIKPCPPCK
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         21 CysGlyGlyGluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrThrValTyr 40
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         61 TGCGGAGGTGAAGACGACATTGAGGCCGACCACGTAGGCTTCTATGGTACAACTGTTTAT 120

         41 GlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr 60
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        181 GTGGACTTGGATAAGAAGAAAACTGTCTGGAGGCTTCCTGAGTTTGGCCAATTGATACTC 240

         81 PheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        241 TTTGAGCCCCAAGGTGGACTGCAAAACATAGCTGCAGAAAAACACAACTTGGGAATCTTG 300

        101 ThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPhePro 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        301 ACTAAGAGGTCAAATTTCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGTTCCCC 360

        121 LysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhe 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        361 AAGTCCCCTGTGCTGCTGGGTCAGCCCAACACCCTTATCTGCTTTGTGGACAACATCTTC 420

        141 ProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyr 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        421 CCACCTGTGATCAACATCACATGGCTCAGAAATAGCAAGTCAGTCACAGACGGCGTTTAT 480

        161 GluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPhe 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        481 GAGACCAGCTTCCTCGTCAACCGTGACCATTCCTTCCACAAGCTGTCTTATCTCACCTTC 540

        181 IleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluPro 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        541 ATCCCTTCTGATGATGACATTTATGACTGCAAGGTGGAGCACTGGGGCCTGGAGGAGCCG 600

        201 ValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThrGly 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        601 GTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAAACTGGA 660

        221 GlyGlyGlySerThrThrAlaProSerAlaGlnLeuGluLysGluLeuGlnAlaLeuGlu 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        661 GGTGGAGGATCCACTACAGCTCCATCAGCTCAGCTCGAAAAAGAGCTCCAGGCCCTGGAG 720

        241 LysGluAsnAlaGlnLeuGluTrpGluLeuGlnAlaLeuGluLysGluLeuAlaGlnAla 260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        721 AAGGAAAATGCACAGCTGGAATGGGAGTTGCAAGCACTGGAAAAGGAACTGGCTCAGGCA 780
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```
Qy      261 AlaSerGluProArgGlyProThrIleLysProCysProProCysLysCysPro 278
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 GCATCTGAGCCCAGAGGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCA 834

RESULT 2
MUSMHIAAD
LOCUS       MUSMHIAAD               978 bp    mRNA    linear   ROD 27-APR-1993
DEFINITION  Mouse MHC class II H2-IA-alpha gene (d haplotype) mRNA, complete
            cds.
ACCESSION   K01923
VERSION     K01923.1  GI:199449
KEYWORDS    antigen; cell surface glycoprotein; class II gene; glycoprotein;
            histocompatibility antigen; integral membrane protein; major
            histocompatibility complex.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 978)
  AUTHORS   Benoist,C.O., Mathis,D.J., Kanter,M.R., Williams,V.E. II and
            McDevitt,H.O.
  TITLE     Regions of allelic hypervariability in the murine A alpha immune
            response gene
  JOURNAL   Cell 34 (1), 169-177 (1983)
   PUBMED   6309407
COMMENT     Original source text: Mus musculus (strain BALB/c, sub_species
            domesticus) spleen cDNA to mRNA.
            The protein domains are as follows: first external protein domain
            (D1) at bases 93-356; second external protein domain (D2) at bases
            357-638; connecting peptide, transmembrane region, and cytoplasmic
            tail (CP,TM,C) at bases 639-791. [1] also sequenced the IA-alpha
            genes from mice of b,f,u and q haplotypes.
FEATURES             Location/Qualifiers
     source          1. .978
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                     /mol_type="mRNA"
                     /strain="BALB/c"
                     /sub_species="domesticus"
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                     /haplotype="d"
                     /tissue_type="spleen"
     gene            1. .978
                     /gene="MHC H2-IA-alpha"
     mRNA            <1. .>978
                     /gene="MHC H2-IA-alpha"
                     /product="IA-alpha mRNA"
     CDS             24. .794
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                     /db_xref="GI:199450"
                     /translation="MPCSRALILGVLALNTMLSLCGGEDDIEADHVGFYGTTVYQSPG
                     DIGQYTHEFDGDELFYVDLDKKKTVWRLPEFGQLILFEPQGGLQNIAAEKHNLGILTK
                     RSNFTPATNEAPQATVFPKSPVLLGQPNTLICFVDNIFPPVINITWLRNSKSVTDGVY
                     ETSFLVNRDHSFHKLSYLTFIPSDDDIYDCKVEHWGLEEPVLKHWEPEIPAPMSELTE
                     TVVCALGLSVGLVGIVVGTIFIIQGLRSGGTSRHPGPL"
     sig_peptide     24. .92
                     /gene="MHC H2-IA-alpha"
     mat_peptide     93. .791
                     /gene="MHC H2-IA-alpha"
                     /product="unnamed"
ORIGIN      44 bp upstream of HinfI site, chromosome 17.

Alignment Scores:
Pred. No.:              2.12e-114       Length:          978
Score:                  1182.00         Matches:         219
Percent Similarity:     100.0%          Conservative:    0
Best Local Similarity:  100.0%          Mismatches:      0
Query Match:            79.0%           Indels:          0
DB:                     6               Gaps:            0
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-10-048-116B-2_COPY_1_278 (1-278) x MUSMHIAAD (1-978)

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         24 ATGCCGTGCAGCAGAGCTCTGATTCTGGGGGTCCTCGCCCTGAACACCATGCTCAGCCTC 83

         21 CysGlyGlyGluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrThrValTyr 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         84 TGCGGAGGTGAAGACGACATTGAGGCCGACCACGTAGGCTTCTATGGTACAACTGTTTAT 143

         41 GlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        144 CAGTCTCCTGGAGACATTGGCCAGTACACACATGAATTTGATGGTGATGAGTTGTTCTAT 203

         61 ValAspLeuAspLysLysLysThrValTrpArgLeuProGluPheGlyGlnLeuIleLeu 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        204 GTGGACTTGGATAAGAAGAAAACTGTCTGGAGGCTTCCTGAGTTTGGCCAATTGATACTC 263

         81 PheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        264 TTTGAGCCCCAAGGTGGACTGCAAAACATAGCTGCAGAAAAACACAACTTGGGAATCTTG 323

        101 ThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPhePro 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        324 ACTAAGAGGTCAAATTTCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGTTCCCC 383

        121 LysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhe 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        384 AAGTCCCCTGTGCTGCTGGGTCAGCCCAACACCCTTATCTGCTTTGTGGACAACATCTTC 443

        141 ProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyr 160
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        444 CCACCTGTGATCAACATCACATGGCTCAGAAATAGCAAGTCAGTCACAGACGGCGTTTAT 503

        161 GluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPhe 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        504 GAGACCAGCTTCCTCGTCAACCGTGACCATTCCTTCCACAAGCTGTCTTATCTCACCTTC 563

        181 IleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluPro 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        564 ATCCCTTCTGATGATGACATTTATGACTGCAAGGTGGAGCACTGGGGCCTGGAGGAGCCG 623

        201 ValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThr 219
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
        624 GTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAAACT 680

SULT 3
199665
CUS       AR199665                4713 bp    DNA     linear   PAT 20-APR-2002
FINITION  Sequence 7 from patent US 6355479.
CESSION   AR199665
RSION     AR199665.1  GI:20249739
YWORDS    .
JRCE      Unknown.
ORGANISM  Unknown.
          Unclassified.
FERENCE   1  (bases 1 to 4713)
AUTHORS   Webb,S.R., Winqvist,O., Karlsson,L., Jackson,M.R. and Peterson,P.A.
ITLE      MHC class II antigen-presenting systems and methods for activating
          CD4+ T cells
JOURNAL   Patent: US 6355479-A 7 12-MAR-2002;
ATURES             Location/Qualifiers
   source          1. .4713
                   /organism="unknown"
                   /mol_type="unassigned DNA"
IGIN

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ed. No.:              2.05e-113      Length:         4713
ore:                  1182.00        Matches:        219
rcent Similarity:     100.0%         Conservative:   0
st Local Similarity:  100.0%         Mismatches:     0
ery Match:            79.0%          Indels:         0

DB:                   2              Gaps:           0

US-10-048-116B-2_COPY_1_278 (1-278) x AR199665 (1-4713)

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Db        459 ATGCCGTGCAGCAGAGCTCTGATTCTGGGGGTCCTCGCCCTGAACACCATGCTCAGCCTC 518

Qy         21 CysGlyGlyGluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrThrValTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        519 TGCGGAGGTGAAGACGACATTGAGGCCGACCACGTAGGCTTCTATGGTACAACTGTTTAT 578

Qy         41 GlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        579 CAGTCTCCTGGAGACATTGGCCAGTACACACATGAATTTGATGGTGATGAGTTGTTCTAT 638

Qy         61 ValAspLeuAspLysLysLysThrValTrpArgLeuProGluPheGlyGlnLeuIleLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         81 PheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 TTTGAGCCCCAAGGTGGACTGCAAAACATAGCTGCAGAAAAACACAACTTGGGAATCTTG 758

Qy        101 ThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPhePro 120
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Db        759 ACTAAGAGGTCAAATTTCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGTTCCCC 818

Qy        121 LysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        819 AAGTCCCCTGTGCTGCTGGGTCAGCCCAACACCCTTATCTGCTTTGTGGACAACATCTTC 878

Qy        141 ProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyr 160
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Db        879 CCACCTGTGATCAACATCACATGGCTCAGGAATAGCAAGTCAGTCACAGACGGCGTTTAT 938

Qy        161 GluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPhe 180
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Db        939 GAGACCAGCTTCCTCGTCAACCGTGACCATTCCTTCCACAAGCTGTCTTATCTCACCTTC 998

Qy        181 IleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluPro 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        999 ATCCCTTCTGATGATGACATTTATGACTGCAAGGTGGAGCACTGGGGCCTGGAGGAGCCG 1058

Qy        201 ValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThr 219
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1059 GTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAAACT 1115

RESULT 4
AY452201
LOCUS       AY452201                771 bp    mRNA    linear   ROD 23-NOV-2003
DEFINITION  Mus musculus H-2 class II histocompatibility antigen, A-D alpha
            chain precursor, mRNA, complete cds.
ACCESSION   AY452201
VERSION     AY452201.1  GI:38373608
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 771)
  AUTHORS   Gao,M., Wang,H. and Wang,Q.
  TITLE     Establishment of pIRES- I-A(d) alpha beta and stable expression of
            BALB/c mouse I-Ad alpha beta chain gene in NIH3T3 cell line
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 771)
  AUTHORS   Gao,M., Wang,H. and Wang,Q.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-OCT-2003) Lab of Transfusion Transfered virus,
            Transfusion Institute Beijing, 27 TaiPing Road, Beijing 100039, PR
            China
FEATURES             Location/Qualifiers
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d. No.:              2.44e-112       Length:         771
re:                  1161.00         Matches:        216
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t Local Similarity:  98.6%           Mismatches:     2
ly Match:            77.6%           Indels:         0
                     6               Gaps:           0

:0-048-116B-2_COPY_1_278 (1-278) x AY452201 (1-771)

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        1 ATGCCGTGCAGCAGAGCTCTGATTCTGGGGGTCCTCGCCCTGAACACCATGCTCAGCCTC 60

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       61 TGCGGAGGTGAAGACGTCATTGAGGCCGACCACGTAGGCTTCTATGGTACAACTGTTTAT 120

       41 GlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      121 CAGTCTCCTGGAGACATTGGCCAGTACACACATGAATTTGATGGTGATGAGTTGTTCTAT 180

       61 ValAspLeuAspLysLysLysThrValTrpArgLeuProGluPheGlyGlnLeuIleLeu 80
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       81 PheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeu 100
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      241 TTTGAGCCCCAAGGTGGACTGCAAAACATAGCTGCAGAAAAACACAACTTGGGAATCTTG 300

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      121 LysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhe 140
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      361 AAGTCCCCTGTGCTGCTGGGTCAGCCCCACACCCTTATCTGCTTTGTGGACAACATCTTC 420

      141 ProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyr 160
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      421 CCACCTGTGATCAACATCACATGGCTCAGAAATAGCAAGTCAGTCACAGACGGCGTTTAT 480

      161 GluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPhe 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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      201 ValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThr 219
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```

```
RESULT 5
BC029620
LOCUS       BC029620                1085 bp    mRNA    linear   ROD 04-OCT-2003
DEFINITION  Mus musculus histocompatibility 2, class II antigen A, alpha, mRNA
            (cDNA clone MGC:25392 IMAGE:2609494), complete cds.
ACCESSION   BC029620
VERSION     BC029620.1  GI:20987326
KEYWORDS    MGC.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1085)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
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            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
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            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  PUBMED    12477932
REFERENCE   2  (bases 1 to 1085)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-MAY-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey Green M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: amg@bcm.tmc.edu
            Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
            Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
            A.N., Gibbs, R.A.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 30 Row: a Column: 2
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 13540710.
FEATURES             Location/Qualifiers
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                /db_xref="MGI:95895"
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                RSNFTPATNEAPQATVFPKSPVLLGQPNTLICFVDNIFPPVINITWLRNSKSVTDGVY
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IGIN

ignment Scores:
ed. No.:              1.94e-106      Length:        1085
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st Local Similarity:  93.6%          Mismatches:    11
ery Match:            74.0%          Indels:        0
:                     6    .         Gaps:          0

-10-048-116B-2_COPY_1_278 (1-278) x BC029620 (1-1085)

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         21 CysGlyGlyGluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrThrValTyr 40
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         91 TGTGGAGGTGAAGACGACATTGAGGCCGACCATGTAGGCTTCTATGGTATAGTTGTATAT 150

         41 GlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr 60
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        151 CAGTCTCCTGGAGACATTGGCCAGTATACACATGAATTTGATGGTGATGAGTGGTTCTAT 210

         61 ValAspLeuAspLysLysLysThrValTrpArgLeuProGluPheGlyGlnLeuIleLeu 80
            ||||||||||||||||:::|||||||||||||||||||||||||||||||||||||||||
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         81 PheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeu 100
            |||:::|||||||||||||||||||||||||||||||||||||||||||||||||||||||
        271 TTTGACCCCCAAGGTGGACTACAAAACATAGCTACAGGAAAACACAACTTGGGAGGCTGG 330

        101 ThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPhePro 120
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        331 ACTAAGAGGTCAAATTTCACCCCAGCTACCAATGAGGCTCCTCAAGCAACTGTGTTCCCC 390

        121 LysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhe 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        391 AAGTCCCCTGTGCTGCTGGGTCAGCCCAATACCCTTATCTGCTTTGTGGACAACATCTTC 450

        141 ProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyr 160
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Qy      161 GluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPhe 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      181 IleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluPro 200
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Db      571 ATCCCTTCTGACGATGACATTTATGACTGCAAGGTGGAACACTGGGGCCTGGACGAGCCA 630

Qy      201 ValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThr 219
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Db      631 GTTCTGAAACACTGGGAACCTGAGATCCCAGCCCCCATGTCAGAGCTGACAGAGACT 687

RESULT 6
BC043925
LOCUS       BC043925               1110 bp    mRNA    linear   ROD 30-MAR-2005
DEFINITION  Mus musculus histocompatibility 2, class II antigen A, alpha, mRNA
            (cDNA clone MGC:49437 IMAGB:4023996), complete cds.
ACCESSION   BC043925
VERSION     BC043925.1  GI:27882597
KEYWORDS    MGC.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1110)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
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            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1110)
  AUTHORS   .
  CONSRTM   NIH MGC Project
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JAN-2003) National Institutes of Health, Mammalian
            Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
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Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 85 Row: f Column: 12
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 31981715.

URES Location/Qualifiers
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/mol_type="mRNA"
/strain="mix FVB/N, C57BL/6J"
/db_xref="taxon:10090"
/clone="MGC:49437 IMAGE:4023996"
/tissue_type="Mammary tumor. WAP-TGF alpha model. 7 months old, gross tissue."
/clone_lib="NCI_CGAP_Mam5"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
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/gene="H2-Aa"
/note="synonyms: Aalpha, IAalpha"
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RSNSTPATNEAPQATVFPKSPVLLGQPNTLICVVDNIFPPVINITWLRNSKSVTDGVY
ETSFLVNRDHSFHKLSYLTFIPSDDDIYDCKVEHWGLEEPVLKHWEPEIPAPMSELTE
TVVCALGLSVGLVGIVVGTIFIIQGLRSGGTSRHPGPL"

IN

nment Scores:
. No.: 1.1e-105 Length: 1110
e: 1100.00 Matches: 204
ent Similarity: 95.0% Conservative: 4
Local Similarity: 93.2% Mismatches: 11
y Match: 73.5% Indels: 0
6 Gaps: 0

0-048-116B-2_COPY_1_278 (1-278) x BC043925 (1-1110)

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 21 CysGlyGlyGluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrThrValTyr 40
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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 41 GlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr 60
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155 CAGTCTCCTGGAGACATTGGCCAGTACACACATGAATTTGATGGTGATGAGTGGTTCTAT 214

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215 GTGGACTTGGATAAGAAGGAGACTATCTGGATGCTTCCTGAGTTTGGCCAATTGACAAGC 274

 81 PheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeu 100
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275 TTTGACCCCCAAGGTGGACTGCAAAACATAGCTACAGGAAAATACACCTTGGGAATCTTG 334

101 ThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPhePro 120
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Qy  141 ProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyr 160
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Qy  161 GluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPhe 180
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Qy  181 IleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluPro 200
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Qy  201 ValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThr 219
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RESULT 7
AR106256
LOCUS AR106256 776 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 4 from patent US 6106840.
ACCESSION AR106256
VERSION AR106256.1 GI:12820786
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 776)
AUTHORS Clark,B.R., Sharma,S.D. and Lerch,B.L.
TITLE MHC conjugates useful in ameliorating autoimmunity
JOURNAL Patent: US 6106840-A 4 22-AUG-2000;
FEATURES Location/Qualifiers
source 1. .776
/organism="unknown"
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ORIGIN

Alignment Scores:
Pred. No.: 1.36e-103 Length: 776
Score: 1078.00 Matches: 201
Percent Similarity: 94.1% Conservative: 5
Best Local Similarity: 91.8% Mismatches: 13
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US-10-048-116B-2_COPY_1_278 (1-278) x AR106256 (1-776)

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Qy   21 CysGlyGlyGluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrThrValTyr 40
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Db   66 TGTGGAGGTGAAGACGACATTGAGGCCGACCACGTAGGCACCTATGGTATAAGTGTATAT 125

Qy   41 GlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr 60
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Qy   61 ValAspLeuAspLysLysLysThrValTrpArgLeuProGluPheGlyGlnLeuIleLeu 80
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Qy   81 PheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeu 100
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Qy  101 ThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPhePro 120
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        366 AAGTCCCCTGTGCTGCTGGGTCAGCCCAACACCCTCATCTGCTTTGTGGACAACATCTTC 425

        141 ProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyr 160
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        426 CCTCCTGTGATCAACATCACATGGCTCAGAAATAGCAAGTCAGTCGCAGACGGTGTTTAT 485

        161 GluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPhe 180
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SULT 8
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FINITION  Sequence 4 from patent US 6451314.
CESSION   AR229608
RSION     AR229608.1  GI:27269264
YWORDS    .
URCE      Unknown.
RGANISM   Unknown.
          Unclassified.
FERENCE   1  (bases 1 to 776)
UTHORS    Clark,B.R., Sharma,S.D. and Lerch,B.L.
ITLE      MHC conjugates useful in ameliorating autoimmunity
OURNAL    Patent: US 6451314-A 4 17-SEP-2002;
          Anergen, Inc.; Seattle, WA
ATURES              Location/Qualifiers
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IGIN

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st Local Similarity:  91.8%          Mismatches:     13
ery Match:            72.1%          Indels:         0
:                     2              Gaps:           0

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         21 CysGlyGlyGluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrThrValTyr 40
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         66 TGTGGAGGTGAAGACGACATTGAGGCCGACCACGTAGGCACCTATGGTATAAGTGTATAT 125

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        126 CAGTCTCCTGGAGACATTGGCCAGTACACATTTGAATTTGATGGTGATGAGTTGTTCTAT 185

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         81 PheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeu 100
            |||:::||||||||||||||||||||||||||||||||||||||||||:::|||
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RESULT 9
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DEFINITION  Sequence 5 from patent US 5194425.
ACCESSION   AR363023
VERSION     AR363023.1  GI:34423771
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 776)
  AUTHORS   Sharma,S.D., Lerch,L.B. and Clark,B.R.
  TITLE     MHC-mediated toxic conjugates useful in ameliorating autoimmunity
  JOURNAL   Patent: US 5194425-A 5 16-MAR-1993;
            Anergen, Inc.; Redwood City, CA
FEATURES              Location/Qualifiers
     source           1. .776
                      /organism="unknown"
                      /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.36e-103      Length:         776
Score:                  1078.00        Matches:        201
Percent Similarity:     94.1%          Conservative:   5
Best Local Similarity:  91.8%          Mismatches:     13
Query Match:            72.1%          Indels:         0
DB:                     2              Gaps:           0

US-10-048-116B-2_COPY_1_278 (1-278) x AR363023 (1-776)

Qy          1 MetProCysSerArgAlaLeuIleLeuGlyValLeuAlaLeuAsnThrMetLeuSerLeu 20
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Db          6 ATGCCGCGCAGCAGAGCTCTGATTCTGGGGGTCCTCGCCCTGACCACCATGCTCAGCCTC 65

Qy         21 CysGlyGlyGluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrThrValTyr 40
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Db         66 TGTGGAGGTGAAGACGACATTGAGGCCGACCACGTAGGCACCTATGGTATAAGTGTATAT 125

Qy         41 GlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr 60
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        126 CAGTCTCCTGGAGACATTGGCCAGTACACATTTGAATTTGATGGTGATGAGTTGTTCTAT 185

Qy         61 ValAspLeuAspLysLysLysThrValTrpArgLeuProGluPheGlyGlnLeuIleLeu 80
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Qy         81 PheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeu 100
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       246 TTTGACCCCCAAGGTGGACTGCAAAACATAGCTGTAGTAAAACACAACTTGGGAGTCTTG 305

       101 ThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPhePro 120
           ||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
       306 ACTAAGAGGTCAAATTCCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGTTCCCC 365

       121 LysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhe 140
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       366 AAGTCCCCTGTGCTGCTGGGTCAGCCCAACACCCTCATCTGCTTTGTGGACAACATCTTC 425

       141 ProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyr 160
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       426 CCTCCTGTGATCAACATCACATGGCTCAGAAATAGCAAGTCAGTCGCAGACGGTGTTTAT 485

       161 GluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPhe 180
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       181 IleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluPro 200
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       201 ValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThr 219
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       606 GTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAGACT 662

LT 10
9721
S       BC019721                1084 bp    mRNA    linear   ROD 30-JUN-2004
NITION  Mus musculus histocompatibility 2, class II antigen A, alpha, mRNA
        (cDNA clone MGC:30249 IMAGE:3669693), complete cds.
SSION   BC019721
ION     BC019721.1  GI:18043825
ORDS    MGC.
CE      Mus musculus (house mouse)
GANISM  Mus musculus
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
        Sciurognathi; Muroidea; Muridae; Murinae; Mus.
RENCE   1  (bases 1 to 1084)
THORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
        Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
        Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
        Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
        Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
        Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
        Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
        Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
        Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
        McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
        Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
        Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
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        Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
        Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
        Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
        Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
        Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TLE     Generation and initial analysis of more than 15,000 full-length
        human and mouse cDNA sequences
URNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
UBMED   12477932
RENCE   2  (bases 1 to 1084)
THORS   Strausberg,R.
TLE     Direct Submission
URNAL   Submitted (19-DEC-2001) National Institutes of Health, Mammalian
        Gene Collection (MGC), Cancer Genomics Office, National Cancer
        Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
        USA
MARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
ENT     Contact: MGC help desk
        Email: cgapbs-r@mail.nih.gov
        Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys

        cDNA Library Preparation: Life Technologies, Inc.
        cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
        DNA Sequencing by: Baylor College of Medicine Human Genome
        Sequencing Center
        Center code: BCM-HGSC
        Web site: http://www.hgsc.bcm.tmc.edu/cdna/
        Contact: amg@bcm.tmc.edu
        Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
        Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
        A.N., Gibbs, R.A.

        Clone distribution: MGC clone distribution information can be found
        through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
        Series: IRAK Plate: 40 Row: d Column: 4
        This clone was selected for full length sequencing because it
        passed the following selection criteria: matched mRNA gi: 13540710.
FEATURES             Location/Qualifiers
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                     /tissue_type="Mammary tumor. WAP-TGF alpha model. 7 months
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                     /note="Vector: pCMV-SPORT6"
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                     /db_xref="MGI:95895"
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                     DIGQYTFEFDGDELFYVDLDKKETVWMLPEFGQLASFDPQGGLQNIAVVKHNLGVLTK
                     RSNSTPATNEAPQATVFPKSPVLLGQPNTLICFVDNIFPPVINITWLRNSKSVADGVY
                     ETSFFVNRDYSFHKLSYLTFIPSDDDIYDCKVEHWGLEEPVLKHWEPEIPAPMSELTE
                     TVVCALGLSVGLVGIVVGTIFIIQGLRSGGTSRHPGPL"
ORIGIN

Alignment Scores:
Pred. No.:                2.2e-103        Length:          1084
Score:                    1078.00         Matches:         201
Percent Similarity:       94.1%           Conservative:    5
Best Local Similarity:    91.8%           Mismatches:      13
Query Match:              72.1%           Indels:          0
DB:                       6               Gaps:            0

US-10-048-116B-2_COPY_1_278 (1-278) x BC019721 (1-1084)

Qy          1 MetProCysSerArgAlaLeuIleLeuGlyValLeuAlaLeuAsnThrMetLeuSerLeu 20
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Db          6 ATGCCGCGCAGCAGAGCTCTGATTCTGGGGGTCCTCGCCCTGACCACCATGCTCAGCCTC 65

Qy         21 CysGlyGlyGluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrThrValTyr 40
              ||||||||||||||||||||||||||||||||||   ||||||   :::||||||
Db         66 TGTGGAGGTGAAGACGACATTGAGGCCGACCACGTAGGCACCTATGGTATAAGTGTATAT 125

Qy         41 GlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr 60
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||
Db        126 CAGTCTCCTGGAGACATTGGCCAGTACACATTTGAATTTGATGGTGATGAGTTGTTCTAT 185

Qy         61 ValAspLeuAspLysLysLysThrValTrpArgLeuProGluPheGlyGlnLeuIleLeu 80
              ||||||||||||||||||:::||||||||   ||||||||||||||||||||||||||
Db        186 GTGGACTTGGATAAGAAGGAGACTGTCTGGATGCTTCCTGAGTTTGGCCAATTGGCAAGC 245
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 81 PheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeu 100
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246 TTTGACCCCCAAGGTGGACTGCAAAACATAGCTGTAGTAAAACACAACTTGGGAGTCTTG 305

101 ThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPhePro 120
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306 ACTAAGAGGTCAAATTCCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGTTCCCC 365

121 LysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhe 140
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366 AAGTCCCCTGTGCTGCTGGGTCAGCCCAACACCCTCATCTGCTTTGTGGACAACATCTTC 425

141 ProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyr 160
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426 CCTCCTGTGATCAACATCACATGGCTCAGAAATAGCAAGTCAGTCGCAGACGGTGTTTAT 485

161 GluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPhe 180
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181 IleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluPro 200
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201 ValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThr 219
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606 GTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAGACT 662
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031711
OUS       BC031711                1109 bp    mRNA    linear   ROD 30-JUN-2004
FINITION  Mus musculus histocompatibility 2, class II antigen A, alpha, mRNA
          (cDNA clone MGC:25391 IMAGE:3670758), complete cds.
CESSION   BC031711
RSION     BC031711.1  GI:21618807
YWORDS    MGC.
URCE      Mus musculus (house mouse)
ORGANISM  Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
          Sciurognathi; Muroidea; Muridae; Murinae; Mus.
FERENCE   1  (bases 1 to 1109)
AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
          Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
          Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
          Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
          Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
          Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
          Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
          Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
          Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
          McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
          Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
          Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
          Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
          Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
          Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
          Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
          Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
          Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
ITLE      Generation and initial analysis of more than 15,000 full-length
          human and mouse cDNA sequences
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 PUBMED   12477932
FERENCE   2  (bases 1 to 1109)
AUTHORS   Strausberg,R.
ITLE      Direct Submission
JOURNAL   Submitted (06-JUN-2002) National Institutes of Health, Mammalian
          Gene Collection (MGC), Cancer Genomics Office, National Cancer
          Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
          USA
EMARK     NIH-MGC Project URL: http://mgc.nci.nih.gov
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COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: amg@bcm.tmc.edu
            Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
            Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
            A.N., Gibbs, R.A.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 30 Row: c Column: 18
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 13540710.
FEATURES              Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.:              2.27e-103       Length:         1109
Score:                  1078.00         Matches:        201
Percent Similarity:     94.1%           Conservative:   5
Best Local Similarity:  91.8%           Mismatches:     13
Query Match:            72.1%           Indels:         0
DB:                     6               Gaps:           0

US-10-048-116B-2_COPY_1_278 (1-278) x BC031711 (1-1109)

Qy          1 MetProCysSerArgAlaLeuIleLeuGlyValLeuAlaLeuAsnThrMetLeuSerLeu 20
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Db         12 ATGCCGCGCAGCAGAGCTCTGATTCTGGGGGTCCTCGCCCTGACCACCATGCTCAGCCTC 71

Qy         21 CysGlyGlyGluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrThrValTyr 40
              ||||||||||||||||||||||||||||||||||||||||  ||||||   :::||||||
Db         72 TGTGGAGGTGAAGACGACATTGAGGCCGACCACGTAGGCACCTATGGTATAAGTGTATAT 131

Qy         41 GlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr 60
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192 GTGGACTTGGATAAGAAGGAGACTGTCTGGATGCTTCCTGAGTTTGGCCAATTGGCAAGC 251

 81 PheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeu 100
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252 TTTGACCCCCAAGGTGGACTGCAAAACATAGCTGTAGTAAAACACAACTTGGGAGTCTTG 311

101 ThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPhePro 120
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312 ACTAAGAGGTCAAATTCCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGTTCCCC 371

121 LysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhe 140
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372 AAGTCCCCTGTGCTGCTGGGTCAGCCCAACACCCTCATCTGCTTTGTGGACAACATCTTC 431

141 ProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyr 160
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161 GluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPhe 180
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181 IleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluPro 200
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552 ATCCCTTCTGACGATGACATTTATGACTGCAAGGTGGAACACTGGGGCCTGGAGGAGCCG 611

201 ValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThr 219
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612 GTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAGACT 668
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LT 12
01
S       MMMH01                  978 bp    mRNA    linear   ROD 12-SEP-1993
NITION  Mouse fragment of mRNA encoding for the Ia antigen (heavy chain)
        from major histocompatibility complex (A-k-alpha). This is coded by
        the I-A region of the MHC and corresponds to the k haplotype.
SSION   V00832 J00399
ION     V00832.1  GI:53076
ORDS    complementary DNA; histocompatibility antigen; signal peptide.
CE      Mus musculus (house mouse)
GANISM  Mus musculus
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
        Sciurognathi; Muroidea; Muridae; Murinae; Mus.
RENCE   1  (bases 31 to 978)
THORS   Benoist,C.O., Mathis,D.J., Kanter,M.R., Williams,V.E. II and
        McDevitt,H.O.
TLE     The murine Ia alpha chains, E alpha and A alpha, show a surprising
        degree of sequence homology
URNAL   Proc. Natl. Acad. Sci. U.S.A. 80 (2), 534-538 (1983)
UBMED   6300851
RENCE   2  (bases 1 to 30)
THORS   Benoist,C.O.
TLE     Direct Submission
URNAL   Submitted (05-MAY-1983)
ENT     Data kindly reviewed (05-MAY-1983) by C.O. Benoist.
URES            Location/Qualifiers
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                /mol_type="mRNA"
                /db_xref="taxon:10090"
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                /product="messenger RNA"
 CDS            24. .794
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                RSNSTPATNEAPQATVFPKSPVLLGQPNTLICFVDNIFPPVINITWLRNSKSVTDGVY
                ETSFFVNRDYSFHKLSYLTFIPSDDDIYDCKVEHWGLEEPVLKHWEPEIPAPMSELTE
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ORIGIN

Alignment Scores:
Pred. No.:              3.92e-103       Length:         978
Score:                  1075.00         Matches:        203
Percent Similarity:     93.6%           Conservative:   2
Best Local Similarity:  92.7%           Mismatches:     14
Query Match:            71.9%           Indels:         0
DB:                     6               Gaps:           0

US-10-048-116B-2_COPY_1_278 (1-278) x MMMH01 (1-978)

Qy          1 MetProCysSerArgAlaLeuIleLeuGlyValLeuAlaLeuAsnThrMetLeuSerLeu 20
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Db         24 ATGCCGCGCAGCAGAGCTCTGATTCTGGGGGTCCTCGCCCTGACCACCATGCTCAGCCTC 83

Qy         21 CysGlyGlyGluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrThrValTyr 40
              ||||||||||||||||||||||||||||||||||||||||  ||||||  |||||||||
Db         84 TGCGGAGGTGAAGACGACATTGAGGCCGACCACGTAGGCTCCTATGGTATAACTGTATAT 143

Qy         41 GlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr 60
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db        144 CAGTCTCCTGGAGACATTGGCCAGTACACATTTGAATTTGATGGTGATGAGTTGTTCTAT 203

Qy         61 ValAspLeuAspLysLysLysThrValTrpArgLeuProGluPheGlyGlnLeuIleLeu 80
              ||||||||||||||||||:::||||||||||   ||||||||||||   ||||||
Db        204 GTGGACTTGGATAAGAAGGAGACTGTCTGGATGCTTCCTGAGTTTGCTCAACTGAGAAGA 263

Qy         81 PheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeu 100
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Db        264 TTTGAGCCCCAAGGTGGACTGCAAAACATAGCTACAGGAAAACACAACTTGGAAATCTTG 323

Qy        101 ThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPhePro 120
              ||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db        324 ACTAAGAGGTCAAATTCCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGTTCCCC 383

Qy        121 LysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AAGTCTCCTGTGCTGCTGGGTCAGCCCAACACCCTTATCTGCTTTGTGGACAACATCTTC 443

Qy        141 ProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 CCTCCTGTGATCAACATCACATGGCTCAGAAATAGCAAGTCAGTCACAGACGGCGTTTAT 503

Qy        161 GluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPhe 180
              ||||||||||||   ||||||||||:::||||||||||||||||||||||||||||||||
Db        504 GAAACCAGCTTCTTCGTCAACCGTGACTATTCCTTCCACAAGCTGTCTTATCTCACCTTC 563

Qy        181 IleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluPro 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 ATCCCTTCTGACGATGACATTTATGACTGCAAGGTGGAGCACTGGGGCCTGGAGGAGCCG 623

Qy        201 ValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThr 219
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 GTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAGACT 680

RESULT 13
MUSMHIAKA
LOCUS       MUSMHIAKA               978 bp    mRNA    linear   ROD 27-APR-1993
DEFINITION  Mouse MHC class II H2-I-A-alpha gene (k haplotype), complete cds.
ACCESSION   M21931
VERSION     M21931.1  GI:199493
KEYWORDS    cell surface glycoprotein; class II gene; integral membrane
            protein; major histocompatibility complex.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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FERENCE   1  (bases 1 to 978)
UTHORS    Bishop,G.A., McMillan,M.S., Haughton,G. and Frelinger,J.A.
ITLE      Signaling to a B-cell clone by Ek, but not Ak, does not reflect
          alteration of Ak genes
OURNAL    Immunogenetics 28 (3), 184-192 (1988)
 UBMED    3137158
MENT      Original source text: Mouse (strain BIO.H-2a4bp/Wts (2a4b)) spleen
          B lymphocyte, cDNA to mRNA, clones alpha-[1,12].
          Draft entry and compute-readable sequence [1] kindly submitted by
          G.Bishop, 18-JAN-1989.
TURES             Location/Qualifiers
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                  /organism="Mus musculus"
                  /mol_type="mRNA"
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                  ETSFFVNRDYSFHKLSYLTFIPSDDDIYDCKVEHWGLEEPVLKHWEPEIPAPMSELTE
                  TVVCALGLSVGLVGIVVGTIFIIQGLRSGGTSRHPGPL"
IGIN      Chromosome 17.

ignment Scores:
ed. No.:              3.92e-103      Length:         978
ore:                  1075.00        Matches:        203
rcent Similarity:     93.6%          Conservative:   2
st Local Similarity:  92.7%          Mismatches:     14
ery Match:            71.9%          Indels:         0
:                     6              Gaps:           0

-10-048-116B-2_COPY_1_278 (1-278) x MUSMHIAKA (1-978)

          1 MetProCysSerArgAlaLeuIleLeuGlyValLeuAlaLeuAsnThrMetLeuSerLeu 20
            |||||| |||||||||||||||||||||||||||||||| ||||||||||||||||
         24 ATGCCGCGCAGCAGAGCTCTGATTCTGGGGGTCCTCGCCCTGACCACCATGCTCAGCCTC 83

         21 CysGlyGlyGluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrThrValTyr 40
            |||||||||||||||||||||||||||||||||||| |||||| |||||||||
         84 TGCGGAGGTGAAGACGACATTGAGGCCGACCACGTAGGCTCCTATGGTATAACTGTATAT 143

         41 GlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr 60
            |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
        144 CAGTCTCCTGGAGACATTGGCCAGTACACATTTGAATTTGATGGTGATGAGTTGTTCTAT 203

         61 ValAspLeuAspLysLysLysThrValTrpArgLeuProGluPheGlyGlnLeuIleLeu 80
            |||||||||||||||||:::|||||||| |||||||||| ||||||
        204 GTGGACTTGGATAAGAAGGAGACTGTCTGGATGCTTCCTGAGTTTGCTCAACTGAGAAGA 263

         81 PheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeu 100
            |||||||||||||||||||||||||||||||| |||||||||||| ||||||
        264 TTTGAGCCCCAAGGTGGACTGCAAAACATAGCTACAGGAAAACACAACTTGGAAATCTTG 323

        101 ThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPhePro 120
            |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
        324 ACTAAGAGGTCAAATTCCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGTTCCCC 383

        121 LysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhe 140
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Qy        141 ProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyr 160
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Qy        161 GluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPhe 180
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Db        504 GAAACCAGCTTCTTCGTCAACCGTGACTATTCCTTCCACAAGCTGTCTTATCTCACCTTC 563

Qy        181 IleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluPro 200
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Db        564 ATCCCTTCTGACGATGACATTTATGACTGCAAGGTGGAGCACTGGGGCCTGGAGGAGCCG 623

Qy        201 ValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThr 219
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 GTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAGACT 680

RESULT 14
AR365183
LOCUS       AR365183                776 bp    DNA     linear   PAT 03-SEP-2003
DEFINITION  Sequence 4 from patent US 5468481.
ACCESSION   AR365183
VERSION     AR365183.1  GI:34428599
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 776)
  AUTHORS   Sharma,S.D., Clark,B.R. and Lerch,B.L.
  TITLE     MHC class II-peptide conjugates useful in ameliorating autoimmunity
  JOURNAL   Patent: US 5468481-A 4 21-NOV-1995;
            Amergen, Inc.; Redwood City, CA
FEATURES             Location/Qualifiers
     source          1. .776
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ORIGIN

Alignment Scores:
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Score:                  1069.00        Matches:        200
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Best Local Similarity:  91.3%          Mismatches:     14
Query Match:            71.5%          Indels:         0
DB:                     2              Gaps:           0

US-10-048-116B-2_COPY_1_278 (1-278) x AR365183 (1-776)

Qy          1 MetProCysSerArgAlaLeuIleLeuGlyValLeuAlaLeuAsnThrMetLeuSerLeu 20
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Db          6 ATGCCGCGCAGCAGAGCTCTGATTCTGGGGGTCCTCGCCCTGACCACCATGCTCAGCCTC 65

Qy         21 CysGlyGlyGluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrThrValTyr 40
              |||||||||||||||||||||||||||||||||||| |||||| :::||||||
Db         66 TGTGGAGGTGAAGACGACATTGAGGCCGACCACGTAGGCACCTATGGTATAAGTGTATAT 125

Qy         41 GlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr 60
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Qy         61 ValAspLeuAspLysLysLysThrValTrpArgLeuProGluPheGlyGlnLeuIleLeu 80
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Qy         81 PheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeu 100
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Qy        101 ThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPhePro 120
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Db        306 ACTAAGAGGTCAAATTCCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGTTCCCC 365

Qy        121 LysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhe 140
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       201 ValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThr 219
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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LT 15
3963
S       AR033963                1508 bp    DNA     linear   PAT 29-SEP-1999
NITION  Sequence 122 from patent US 5869270.
SSION   AR033963
ION     AR033963.1  GI:5949568
ORDS    .
CE      Unknown.
GANISM  Unknown.
        Unclassified.
RENCE   1  (bases 1 to 1508)
THORS   Rhode,P.R., Jiao,J.-A., Burkhardt,M. and Wong,H.C.
TLE     Single chain MHC complexes and uses thereof
URNAL   Patent: US 5869270-A 122 09-FEB-1999;
URES            Location/Qualifiers
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d. No.:             7.34e-102       Length:         1508
e:                  1065.50         Matches:        198
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t Local Similarity: 98.5%           Mismatches:     0
y Match:            71.2%           Indels:         3
                    2               Gaps:           1

 0-048-116B-2_COPY_1_278 (1-278) x AR033963 (1-1508)

        22 GlyGly---------GluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrThr 38
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       792 GGCGGTTCCTCGAGTGAAGACGACATTGAGGCCGACCACGTAGGCTTCTATGGTACAACT 851

        39 ValTyrGlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeu 58
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       852 GTTTATCAGTCTCCTGGAGACATTGGCCAGTACACACATGAATTTGATGGTGATGAGTTG 911

        59 PheTyrValAspLeuAspLysLysLysThrValTrpArgLeuProGluPheGlyGlnLeu 78
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       912 TTCTATGTGGACTTGGATAAGAAGAAAACTGTCTGGAGGCTTCCTGAGTTTGGCCAATTG 971

        79 IleLeuPheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGly 98
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       972 ATACTCTTTGAGCCCCAAGGTGGACTGCAAAACATAGCTGCAGAAAAACACAACTTGGGA 1031

        99 IleLeuThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrVal 118
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1032 ATCTTGACTAAGAGGTCAAATTTCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTG 1091

       119 PheProLysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsn 138
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       139 IleProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGly 158
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Qy       159 ValTyrGluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeu 178
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Db      1212 GTTTATGAGACCAGCTTCCTCGTCAACCGTGACCATTCCTTCCACAAGCTGTCTTATCTC 1271

Qy       179 ThrPheIleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGlu 198
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1272 ACCTTCATCCCTTCTGATGATGACATTTATGACTGCAAGGTGGAGCACTGGGGCCTGGAG 1331

Qy       199 GluProValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGlu 218
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       219 Thr 219
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Db      1392 ACT 1394

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Job time : 5235.37 secs
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GenCore version 5.1.8

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on: May 31, 2006, 23:08:35 ; Search time 6465 Seconds
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Ygapop 10.0 , Ygapext 0.5
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il number of hits satisfying chosen parameters: 12732272

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Maximum Match 100%
Listing first 45 summaries

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\POP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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1: gb_env:*
2: gb_pat:*
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5: gb_pr:*
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7: gb_sts:*
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9: gb_un:*
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12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ılt No.	Score	% Query Match	Length	DB	ID	Description
1	1620	100.0	921	2	AX081281	AX081281 Sequence
2	1255.5	77.5	893	2	AR047947	AR047947 Sequence
3	1161.5	71.7	4724	2	AR199666	AR199666 Sequence
4	1154	71.2	1013	2	AR047957	AR047957 Sequence
5	1145	70.7	1382	2	AR033964	AR033964 Sequence
6	1145	70.7	1382	2	AR175097	AR175097 Sequence
7	1145	70.7	1382	2	CS079301	CS079301 Sequence
8	1145	70.7	1382	2	AX032545	AX032545 Sequence
9	1145	70.7	1385	2	AR033962	AR033962 Sequence
10	1145	70.7	1385	2	AR175095	AR175095 Sequence
11	1145	70.7	1385	2	CS079299	CS079299 Sequence
12	1145	70.7	1385	2	AX032543	AX032543 Sequence
13	1145	70.7	1508	2	AR033963	AR033963 Sequence
14	1145	70.7	1508	2	AR152030	AR152030 Sequence
15	1145	70.7	1508	2	AR175096	AR175096 Sequence
16	1145	70.7	1508	2	CS079300	CS079300 Sequence
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20	1102.5	68.1	798	6	MUSMHIABQ	M13537 Mouse MHC c
21	1096.5	67.7	798	2	CQ777552	CQ777552 Sequence
22	1054.5	65.1	888	6	MUSMHABNO	M15848 Mouse MHC c
23	1054.5	65.1	1204	6	BC008168	BC008168 Mus muscu
24	1050.5	64.8	792	6	AY452202	AY452202 Mus muscu
25	1042.5	64.4	777	6	AF065913	AF065913 Mus muscu
26	1042.5	64.4	792	6	AF293060	AF293060 Mus muscu
27	1042.5	64.4	792	6	MUSMHIH2	M66213 Mouse MHC c
28	1042.5	64.4	1162	6	BC057998	BC057998 Mus muscu
29	1041.5	64.3	792	6	MUSMHIABS	M13540 Mouse MHC c
30	1036.5	64.0	792	6	AF119251	AF119251 Mus muscu
31	1036.5	64.0	792	6	AF119252	AF119252 Mus muscu
32	1033.5	63.8	750	6	AF065912	AF065912 Mus muscu
33	1030.5	63.6	1078	6	AF293061	AF293061 Mus muscu
34	1028.5	63.5	792	6	MUSMHIABK	M13538 Mouse MHC c
35	1016.5	62.7	792	6	MUSMHIABU	M13539 Mouse MHC c
36	998.5	61.6	1070	6	AF015280	AF015280 Mus muscu
37	993.5	61.3	760	6	MUSMHIABF	M13541 Mouse MHC c
38	979.5	60.5	702	2	AR106257	AR106257 Sequence
39	979.5	60.5	702	2	AR229609	AR229609 Sequence
40	979.5	60.5	702	2	AR363024	AR363024 Sequence
41	972	60.0	575	6	AY303785	AY303785 Mus muscu
42	972	60.0	578	6	AY303784	AY303784 Mus muscu
43	972	60.0	1243	2	AX490802	AX490802 Sequence
44	964.5	59.5	792	6	AY626181	AY626181 Rattus no
45	964.5	59.5	792	6	AY626184	AY626184 Rattus no

ALIGNMENTS

RESULT 1
AX081281
LOCUS AX081281 921 bp DNA linear PAT 27-FEB-2001
DEFINITION Sequence 2 from Patent WO0109194.
ACCESSION AX081281
VERSION AX081281.1 GI:13170131
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Glaichenhaus,N. and Malherbe,L.
TITLE Recombinant proteins and molecular complexes derived therefrom, analogous to molecules involved in immune responses
JOURNAL Patent: WO 0109194-A 2 08-FEB-2001;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
FEATURES Location/Qualifiers
source 1. .921
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Ligation de fragments d'ADNc"
CDS 1. .921
/note="unnamed protein product"
/codon_start=1
/transl_table=11
/protein_id="CAC33123.1"

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                /db_xref="GI:13170132"
                /translation="MALQIPSLLLSAAVVVLMVLSSPGTEGGNSICFSPSLEHPIVVS
                GSWDGGGGSLVPRGSGGGGSERHFVVQFKGECYYTNGTQRIRLVTRYIYNREEYVRYD
                SDVGEYRAVTELGRPDAEYWNSQPEILERTRAEVDTACRHNYEGPETSTSLRRLEQPN
                VAISLSRTEALNHHNTLVCSVTDFYPAKIKVRWFRNGQEETVGVSSTQLIRNGDWTFQ
                VLVMLEMTPHQGEVYTCHVEHPSLKSPITVEWRAQSESARSKGGGGSTTAPSAQLKKK
                LQALKKKNAQLKWKLQALKKKLAQHHHHHH"
IN

nment Scores:
. No.:              8.59e-161       Length:         921
e:                  1620.00         Matches:        306
ent Similarity:     100.0%          Conservative:   0
 Local Similarity:  100.0%          Mismatches:     0
y Match:            100.0%          Indels:         0
                    2               Gaps:           0

)-048-116B-6 (1-306) x AX081281 (1-921)

        1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        1 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 60

       21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       61 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120

       41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      121 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 180

       61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      181 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 240

       81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      241 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 300

      101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      301 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 360

      121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      361 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 420

      141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      421 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 480

      161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      481 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 540

      181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      541 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 600

      201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      601 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 660

      221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      661 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 720

      241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      721 AGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCCGAGTCTGCCCGGAGCAAG 780

      261 GlyGlyGlyGlySerThrThrAlaProSerAlaGlnLeuLysLysLysLeuGlnAlaLeu 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        781 GGAGGTGGAGGATCCACTACAGCTCCATCAGCTCAGTTGAAAAAGAAATTGCAAGCACTG 840

Qy        281 LysLysLysAsnAlaGlnLeuLysTrpLysLeuGlnAlaLeuLysLysLysLeuAlaGln 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAAAAAGAACGCTCAGCTGAAGTGGAAACTTCAAGCCCTCAAGAAGAAACTCGCCCAG 900

Qy        301 HisHisHisHisHisHis 306
              ||||||||||||||||||
Db        901 CATCATCATCATCATCAT 918

RESULT 2
AR047947
LOCUS       AR047947                 893 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 25 from patent US 5820866.
ACCESSION   AR047947
VERSION     AR047947.1  GI:5970290
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 893)
  AUTHORS   Kappler,J.W. and Marrack,P.
  TITLE     Product and process for T cell regulation
  JOURNAL   Patent: US 5820866-A 25 13-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .893
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              2.4e-122        Length:         893
Score:                  1255.50         Matches:        242
Percent Similarity:     95.4%           Conservative:   6
Best Local Similarity:  93.1%           Mismatches:     7
Query Match:            77.5%           Indels:         5
DB:                     2               Gaps:           1

US-10-048-116B-6 (1-306) x AR047947 (1-893)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 120

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              ||||||||||||||||||||||||||||||:::     :::   :::
Db        121 AGCAGCCCCGGGACTGAGGGCGGAAACTCCGTACATGCTGCCCATGCT------------ 168

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
                  ::::::   :::      ||||||||||||||||||||||||||||||||||||||
Db        169 ---GAGATCAATGAGGCTGGCAGAGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 225

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 285

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 345

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 405

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 465

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 525

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
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      526 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 585

      181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      586 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 645

      201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      646 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 705

      221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      706 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 765

      241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      766 AGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCCGAGTCTGCCCGGAGCAAG 825

JLT 3
:9666
'S       AR199666                4724 bp    DNA     linear   PAT 20-APR-2002
:NITION  Sequence 8 from patent US 6355479.
:SSION   AR199666
:ION     AR199666.1  GI:20249740
VORDS    .
:CE      Unknown.
:GANISM  Unknown.
         Unclassified.
:ERENCE  1  (bases 1 to 4724)
JTHORS   Webb,S.R., Winqvist,O., Karlsson,L., Jackson,M.R. and Peterson,P.A.
:TLE     MHC class II antigen-presenting systems and methods for activating
         CD4+ T cells
)URNAL   Patent: US 6355479-A 8 12-MAR-2002;
:URES              Location/Qualifiers
  source           1. .4724
                   /organism="unknown"
                   /mol_type="unassigned DNA"
:IN

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i. No.:              1.64e-111      Length:         4724
:e:                  1161.50        Matches:        228
:ent Similarity:     85.8%          Conservative:   1
: Local Similarity:  85.4%          Mismatches:     1
:y Match:            71.7%          Indels:         37
                     2              Gaps:           2

!0-048-116B-6 (1-306) x AR199666 (1-4724)

        1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
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      451 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 510

       21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
          |||||||||||||||||||||||||||
      511 AGCAGCCCAGGGACTGAGGGCGGAAAC------------------------------ 537

       41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60

      537 ------------------------------------------------------------ 537

       61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
      538 ---------TCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 588

       81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      589 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 648

      101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      649 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 708

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        709 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 768

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        769 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 828

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              :::|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        829 ATCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 888

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        889 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 948

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        949 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 1008

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1009 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 1068

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1069 AGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCCGAGTCTGCCCGGAGCAAG 1128

Qy        261 ---------GlyGlyGlyGly 264
                     |||   ||||||
Db       1129 ATGTTGAGCGGCATCGGGGGC 1149

RESULT 4
AR047957
LOCUS       AR047957                1013 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 38 from patent US 5820866.
ACCESSION   AR047957
VERSION     AR047957.1  GI:5970300
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1013)
  AUTHORS   Kappler,J.W. and Marrack,P.
  TITLE     Product and process for T cell regulation
  JOURNAL   Patent: US 5820866-A 38 13-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .1013
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.44e-111      Length:         1013
Score:                  1154.00        Matches:        231
Percent Similarity:     86.8%          Conservative:   5
Best Local Similarity:  84.9%          Mismatches:     22
Query Match:            71.2%          Indels:         14
DB:                     2              Gaps:           4

US-10-048-116B-6 (1-306) x AR047957 (1-1013)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCGGCTGCTGTGGTGGTGCTGATGGTGCTG 122

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              ||||||||||||||||||||||:::|||                |||   |||
Db        123 AGCAGCCCAGGGACTGAGGGCGGAGACTCC---------GAAGCTAGCTTTGAGGCTCAG 173

Qy         41 --------------IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuVal 55
                           |||   |||      :::      ||||||   |||
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174 GGTGCACTGGCCAACATTGCTGTCGACAAGGCTGGAGGTGGTGGATCCGGTGGA------ 227

 56 ProArgGlySerGlyGlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGlu 75
228 ---GGGGGAAGTGGAGGTGGAGGGTCTGAAAGGCATTTCGTGTACCAGTTCATGGGCGAG 284

 76 CysTyrTyrThrAsnGlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArg 95
285 TGCTACTTCACCAACGGGACGCAGCGCATACGATATGTGACCAGATACATCTACAACCGG 344

 96 GluGluTyrValArgTyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGly 115
345 GAGGAGTACGTGCGCTACGACAGCGACGTGGGCGAGCACCGCGCGGTGACCGAGCTGGGG 404

116 ArgProAspAlaGluTyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGlu 135
405 CGGCCAGACGCCGAGTACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAG 464

136 ValAspThrAlaCysArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArg 155
465 GTGGACACGGTGTGCAGACACAACTACGAGGGGCCGGAGACCCACACCTCCCTGCGGCGG 524

156 LeuGluGlnProAsnValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsn 175
525 CTTGAACAGCCCAATGTCGTCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAAC 584

176 ThrLeuValCysSerValThrAspPheTyrProAlaLysIleLysValArgTrpPheArg 195
585 ACTCTGGTCTGCTCAGTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCCGG 644

196 AsnGlyGlnGluGluThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrp 215
645 AATGGCCAGGAGGAGACGGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGG 704

216 ThrPheGlnValLeuValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCys 235
705 ACCTTCCAGGTCCTGGTCATGCTGGAGATGACCCCTCGGCGGGGAGAGGTCTACACCTGT 764

236 HisValGluHisProSerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGlu 255
765 CACGTGGAGCATCCCAGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCTGAG 824

256 SerAlaArgSerLys---------GlyGlyGlyGly 264
825 TCTGCCTGGAGCAAGATGTTGAGCGGCATCGGGGGC 860
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LT 5
3964
S       AR033964                1382 bp    DNA     linear   PAT 29-SEP-1999
NITION  Sequence 123 from patent US 5869270.
SSION   AR033964
ION     AR033964.1  GI:5949569
ORDS    .
CE      Unknown.
GANISM  Unknown.
        Unclassified.
RENCE   1  (bases 1 to 1382)
THORS   Rhode,P.R., Jiao,J.-A., Burkhardt,M. and Wong,H.C.
TLE     Single chain MHC complexes and uses thereof
JRNAL   Patent: US 5869270-A 123 09-FEB-1999;
JRES            Location/Qualifiers
 source         1. .1382
                /organism="unknown"
                /mol_type="unassigned DNA"
IN

nment Scores:
. No.:              1.91e-110       Length:         1382
e:                  1145.00         Matches:        227
ent Similarity:     87.2%           Conservative:   4
 Local Similarity:  85.7%           Mismatches:     24
y Match:            70.7%           Indels:         10
                    2               Gaps:           3
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US-10-048-116B-6 (1-306) x AR033964 (1-1382)

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Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC--------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy        261 GlyGlyGlyGlySer 265
Db        756 GGCGGTGGTGGTTCC 770
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RESULT 6
AR175097
LOCUS       AR175097                1382 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 123 from patent US 6309645.
ACCESSION   AR175097
VERSION     AR175097.1  GI:17916396
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1382)
  AUTHORS   Rhode,P.R., Jiao,J.-A., Burkhardt,M. and Wong,H.C.
  TITLE     MHC molecules and uses thereof
  JOURNAL   Patent: US 6309645-A 123 30-OCT-2001;
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URES             Location/Qualifiers
  source         1. .1382
                 /organism="unknown"
                 /mol_type="unassigned DNA"
IN

nment Scores:
i. No.:              1.91e-110      Length:         1382
e:                   1145.00        Matches:        227
ent Similarity:      87.2%          Conservative:   4
: Local Similarity:  85.7%          Mismatches:     24
y Match:             70.7%          Indels:         10
                     2              Gaps:           3

0-048-116B-6 (1-306) x AR175097 (1-1382)

        1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
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        6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

       21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
          |||||||||   |||          :::          :::          |||
       66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

       41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
          |||      :::|||          ||||||||||||||                  |||
      120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC--------------GGCGGA 164

       61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
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      165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

       81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

      101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

      121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

      141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
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      181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
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      201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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      221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
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      645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

      241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

      261 GlyGlyGlyGlySer 265
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      756 GGCGGTGGTGGTTCC 770

LT 7
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CS079301
LOCUS       CS079301                1382 bp    DNA     linear   PAT 06-MAY-2005
DEFINITION  Sequence 123 from Patent EP1526141.
ACCESSION   CS079301
VERSION     CS079301.1  GI:63093743
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1
  AUTHORS   Rhode,P.R., Jiao,J.A., Burkhardt,M. and Wong,H.C.
  TITLE     MHC complexes and uses thereof
  JOURNAL   Patent: EP 1526141-A 123 27-APR-2005;
            Altor BioScience Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .1382
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:              1.91e-110      Length:         1382
Score:                  1145.00        Matches:        227
Percent Similarity:     87.2%          Conservative:   4
Best Local Similarity:  85.7%          Mismatches:     24
Query Match:            70.7%          Indels:         10
DB:                     2              Gaps:           3

US-10-048-116B-6 (1-306) x CS079301 (1-1382)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
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Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              |||||||||   |||          :::          :::          |||
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              |||      :::|||          ||||||||||||||                  |||
Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC--------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
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Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
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Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
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Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
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      585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

      221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

      241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
          |||||||||||||||||||||||||||||||||         :::
      705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

      261 GlyGlyGlyGlySer 265
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      756 GGCGGTGGTGGTTCC 770


LT 8
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NITION  Sequence 123 from Patent EP0997477.
3SION   AX032545
ION     AX032545.1  GI:10279486
ORDS    .
CE      unidentified
3ANISM  unidentified
        unclassified sequences.
RENCE   1
THORS   Chavaillaz,P.A., Edwards,A.C., Grammer,S., Jiao,J.A., Rhode,P.R.,
        Weidanz,J.A. and Wong,H.C.
TLE     Mhc complexes and uses thereof
URNAL   Patent: EP 0997477-A 123 03-MAY-2000;
        SUNOL MOLECULAR CORP (US)
URES            Location/Qualifiers
 source         1. .1382
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                /mol_type="unassigned DNA"
                /db_xref="taxon:32644"
IN

ıment Scores:
. No.:              1.91e-110       Length:         1382
e:                  1145.00         Matches:        227
ent Similarity:     87.2%           Conservative:   4
 Local Similarity:  85.7%           Mismatches:     24
y Match:            70.7%           Indels:         10
                    2               Gaps:           3

)-048-116B-6 (1-306) x AX032545 (1-1382)

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       21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
          |||||||||   |||         :::         :::         |||
       66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

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          |||      :::|||          ||||||||||||||                  |||
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      101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

      121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
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Db      345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy      141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
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Db      405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy      161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy      181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy      201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy      221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
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Db      645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy      241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
            |||||||||||||||||||||||||||||||||         :::
Db      705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy      261 GlyGlyGlyGlySer 265
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Db      756 GGCGGTGGTGGTTCC 770

RESULT 9
AR033962
LOCUS       AR033962                1385 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 121 from patent US 5869270.
ACCESSION   AR033962
VERSION     AR033962.1  GI:5949567
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1385)
  AUTHORS   Rhode,P.R., Jiao,J.-A., Burkhardt,M. and Wong,H.C.
  TITLE     Single chain MHC complexes and uses thereof
  JOURNAL   Patent: US 5869270-A 121 09-FEB-1999;
FEATURES            Location/Qualifiers
     source         1. .1385
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                    /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.91e-110       Length:         1385
Score:                  1145.00         Matches:        227
Percent Similarity:     87.2%           Conservative:   4
Best Local Similarity:  85.7%           Mismatches:     24
Query Match:            70.7%           Indels:         10
DB:                     2               Gaps:           3

US-10-048-116B-6 (1-306) x AR033962 (1-1385)

Qy        1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
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Db        6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy       21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
            |||||||||   |||         :::         :::         |||
Db       66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy       41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
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Qy       61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
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      225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

      101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
      285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

      121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
      345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

      141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
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      181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
      525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

      201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
      585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

      221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
      645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

      241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
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      756 GGCGGTGGTGGTTCC 770
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JLT 10
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JS       AR175095                1385 bp    DNA     linear   PAT 17-DEC-2001
INITION  Sequence 121 from patent US 6309645.
ESSION   AR175095
SION     AR175095.1  GI:17916394
WORDS    .
CE       Unknown.
RGANISM  Unknown.
         Unclassified.
ERENCE   1  (bases 1 to 1385)
JTHORS   Rhode,P.R., Jiao,J.-A., Burkhardt,M. and Wong,H.C.
ITLE     MHC molecules and uses thereof
OURNAL   Patent: US 6309645-A 121 30-OCT-2001;
TURES             Location/Qualifiers
  source          1. .1385
                  /organism="unknown"
                  /mol_type="unassigned DNA"
IN
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gnment Scores:
i. No.:              1.91e-110      Length:         1385
e:                   1145.00        Matches:        227
ent Similarity:      87.2%          Conservative:   4
 Local Similarity:   85.7%          Mismatches:     24
y Match:             70.7%          Indels:         10
                     2              Gaps:           3

0-048-116B-6 (1-306) x AR175095 (1-1385)
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Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC--------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
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Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
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Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy        261 GlyGlyGlyGlySer 265
Db        756 GGCGGTGGTGGTTCC 770
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RESULT 11
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LOCUS       CS079299                1385 bp    DNA     linear   PAT 06-MAY-2005
DEFINITION  Sequence 121 from Patent EP1526141.
ACCESSION   CS079299
VERSION     CS079299.1  GI:63093741
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1
  AUTHORS   Rhode,P.R., Jiao,J.A., Burkhardt,M. and Wong,H.C.
  TITLE     MHC complexes and uses thereof
  JOURNAL   Patent: EP 1526141-A 121 27-APR-2005;
            Altor BioScience Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .1385
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IN

ıment Scores:
. No.:              1.91e-110       Length:         1385
3:                  1145.00         Matches:        227
ent Similarity:     87.2%           Conservative:   4
 Local Similarity:  85.7%           Mismatches:     24
/ Match:            70.7%           Indels:         10
                    2               Gaps:           3

)-048-116B-6 (1-306) x CS079299 (1-1385)

        1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

       21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
          |||||||||   |||         :::             :::           |||
       66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

       41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
          |||      :::|||          ||||||||||||||                 |||
      120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC--------------GGCGGA 164

       61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
          ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
      165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

       81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

      101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

      121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

      141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

      161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
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      465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

      181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
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      525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

      201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

      221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

      241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
          ||||||||||||||||||||||||||||||||         :::
      705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

      261 GlyGlyGlyGlySer 265
          |||||||||||||||
      756 GGCGGTGGTGGTTCC 770

LT 12
2543
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LOCUS       AX032543                1385 bp    DNA     linear   PAT 20-SEP-2000
DEFINITION  Sequence 121 from Patent EP0997477.
ACCESSION   AX032543
VERSION     AX032543.1  GI:10279484
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1
  AUTHORS   Chavaillaz,P.A., Edwards,A.C., Grammer,S., Jiao,J.A., Rhode,P.R.,
            Weidanz,J.A. and Wong,H.C.
  TITLE     Mhc complexes and uses thereof
  JOURNAL   Patent: EP 0997477-A 121 03-MAY-2000;
            SUNOL MOLECULAR CORP (US)
FEATURES             Location/Qualifiers
     source          1. .1385
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ORIGIN

Alignment Scores:
Pred. No.:              1.91e-110       Length:         1385
Score:                  1145.00         Matches:        227
Percent Similarity:     87.2%           Conservative:   4
Best Local Similarity:  85.7%           Mismatches:     24
Query Match:            70.7%           Indels:         10
DB:                     2               Gaps:           3

US-10-048-116B-6 (1-306) x AX032543 (1-1385)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
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Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              |||||||||   |||         :::             :::           |||
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              |||      :::|||          ||||||||||||||                 |||
Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC--------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
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Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
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Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
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Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
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Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
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       585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

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       645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

       241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
           |||||||||||||||||||||||||||||||      :::
       705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

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       756 GGCGGTGGTGGTTCC 770

JLT 13
13963
JS       AR033963                1508 bp    DNA     linear   PAT 29-SEP-1999
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:SSION   AR033963
:ION     AR033963.1  GI:5949568
VORDS    .
:CE      Unknown.
:GANISM  Unknown.
         Unclassified.
:RENCE   1  (bases 1 to 1508)
JTHORS   Rhode,P.R., Jiao,J.-A., Burkhardt,M. and Wong,H.C.
:TLE     Single chain MHC complexes and uses thereof
)URNAL   Patent: US 5869270-A 122 09-FEB-1999;
TURES             Location/Qualifiers
  source          1. .1508
                  /organism="unknown"
                  /mol_type="unassigned DNA"
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nment Scores:
i. No.:              2.13e-110      Length:         1508
:e:                  1145.00        Matches:        227
:ent Similarity:     87.2%          Conservative:   4
: Local Similarity:  85.7%          Mismatches:     24
:y Match:            70.7%          Indels:         10
                     2              Gaps:           3

:0-048-116B-6 (1-306) x AR033963 (1-1508)

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         6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

        21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
           |||||||||  |||       :::       :::       |||
        66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

        41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
           |||      :::|||          ||||||||||||||                  |||
       120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC--------------GGCGGA 164

        61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
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       225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

       101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

       121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
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       141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
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       181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
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       201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
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       585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

       221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
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       645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

       241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
           |||||||||||||||||||||||||||||||      :::
       705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

       261 GlyGlyGlyGlySer 265
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       756 GGCGGTGGTGGTTCC 770

RESULT 14
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LOCUS       AR152030                1508 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 24 from patent US 6232445.
ACCESSION   AR152030
VERSION     AR152030.1  GI:15118080
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1508)
  AUTHORS   Rhode,P.R., Acevedo,J., Burkhardt,M., Jiao,J.-a. and Wong,H.C.
  TITLE     Soluble MHC complexes and methods of use thereof
  JOURNAL   Patent: US 6232445-A 24 15-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .1508
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                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              2.13e-110      Length:         1508
Score:                  1145.00        Matches:        227
Percent Similarity:     87.2%          Conservative:   4
Best Local Similarity:  85.7%          Mismatches:     24
Query Match:            70.7%          Indels:         10
DB:                     2              Gaps:           3

US-10-048-116B-6 (1-306) x AR152030 (1-1508)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              |||||||||  |||       :::       :::       |||
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              |||      :::|||          ||||||||||||||                  |||
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Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
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Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224
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 81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
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225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
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405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
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465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
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525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
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221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
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645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
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705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

261 GlyGlyGlyGlySer 265
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756 GGCGGTGGTGGTTCC 770
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LT 15
5096
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NITION  Sequence 122 from patent US 6309645.
3SION   AR175096
ION     AR175096.1  GI:17916395
ORDS    .
CE      Unknown.
3ANISM  Unknown.
        Unclassified.
RENCE   1  (bases 1 to 1508)
THORS   Rhode,P.R., Jiao,J.-A., Burkhardt,M. and Wong,H.C.
TLE     MHC molecules and uses thereof
JRNAL   Patent: US 6309645-A 122 30-OCT-2001;
URES            Location/Qualifiers
 source         1. .1508
                /organism="unknown"
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IN

ıment Scores:
. No.:              2.13e-110       Length:         1508
3:                  1145.00         Matches:        227
ent Similarity:     87.2%           Conservative:   4
 Local Similarity:  85.7%           Mismatches:     24
/ Match:            70.7%           Indels:         10
                    2               Gaps:           3

)-048-116B-6 (1-306) x AR175096 (1-1508)

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Qy        21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
             |||||||||  |||          :::                 :::          |||
Db        66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy        41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
             |||      :::|||        ||||||||||||||                   |||
Db       120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC---------------GGCGGA 164

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Db       225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy       101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
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Db       285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy       121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
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Qy       141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
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Qy       161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
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Db       465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy       181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
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Qy       221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
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Db       645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy       241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
             ||||||||||||||||||||||||||||||||  :::
Db       705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy       261 GlyGlyGlyGlySer 265
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Search completed: June  1, 2006, 01:03:44
Job time : 6473 secs
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GenCore version 5.1.9

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 30, 2006, 01:23:04 ; Search time 522.277 Seconds
(without alignments)
6007.369 Million cell updates/sec

Title: US-10-048-116B-6_COPY_1_300
Perfect score: 1572
Sequence: 1 MALQIPSLLLSAAVVVLMVL.....KKKNAQLKWKLQALKKKLAQ 300

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10048116/runat_29062006_093309_10102/app_query.fasta_1
-DB=N_Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss05p
-USER=US10048116_@CGN_1_1_1423_@runat_29062006_093309_10102 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
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9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1572	100.0	921	5	AAF55099	Aaf55099 DNA encod
2	1255.5	79.9	893	2	AAT04262	Aat04262 Hybrid IA
3	1222	77.7	945	12	ADQ31225	Adq31225 I-Ab(beta
4	1206	76.7	915	12	ADQ31228	Adq31228 I-Ab(beta
5	1161.5	73.9	4724	2	AAV12068	Aav12068 Murine IA
6	1151	73.2	1013	2	AAT04269	Aat04269 Hybrid IA
7	1145	72.8	1382	2	AAT17588	Aat17588 Vector SC
8	1145	72.8	1382	2	AAT86989	Aat86989 SCE1 sing
9	1145	72.8	1382	8	ACA60744	Aca60744 Mouse MHC
10	1145	72.8	1385	2	AAT17586	Aat17586 Vector SS
11	1145	72.8	1385	2	AAT86987	Aat86987 SSC1 sing
12	1145	72.8	1385	8	ACA60742	Aca60742 Mouse MHC
13	1145	72.8	1508	2	AAT17587	Aat17587 Vector SC
14	1145	72.8	1508	2	AAT86988	Aat86988 SCT1 sing
15	1145	72.8	1508	2	AAX89069	Aax89069 Single ch
16	1145	72.8	1508	8	ACA60743	Aca60743 Mouse MHC
17	1096.5	69.8	798	12	ADJ75986	Adj75986 Marker ge
18	1096.5	69.8	798	14	ADX26090	Adx26090 Novel cel
19	1093	69.5	1085	4	ABI99040	Abi99040 Murine pC
20	1049.5	66.8	1698	4	ABI99038	Abi99038 Murine pC
21	1044.5	66.4	1662	4	ABI99039	Abi99039 Murine pC
22	979.5	62.3	702	2	AAQ03170	Aaq03170 Sequence
23	979.5	62.3	702	2	AAT06286	Aat06286 I-Ab-beta
24	979.5	62.3	702	2	AAQ56920	Aaq56920 Mouse I-A
25	972	61.8	1243	6	ABN84048	Abn84048 Single ch
26	963.5	61.3	702	2	AAQ35055	Aaq35055 IAB beta
27	957	60.9	1686	4	ABI99031	Abi99031 MBP 1-14
28	957	60.9	1701	4	ABI99028	Abi99028 IAS MBP 1
29	957	60.9	2059	4	ABI99032	Abi99032 MBP 1-14
30	957	60.9	2346	4	ABI99027	Abi99027 IAS MBP 1
31	952	60.6	1707	4	ABI99030	Abi99030 IAS MBP 9
32	949	60.4	1680	4	ABI99021	Abi99021 I-As MBP.
33	949	60.4	2053	4	ABI99029	Abi99029 IAS MBP 9
34	949	60.4	2343	4	ABI99033	Abi99033 MBP 90-10
35	871	55.4	1344	2	AAT60705	Aat60705 cDNA enco
36	854.5	54.4	1323	2	AAT60700	Aat60700 cDNA enco
37	844.5	53.7	861	14	AEC64482	Aec64482 DRB1-biot
38	839.5	53.4	1192	10	AAD63150	Aad63150 Human maj
39	839.5	53.4	1192	10	AAD62751	Aad62751 Human maj
40	839.5	53.4	1192	11	ADP88246	Adp88246 Lung canc
41	839.5	53.4	1192	13	ADR24869	Adr24869 Breast ca
42	833.5	53.0	941	12	ADO40822	Ado40822 DNA encod
43	829	52.7	562	6	ABK63510	Abk63510 Rat seque
44	829	52.7	562	10	ADB57995	Adb57995 Toxicity-
45	829	52.7	562	10	ABT41775	Abt41775 Toxicity

ALIGNMENTS

RESULT 1
AAF55099
ID AAF55099 standard; DNA; 921 BP.
XX
AC AAF55099;
XX
DT 15-MAY-2001 (first entry)
XX
DE DNA encoding a fusion protein comprising a beta chain of MHC.
XX
KW Recombinant protein; alpha chain; beta chain; MHC; immunoglobulin;
KW major histocompatibility complex; Fc region; antigen; T lymphocyte;
KW immunostimulant; vaccine; infection; tumour; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1. .921
FT /*tag= a
XX
PN WO200109194-A1.
XX
PD 08-FEB-2001.
XX
PF 28-JUL-2000; 2000WO-FR002193.
XX
PR 29-JUL-1999; 99FR-00009862.

```
XX
PA   (CNRS ) CNRS CENT NAT RECH SCI.
XX
PI   Glaichenhaus N,  Malherbe L;
XX
DR   WPI; 2001-182944/18.
DR   P-PSDB; AAB67481.
XX
PT   New soluble recombinant protein, useful e.g. as immunostimulant,
PT   comprises dimeric major histocompatibility complex molecule fused to
PT   immunoglobulin Fc region.
XX
PS   Example 1; Page 34-35; 43pp; French.
XX
CC   The specification describes soluble recombinant proteins that comprise at
CC   least a dimer formed from the alpha and beta-chains of MHC (major
CC   histocompatibility complex) Class I and II molecules in which at least
CC   one chain has, attached to its C-terminus, at least part of the Fc region
CC   of an immunoglobulin. The recombinant proteins, when linked to an
CC   antigenic peptide, are used to count and/or purify antigen-reactive T
CC   lymphocytes and to characterize their phenotype, e.g. in preclinical
CC   evaluation of vaccines. They are also used as immunostimulants,
CC   particularly for vaccine development (against infections and tumours), to
CC   count and determine phenotype of autoreactive T cells in subjects with,
CC   or at risk of developing, autoimmune diseases, e.g. for staging or
CC   evaluating treatments, and (to purify and/or enrich Ag-reactive T cells
CC   from cell cultures or patient samples, for use in subsequent curative or
CC   preventative cellular therapy. The present sequence encodes a recombinant
CC   protein of the invention, comprising a beta chain of MHC molecules
XX
SQ   Sequence 921 BP; 214 A; 265 C; 286 G; 156 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.21e-142       Length:         921
Score:                  1572.00         Matches:        300
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     5               Gaps:           0

US-10-048-116B-6_COPY_1_300 (1-300) x AAF55099 (1-921)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 60

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlySerLeuValProArgGlySerGly 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 180

Qy         61 GlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 240

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 300

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 360

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 420

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 480

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 540

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 600

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 660

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 720

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCCGAGTCTGCCCGGAGCAAG 780

Qy        261 GlyGlyGlyGlySerThrThrAlaProSerAlaGlnLeuLysLysLysLeuGlnAlaLeu 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGAGGTGGAGGATCCACTACAGCTCCATCAGCTCAGTTGAAAAAGAAATTGCAAGCACTG 840

Qy        281 LysLysLysAsnAlaGlnLeuLysTrpLysLeuGlnAlaLeuLysLysLysLeuAlaGln 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAAAAAGAACGCTCAGCTGAAGTGGAAACTTCAAGCCCTCAAGAAGAAACTCGCCCAG 900

RESULT 2
AAT04262
ID   AAT04262 standard; DNA; 893 BP.
XX
AC   AAT04262;
XX
DT   16-APR-1996  (first entry)
XX
DE   Hybrid IA beta chain gene.
XX
KW   Polymerase chain reaction; PCR; primer; amplify;
KW   major histocompatability complex; MHC; T-cell receptor; TCR;
KW   autoimmune disease; immunodeficiency disease; immune response;
KW   immunoproliferation disease; graft-host rejection; therapy; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   primer_bind     1. .16
FT                   /*tag= a
FT                   /note= "probable primer binding site (primer #233)"
FT   primer_bind     complement(45. .74)
FT                   /*tag= b
FT                   /note= "binding site for primer #261 (see AAT04260)"
FT   CDS             61. .828
FT                   /*tag= c
FT                   /product= "hybrid IA beta chain"
FT   sig_peptide     61. .141
FT                   /*tag= d
FT                   /note= "leader region"
FT   primer_bind     complement(119. .172)
FT                   /*tag= e
FT                   /note= "binding site for primer #331 (see AAT04261)"
FT   primer_bind     complement(158. .212)
FT                   /*tag= f
FT                   /note= "primer #332 binding site"
FT   primer_bind     complement(199. .250)
FT                   /*tag= g
FT                   /note= "primer #333 (see AAT04263) binding site"
FT   misc_feature    371. .389
FT                   /*tag= h
FT                   /note= "probable primer binding site (primer #270)"
FT   mat_peptide     511. .825
FT                   /*tag= i
```

```
FT                   /product= "IA beta chain beta 2 region"
FT   primer_bind     521. .550
FT                   /*tag=  j
FT                   /note= "probable primer binding site (primer #271)"
FT   primer_bind     532. .554
FT                   /*tag=  k
FT                   /note= "probable primer binding site (primer #272)"
FT   primer_bind     808. .836
FT                   /*tag=  l
FT                   /note= "probable primer binding site (primer #259)"
FT   primer_bind     877. .893
FT                   /*tag=  m
FT                   /note= "probable primer binding site (primer #232)"
XX
PN   WO9523814-A1.
XX
PD   08-SEP-1995.
XX
PF   03-MAR-1995;   95WO-US002689.
XX
PR   04-MAR-1994;   94US-00207481.
XX
PA   (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
XX
PI   Kappler JW,  Marrack P;
XX
DR   WPI; 1995-320543/41.
DR   P-PSDB; AAR82533.
XX
PT   Peptide-MHC complex comprising antigenic peptide, linker and MHC segment
PT   - useful as reagents for the treatment of diseases including auto-immune
PT   diseases, immuno-stimulatory diseases or graft-host rejection.
XX
PS   Example 1; Page 53; 94pp; English.
XX
CC   This sequence represents a hybrid IA beta chain gene, containing the
CC   chicken ovalbumin peptide (cOVA). This sequence was used in the
CC   construction of a hybrid IA alpha beta dimer. The encoded protein (pIAd-
CC   OVA) was found to be more stable than the IA alpha beta dimer. The
CC   stability was decreased by the addition of a MHC groove specific binding
CC   peptide (e.g. see AAR82527, AAR82528 and AAR82531), compared to an
CC   increase seen on the addition of a MHC binding peptide to IE k/d-MCC.
CC   These complexes may be used to regulate an immune response. The complexes
CC   are capable of being recognised by a TCR alone or in combination with
CC   additional MHC proteins. These complexes are useful for therapeutic
CC   purposes and experimental purposes. They can also be used as reagents for
CC   the treatment of diseases including autoimmune diseases, immunodeficiency
CC   diseases, immunoproliferation diseases, and graft-host rejection
XX
SQ   Sequence 893 BP; 204 A; 239 C; 275 G; 175 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              9.23e-112       Length:         893
Score:                  1255.50         Matches:        242
Percent Similarity:     95.4%           Conservative:   6
Best Local Similarity:  93.1%           Mismatches:     7
Query Match:            79.9%           Indels:         5
DB:                     2               Gaps:           1

US-10-048-116B-6_COPY_1_300 (1-300) x AAT04262 (1-893)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 120

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              ||||||||||||||||||||||||||||||:::      :::   :::
Db        121 AGCAGCCCCGGGACTGAGGGCGGAAACTCCGTACATGCTGCCCATGCT---------- 168

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
                  ::::::   :::      ||||||||||||||||||||||||||||||||
Db        169 ---GAGATCAATGAGGCTGGCAGAGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 225

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 285

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 345

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 405

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 465

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 525

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        526 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 585

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 645

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 705

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        706 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 765

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        766 AGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCCGAGTCTGCCCGGAGCAAG 825

RESULT 3
ADQ31225
ID   ADQ31225 standard; cDNA; 945 BP.
XX
AC   ADQ31225;
XX
DT   07-OCT-2004  (first entry)
XX
DE   I-Ab(beta)-Cholera toxin B subunit-leucine zipper (LZ)-BirA fusion cDNA.
XX
KW   class II major histocompatibility complex; MHC; CD4+ T-cell detection;
KW   flow cytometry; mucous membrane invasive antigen;
KW   I-Ab(beta)-cholera toxin B subunit-leucine zipper-BirA fusion; CTB; ss;
KW   gene.
XX
OS   Vibrio cholerae.
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .945
FT                   /*tag=  a
FT                   /product= "I-Ab(beta)-Cholera toxin B subunit (CTB)-
FT                   leucine zipper (LZ)-BirA fusion cDNA"
XX
PN   JP2004196789-A.
XX
PD   15-JUL-2004.
XX
PF   03-DEC-2003; 2003JP-00404367.
XX
PR   03-DEC-2002; 2002JP-00351818.
XX
PA   (SENT-) SENTAN KAGAKU GIJUTSU INCUBATION CENT KK.
```

```
XX
DR   WPI; 2004-546819/53.
DR   P-PSDB; ADQ31224.
XX
PT   Peptide-Class II major histocompatibility complex (MHC) composite, useful
PT   for detecting antigen specific CD4+ T-cell, comprises antigen peptide
PT   containing epitope of mucous membrane invasive protein, and extracellular
PT   region of MHC.
XX
PS   Example 1; SEQ ID NO 10; 30pp; Japanese.
XX
CC   The invention relates to a novel class II major histocompatibility
CC   complex (MHC) antigenic peptide composite comprising a peptide containing
CC   the T-cell antigenic determinant of a mucous membrane invasive protein
CC   and the extracellular region of a class II MHC molecule or at least part
CC   of the extracellular region of the class II MHC molecule having an amino
CC   acid sequence comprising one or more deletions, substitutions or
CC   additions. The molecule of the invention may be useful for detecting an
CC   antigen-specific CD4+ T-cell by flow cytometry and for presenting a
CC   microorganism-derived mucous membrane invasive protein as an antigen. The
CC   method of the invention enables efficient detection of antigen-specific
CC   activation of CD4+ T-cells in the mucous membrane. The current sequence
CC   is that of the class II major histocompatibility complex-related I-
CC   Ab(alpha)-Cholera toxin B subunit (CTB)-leucine zipper (LZ)-BirA fusion
CC   cDNA of the invention.
XX
SQ   Sequence 945 BP; 230 A; 256 C; 294 G; 165 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.74e-108      Length:         945
Score:                  1222.00        Matches:        242
Percent Similarity:     85.0%          Conservative:   14
Best Local Similarity:  80.4%          Mismatches:     41
Query Match:            77.7%          Indels:         4
DB:                     12             Gaps:           3

US-10-048-116B-6_COPY_1_300 (1-300) x ADQ31225 (1-945)

Qy          1 MetAlaLeuGlnIlePro---SerLeuLeuLeuSerAlaAlaValValValLeuMetVal 19
              :::   |||:::::::|||           ::::::         |||   |||||||||
Db          4 GTGTGTCTGAAGCTCCCTGGAGGTTCCTACATGGCAAAGCTGACAGTGACACTGATGGTG 63

Qy         20 LeuSerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHis 39
              ||||||||||||          |||:::|||      ::::::           |||
Db         64 CTGAGCTCCCCACTGGCTTTGGCTGGAGACTCCTGCGTGTGGAACAATAAGACGCCGCAC 123

Qy         40 ProIleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySer 59
                 |||                :::|||||||||||||||          ||||||
Db        124 GCGATCGCGGCCATCAGCATGGCGAACGGAGGTGGTGGGTCC---GGTGGAGGGGGAAGT 180

Qy         60 GlyGlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThr 79
              ||||||||||||||||||||||||||   ||||||   ||||||||||||:::|||
Db        181 GGAGGTGGAGGGTCTGAAAGGCATTTCGTGTACCAGTTCATGGGCGAGTGCTACTTCACC 240

Qy         80 AsnGlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrVal 99
              ||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db        241 AACGGGACGCAGCGCATACGATATGTGACCAGATACATCTACAACCGGGAGGAGTACGTG 300

Qy        100 ArgTyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAla 119
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db        301 CGCTACGACAGCGACGTGGGCGAGCACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCC 360

Qy        120 GluTyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAla 139
              ||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        361 GAGTACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGCTGGACACGGTG 420

Qy        140 CysArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnPro 159
              ||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        421 TGCAGACACAACTACGAGGGGCCGGAGACCCACACCTCCCTGCGGCGGCTTGAACAGCCC 480

Qy        160 AsnValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCys 179
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AATGTCGTCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGC 540

Qy        180 SerValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGlu 199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCAGTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCCGGAATGGCCAGGAG 600

Qy        200 GluThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnVal 219
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GAGACGGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTC 660

Qy        220 LeuValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHis 239
              ||||||||||||||||||||||   :::||||||||||||||||||||||||||||||||
Db        661 CTGGTCATGCTGGAGATGACCCCTCGGCGGGGAGAGGTCTACACCTGTCACGTGGAGCAT 720

Qy        240 ProSerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSer 259
              ||||||||||||||||||||||||||||||||||||||||||||   :::
Db        721 CCCAGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCGTCAGCA------GAC 774

Qy        260 LysGlyGlyGlyGlySerThrThrAlaProSerAlaGlnLeuLysLysLysLeuGlnAla 279
                          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        775 CTGGTTCCGCGCGGATCCACTACAGCTCCATCAGCTCAGTTGAAAAAGAAACTGCAGGCA 834

Qy        280 LeuLysLysLysAsnAlaGlnLeuLysTrpLysLeuGlnAlaLeuLysLysLysLeuAla 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        835 CTTAAGAAAAAGAACGCTCAGCTGAAGTGGAAACTTCAAGCCCTCAAGAAGAAACTCGCC 894

Qy        300 Gln 300
              |||
Db        895 CAG 897

RESULT 4
ADQ31228
ID   ADQ31228 standard; cDNA; 915 BP.
XX
AC   ADQ31228;
XX
DT   07-OCT-2004  (first entry)
XX
DE   I-Ab(beta)-E. coli heat-labile toxin B subunit-LZ-BirA fusion cDNA.
XX
KW   class II major histocompatibility complex; MHC; CD4+ T-cell detection;
KW   flow cytometry; mucous membrane invasive antigen;
KW   I-Ab(beta)-heat-labile toxin B subunit-leucine zipper-BirA fusion; LTB;
KW   ss; gene.
XX
OS   Escherichia coli.
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .915
FT                   /*tag= a
FT                   /product= "I-Ab(beta)-Escherichia coli heat-labile toxin
FT                   B subunit (LTB)-leucine zipper (LZ)-BirA fusion protein"
XX
PN   JP2004196789-A.
XX
PD   15-JUL-2004.
XX
PF   03-DEC-2003; 2003JP-00404367.
XX
PR   03-DEC-2002; 2002JP-00351818.
XX
PA   (SENT-) SENTAN KAGAKU GIJUTSU INCUBATION CENT KK.
XX
DR   WPI; 2004-546819/53.
DR   P-PSDB; ADQ31227.
XX
PT   Peptide-Class II major histocompatibility complex (MHC) composite, useful
PT   for detecting antigen specific CD4+ T-cell, comprises antigen peptide
PT   containing epitope of mucous membrane invasive protein, and extracellular
PT   region of MHC.
XX
PS   Example 3; SEQ ID NO 13; 30pp; Japanese.
XX
```

```
CC   The invention relates to a novel class II major histocompatibility
CC   complex (MHC) antigenic peptide composite comprising a peptide containing
CC   the T-cell antigenic determinant of a mucous membrane invasive protein
CC   and the extracellular region of a class II MHC molecule or at least part
CC   of the extracellular region of the class II MHC molecule having an amino
CC   acid sequence comprising one or more deletions, substitutions or
CC   additions. The molecule of the invention may be useful for detecting an
CC   antigen-specific CD4+ T-cell by flow cytometry and for presenting a
CC   microorganism-derived mucous membrane invasive protein as an antigen. The
CC   method of the invention enables efficient detection of antigen-specific
CC   activation of CD4+ T-cells in the mucous membrane. The current sequence
CC   is that of the class II major histocompatibility complex-related I-
CC   Ab(alpha)-Escherichia coli heat-labile toxin B subunit (LTB)-leucine
CC   zipper (LZ)-BirA fusion cDNA of the invention.
XX
SQ   Sequence 915 BP; 228 A; 242 C; 271 G; 174 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                5.91e-107      Length:          915
Score:                    1206.00        Matches:         240
Percent Similarity:       85.0%          Conservative:    16
Best Local Similarity:    79.7%          Mismatches:      31
Query Match:              76.7%          Indels:          14
DB:                       12             Gaps:            5

US-10-048-116B-6_COPY_1_300 (1-300) x ADQ31228 (1-915)

Qy          1 MetAlaLeuGlnIlePro---SerLeuLeuLeuSerAlaAlaValValValLeuMetVal 19
              :::   |||::::::|||           ::::::         |||   |||||||||
Db          4 GTGTGTCTGAAGCTCCCTGGAGGTTCCTACATGGCAAAGCTGACAGTGACACTGATGGTG 63

Qy         20 LeuSerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHis 39
              ||||||||||||          |||:::|||
Db         64 CTGAGCTCCCCACTGGCTTTGGCTGGAGACTCC--------------GGTAAAAGAGAA 108

Qy         40 ProIleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySer 59
                 :::::::::      ::::::   ||||||||||||||||||||||||||
Db        109 ATGGTTATCATT------ACATTTAAGGGTGGTGGTGGTTCTTTAGTTCCTAGA------ 156

Qy         60 GlyGlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThr 79
              ||||||||||||||||||||||||    ||||||   ||||||||||||:::|||
Db        157 ------GGTGGTAGTGAAAGGCATTTCGTGTACCAGTTCATGGGCGAGTGCTACTTCACC 210

Qy         80 AsnGlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrVal 99
              ||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db        211 AACGGGACGCAGCGCATACGATATGTGACCAGATACATCTACAACCGGGAGGAGTACGTG 270

Qy        100 ArgTyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAla 119
              ||||||||||||||||||||||:::||||||||||||||||||||||||||||||||||
Db        271 CGCTACGACAGCGACGTGGGCGAGCACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCC 330

Qy        120 GluTyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAla 139
              ||||||||||||||||||||||||||||||||||||||||||||:::|||||||
Db        331 GAGTACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGCTGGACACGGTG 390

Qy        140 CysArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnPro 159
              ||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        391 TGCAGACACAACTACGAGGGGCCGGAGACCCACACCTCCCTGCGGCGGCTTGAACAGCCC 450

Qy        160 AsnValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCys 179
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 AATGTCGTCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGC 510

Qy        180 SerValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGlu 199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 TCAGTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCCGGAATGGCCAGGAG 570

Qy        200 GluThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnVal 219
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 GAGACGGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTC 630

Qy        220 LeuValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHis 239
              ||||||||||||||||||||||||   :::|||||||||||||||||||||||||||||

Db        631 CTGGTCATGCTGGAGATGACCCCTCGGCGGGGAGAGGTCTACACCTGTCACGTGGAGCAT 690

Qy        240 ProSerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSer 259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   :::
Db        691 CCCAGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCGTCAGCA------GAC 744

Qy        260 LysGlyGlyGlyGlySerThrThrAlaProSerAlaGlnLeuLysLysLysLeuGlnAla 279
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 CTGGTTCCGCGCGGATCCACTACAGCTCCATCAGCTCAGTTGAAAAAGAAACTGCAGGCA 804

Qy        280 LeuLysLysLysAsnAlaGlnLeuLysTrpLysLeuGlnAlaLeuLysLysLysLeuAla 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 CTTAAGAAAAAGAACGCTCAGCTGAAGTGGAAACTTCAAGCCCTCAAGAAGAAACTCGCC 864

Qy        300 Gln 300
              |||
Db        865 CAG 867
```

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RESULT 5
AAV12068
ID   AAV12068 standard; cDNA; 4724 BP.
XX
AC   AAV12068;
XX
DT   08-JUN-1998  (first entry)
XX
DE   Murine IAd beta chain cDNA.
XX
KW   Major histocompatibility class II antigen; MHC class II; T cell;
KW   T lymphocyte; Th1; Th2; activation; CD4+; antigen presenting cell; APC;
KW   autoimmune disease; diabetes; multiple sclerosis; autoimmune thyroiditis;
KW   systemic lupus erythromatosus; myasthenia gravis; Crohn's disease;
KW   inflammatory bowel disease; allergy; asthma; contact sensitivity;
KW   immunotherapy; therapy; IAd beta chain; mouse; ds; circular; cyclic.
XX
OS   Mus musculus.
XX
PN   WO9746256-A1.
XX
PD   11-DEC-1997.
XX
PF   22-MAY-1997;   97WO-US008697.
XX
PR   23-MAY-1996;   96US-0018175P.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Webb SR,  Winqvist O,  Karlsson L,  Jackson MR,  Peterson PA;
XX
DR   WPI; 1998-041895/04.
XX
PT   Synthetic antigen presenting cell for activating CD4+ T cells - useful to
PT   treat autoimmune disease, e.g. diabetes, multiple sclerosis, Crohn's
PT   disease and inflammatory bowel disease, or allergy, e.g. asthma and
PT   contact sensitivity.
XX
PS   Example 2; Page 94-96; 141pp; English.
XX
CC   This nucleotide sequence comprises a PCR product obtained by
CC   amplification of mouse splenocyte cDNA using primers (see AAV12065 and
CC   AAV12066) designed for the amplification of IAd beta chain full-length
CC   cDNA. IAd alpha chain cDNA (see AAV12067) has been similarly obtained.
CC   The IAd sequences were cloned into metallothionein promoter (see
CC   AAV12062)-driven vector pRmHa-3 prior to sequencing. Major
CC   histocompatibility complex (MHC) class II IAd heterodimers were expressed
CC   at the cell surface of transfected Drosophila Schneider 2 (ATCC CRL
CC   10974) cells. The invention relates to the preparation and use of
CC   synthetic antigen presenting matrices, in particular antigen presenting
CC   cells such as insect cells that have been transfected to produce MHC
CC   antigen presenting molecules with one or more accessory molecules. The
CC   matrices are used to activate naive CD4+ T cells and to shift the ongoing
CC   activation state into a preferred differentiated population of Th1 or Th2
CC   cells. Applications include the treatment of autoimmune disease, e.g.
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CC   diabetes, multiple sclerosis, autoimmune thyroiditis, systemic lupus
CC   erythematosus, myasthenia gravis, Crohn's disease and inflammatory bowel
CC   disease, or an allergy, e.g. asthma and contact sensitivity
XX
SQ   Sequence 4724 BP; 1196 A; 1194 C; 1200 G; 1134 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.11e-101      Length:         4724
Score:                  1161.50        Matches:        228
Percent Similarity:     85.8%          Conservative:   1
Best Local Similarity:  85.4%          Mismatches:     1
Query Match:            73.9%          Indels:         37
DB:                     2              Gaps:           2

US-10-048-116B-6_COPY_1_300 (1-300) x AAV12068 (1-4724)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 510

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              ||||||||||||||||||||||||||
Db        511 AGCAGCCCAGGGACTGAGGGCGGAAAC------------------------------ 537

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60

Db        537 ------------------------------------------------------------ 537

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
                         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 ---------TCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 588

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        589 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 648

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        649 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 708

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        709 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 768

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        769 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 828

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              :::||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        829 ATCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 888

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        889 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 948

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        949 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 1008

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1009 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 1068

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1069 AGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCCGAGTCTGCCCGGAGCAAG 1128

Qy        261 ---------GlyGlyGlyGly 264
                       |||  ||||||
Db       1129 ATGTTGAGCGGCATCGGGGGC 1149

RESULT 6
```

```
AAT04269
ID   AAT04269 standard; DNA; 1013 BP.
XX
AC   AAT04269;
XX
DT   16-APR-1996  (first entry)
XX
DE   Hybrid IA beta chain gene.
XX
KW   Major histocompatability complex; MHC; T-cell receptor; TCR;
KW   autoimmune disease; immunodeficiency disease; immune response;
KW   immunoproliferation disease; graft-host rejection; therapy; B cell;
KW   M12.C3; pM12-IAb-Ea; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   primer_bind     1. .18
FT                   /*tag= a
FT                   /note= "probable primer binding site (primer #76)"
FT   primer_bind     complement(40. .74)
FT                   /*tag= b
FT                   /note= "binding site for primer #362 (see AAT04270)"
FT   CDS             63. .959
FT                   /*tag= c
FT                   /product= "hybrid IA beta chain"
FT   sig_peptide     63. .143
FT                   /*tag= d
FT                   /note= "leader region"
FT   primer_bind     complement(140. .191)
FT                   /*tag= e
FT                   /note= "binding site for primer #363 (see AAT04271)"
FT   primer_bind     complement(177. .226)
FT                   /*tag= f
FT                   /note= "primer #364 binding site"
FT   primer_bind     complement(212. .266)
FT                   /*tag= g
FT                   /note= "primer #365 (see AAT04272) binding site"
FT   primer_bind     385. .403
FT                   /*tag= h
FT                   /note= "probable primer binding site (primer #270)"
FT   mat_peptide     531. .959
FT                   /*tag= i
FT                   /product= "IA beta chain beta 2 region"
FT   primer_bind     535. .564
FT                   /*tag= j
FT                   /note= "probable primer binding site (primer #271)"
FT   primer_bind     544. .568
FT                   /*tag= k
FT                   /note= "probable primer binding site (primer #272)"
FT   primer_bind     823. .850
FT                   /*tag= l
FT                   /note= "probable primer binding site (primer #259)"
FT   primer_bind     942. .976
FT                   /*tag= m
FT                   /note= "probable primer binding site (primer #366)"
FT   primer_bind     1000. .1013
FT                   /*tag= n
FT                   /note= "probable primer binding site (primer #59)"
XX
PN   WO9523814-A1.
XX
PD   08-SEP-1995.
XX
PF   03-MAR-1995;   95WO-US002689.
XX
PR   04-MAR-1994;   94US-00207481.
XX
PA   (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
XX
PI   Kappler JW,  Marrack P;
XX
DR   WPI; 1995-320543/41.
```

```
DR   P-PSDB; AAR82538.
XX
PT   Peptide-MHC complex comprising antigenic peptide, linker and MHC segment
PT   - useful as reagents for the treatment of diseases including auto-immune
PT   diseases, immuno-stimulatory diseases or graft-host rejection.
XX
PS   Example 2; Page 65; 94pp; English.
XX
CC   This sequence represents a hybrid IA beta chain gene. This sequence
CC   contains a fragment of the IE alpha chain (residues 56-73), as well as a
CC   linker and cleavage site. This sequence was transfected into a B cell
CC   line (M12.C3) using plasmid pM12-IAb-Ea. It was found that the encoded
CC   sequence was expressed in these cells. Complexes such as this may be used
CC   to regulate an immune response. The complexes are capable of being
CC   recognised by a TCR alone or in combination with additional MHC proteins.
CC   These complexes are useful for therapeutic purposes and experimental
CC   purposes. They can also be used as reagents for the treatment of diseases
CC   including autoimmune diseases, immunodeficiency diseases,
CC   immunoproliferation diseases, and graft-host rejection
XX
SQ   Sequence 1013 BP; 220 A; 272 C; 327 G; 192 T; 0 U; 2 Other;

Alignment Scores:
Pred. No.:              1.43e-101     Length:          1013
Score:                  1151.00       Matches:         230
Percent Similarity:     86.8%         Conservative:    6
Best Local Similarity:  84.6%         Mismatches:      22
Query Match:            73.2%         Indels:          14
DB:                     2             Gaps:            4

US-10-048-116B-6_COPY_1_300 (1-300) x AAT04269 (1-1013)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCGGCTGCTGTGGTGGTGCTCATGGTGCTG 122

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              ||||||||||||||||||||||:::|||              |||   |||
Db        123 AGCAGCCCAGGGACTGAGGGCGGAGACTCC---------GAAGCTAGCTTTGAGGCTCAG 173

Qy         41 --------------IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuVal 55
                           |||   |||      :::      ||||||   |||
Db        174 GGTGCACTGGCCAACATTGCTGTCGACAAGGCTGGAGGTGGTGGATCCGGTGGA------ 227

Qy         56 ProArgGlySerGlyGlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGlu 75
              |||||||||||||||||||||||||||||||||||   ||||||   ||||||
Db        228 ---GGGGGAAGTGGAGGTGGAGGGTCTGAAAGGCATTTCGTGTACCAGTTCATGGGCGAG 284

Qy         76 CysTyrTyrThrAsnGlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArg 95
              ||||||:::|||||||||||||||||||||||||   |||||||||||||||||||||||
Db        285 TGCTACTTCACCAACGGGACGCAGCGCATACGATATGTGACCAGATACATCTACAACCGG 344

Qy         96 GluGluTyrValArgTyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGly 115
              ||||||||||||||||||||||||||||||||||:::|||||||||||||||||||||||
Db        345 GAGGAGTACGTGCGCTACGACAGCGACGTGGGCGAGCACCGCGCGGTGACCGAGCTGGGG 404

Qy        116 ArgProAspAlaGluTyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGlu 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 CGGCCAGACGCCGAGTACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAG 464

Qy        136 ValAspThrAlaCysArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArg 155
              |||||||||   ||||||||||||||||||||||||||||||   |||||||||||||||
Db        465 GTGGACACGGTGTGCAGACACAACTACGAGGGGCCGGAGACCCACACCTCCCTGCGGCGG 524

Qy        156 LeuGluGlnProAsnValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsn 175
              |||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db        525 CTTGAACAGCCCAATGTCGTCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAAC 584

Qy        176 ThrLeuValCysSerValThrAspPheTyrProAlaLysIleLysValArgTrpPheArg 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACTCTGGTCTGCTCAGTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCCGG 644

Qy        196 AsnGlyGlnGluGluThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrp 215
              |||||||||||||||||||||||:::|||||||||||||||||||||||||||||||||||||||
Db        645 AATGGCCAGGAGGAGACGGTGGGGCTCTCATCCACACAGCTTATTAGGAATGGGGACTGG 704

Qy        216 ThrPheGlnValLeuValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCys 235
              ||||||||||||||||||||||||||||||||||||   :::|||||||||||||||||||
Db        705 ACCTTCCAGGTCCTGGTCATGCTGGAGATGACCCCTCGGCGGGGAGAGGTCTAYACCTGT 764

Qy        236 HisValGluHisProSerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGlu 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        765 CACGTGGAGCATCCCAGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCTGAG 824

Qy        256 SerAlaArgSerLys---------GlyGlyGlyGly 264
              ||||||   ||||||         |||   ||||||
Db        825 TCTGCCTGGAGCAAGATGTTGAGCGGCATCGGGGGC 860

RESULT 7
AAT17588
ID   AAT17588 standard; DNA; 1382 BP.
XX
AC   AAT17588;
XX
DT   26-SEP-1996  (first entry)
XX
DE   Vector SCE1-derived single chain gene encoding MHC fusion complex.
XX
KW   MHC; major histocompatibility complex; PCR; polymerase chain reaction;
KW   T cell activity modulator; antagonist; immune disorder; allergy;
KW   multiple sclerosis; insulin-dependent diabetes mellitus;
KW   rheumatoid arthritis; myasthenia gravis; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             6. .1382
FT                   /*tag=  a
FT   sig_peptide     6. .86
FT                   /*tag=  b
FT                   /label= I-Ad_beta_chain_leader
FT                   /note= "murine MHC class II I-Ad gene beta chain leader
FT                   sequence"
FT   misc_feature    87. .137
FT                   /*tag=  c
FT                   /label= OVA_323-339
FT                   /note= "chicken ovalbumin residues 323-339"
FT   misc_feature    138. .167
FT                   /*tag=  d
FT                   /note= "10 residue linker peptide"
FT   misc_feature    168. .452
FT                   /*tag=  e
FT                   /label= I-Ad_beta1
FT                   /note= "murine MHC class II I-Ad gene beta-1 domain"
FT   misc_feature    453. .734
FT                   /*tag=  f
FT                   /label= I-Ad_beta2
FT                   /note= "murine MHC class II I-Ad gene beta-2 domain"
FT   misc_feature    735. .806
FT                   /*tag=  g
FT                   /note= "24 residue peptide linker"
FT   misc_feature    807. .1067
FT                   /*tag=  h
FT                   /label= I-Ad_alpha1
FT                   /note= "murine MHC class II I-Ad gene alpha-2 domain"
FT   misc_feature    1068. .1352
FT                   /*tag=  i
FT                   /label= I-Ad_alpha2
FT                   /note= "murine MHC class II I-Ad gene alpha-2 domain"
FT   misc_feature    1353. .1379
FT                   /*tag=  j
FT                   /note= "EE tag"
XX
PN   WO9604314-A1.
XX
PD   15-FEB-1996.
```

```
XX
PF   31-JUL-1995;   95WO-US009816.
XX
PR   29-JUL-1994;   94US-00283302.
PR   01-FEB-1995;   95US-00382454.
XX
PA   (DADE-) DADE INT INC.
XX
PI   Wong HC,  Rhode PR,  Weidanz JA,  Grammer S,  Edwards AC;
PI   Chavaillaz P,  Jiao J;
XX
DR   WPI; 1996-129343/13.
DR   P-PSDB; AAR98907.
XX
PT   Major histocompatability complex fusion complex for modulating T cell
PT   activity - used in the treatment of immune disorders, e.g. multiple
PT   sclerosis, IDDM and rheumatoid arthritis.
XX
PS   Example 17; Fig 29; 210pp; English.
XX
CC   AAT17588 encodes a murine MHC fusion complex capable of modulating T cell
CC   activity encoded by the vector SCE1. The MHC fusion complex comprises at
CC   least one MHC molecule containing a peptide-binding groove and a
CC   presenting peptide covalently linked to the MHC molecule and opt. a
CC   transmembrane domain. DNA encoding a MHC fusion complex may be cloned
CC   into a host cell to express the complex. The transformed cells may then
CC   be used to identify peptides that modulate, pref. antagonise, T cell
CC   activity. DNA encoding a MHC fusion complex or a single chain fusion
CC   molecule may be used to vaccinate a mammal against a targeted disorder.
CC   The fusion complexes may be used to suppress an immune response in an
CC   animal suffering from an immune disorder e.g. multiple sclerosis, insulin
CC   -dependent diabetes mellitus, rheumatoid arthritis, myasthenia gravis or
CC   chronic allergies. The complexes may also be used in the treatment of
CC   livestock and pets such as cats and dogs. The MHC fusion complexes can be
CC   produced such that they contain a single antigenic peptide including one
CC   of known structure, additionally a wide range of peptides can be
CC   presented for T cell interaction
XX
SQ   Sequence 1382 BP; 320 A; 374 C; 404 G; 284 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              8.31e-101      Length:          1382
Score:                  1145.00        Matches:         227
Percent Similarity:     87.2%          Conservative:    4
Best Local Similarity:  85.7%          Mismatches:      24
Query Match:            72.8%          Indels:          10
DB:                     2              Gaps:            3

US-10-048-116B-6_COPY_1_300 (1-300) x AAT17588 (1-1382)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              |||||||||   |||        :::          :::        |||
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              |||      :::|||         ||||||||||||||                 |||
Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC--------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTCGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              ||||||||||||||||||||||||||||||||          :::
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy        261 GlyGlyGlyGlySer 265
              |||||||||||||||
Db        756 GGCGGTGGTGGTTCC 770

RESULT 8
AAT86989
ID   AAT86989 standard; DNA; 1382 BP.
XX
AC   AAT86989;
XX
DT   27-MAR-1998  (first entry)
XX
DE   SCE1 single chain gene.
XX
KW   Construction; major histocompatibility complex; MHC; fusion complex;
KW   SCE1 single chain gene; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             6. .1382
FT                   /*tag=  a
XX
PN   WO9728191-A1.
XX
PD   07-AUG-1997.
XX
PF   30-JAN-1997;   97WO-US001617.
XX
PR   31-JAN-1996;   96US-00596387.
XX
PA   (DADE-) DADE INT INC.
XX
PI   Rhode PR,  Jiao J,  Burkhardt M,  Wong HC;
XX
DR   WPI; 1997-402555/37.
DR   P-PSDB; AAW29214.
XX
PT   Single chain major histocompatibility complex comprising linked alpha and
PT   beta chains - useful for suppressing an immune response to an auto:immune
PT   disease, e.g. multiple sclerosis, rheumatoid arthritis, diabetes
PT   mellitus, etc.
XX
PS   Example 17; Page 140-141; 217pp; English.
```

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XX
CC   The present sequence was used in the construction of major
CC   histocompatibility complex (MHC) fusion complexes
XX
SQ   Sequence 1382 BP; 320 A; 373 C; 405 G; 284 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              8.31e-101      Length:          1382
Score:                  1145.00        Matches:         227
Percent Similarity:     87.2%          Conservative:    4
Best Local Similarity:  85.7%          Mismatches:      24
Query Match:            72.8%          Indels:          10
DB:                     2              Gaps:            3

US-10-048-116B-6_COPY_1_300 (1-300) x AAT86989 (1-1382)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              |||||||||   |||         :::           :::          |||
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              |||      :::|||          ||||||||||||||                 |||
Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC---------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              ||||||||||||||||||||||||||||||         :::
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy        261 GlyGlyGlyGlySer 265
              |||||||||||||||
Db        756 GGCGGTGGTGGTTCC 770

RESULT 9
```

```
ACA60744
ID   ACA60744 standard; DNA; 1382 BP.
XX
AC   ACA60744;
XX
DT   16-JUN-2003  (first entry)
XX
DE   Mouse MHC I-Ad/Ova 323-339 synthetic gene SCE1.
XX
KW   MHC; major histocompatibility complex; gene therapy; fusion complex;
KW   peptide-binding groove; T cell modulation; class II MHC; vaccine;
KW   autoimmune disorder; multiple sclerosis; rheumatoid arthritis;
KW   insulin-dependent diabetes mellitus; myasthenia gravis; immunogen;
KW   chronic allergy; mouse; ds; I-Ad; gene.
XX
OS   Mus sp.
OS   Synthetic.
XX
PN   US2002198144-A1.
XX
PD   26-DEC-2002.
XX
PF   06-JUL-2001; 2001US-00900379.
XX
PR   29-JUL-1994;   94US-00283302.
PR   01-FEB-1995;   95US-00382454.
PR   17-JAN-1997;   97US-00776084.
XX
PA   (DADE-) DADE INT INC.
XX
PI   Wong HC,  Rhode PR,  Weidanz JA,  Grammer S,  Edwards AC;
PI   Chavaillaz P,  Jiao JJJ;
XX
DR   WPI; 2003-341126/32.
DR   P-PSDB; ABU72108.
XX
PT   Novel major histocompatibility complex fusion complex having presenting
PT   peptide covalently linked to MHC molecule containing peptide-binding
PT   groove, used for suppressing immune response in multiple sclerosis,
PT   allergies.
XX
PS   Example 17; Fig 29; 126pp; English.
XX
CC   The invention relates to a major histocompatibility complex (MHC) fusion
CC   complex (I) comprising an MHC molecule that contains a peptide-binding
CC   groove, and a presenting peptide covalently (e.g. an antigenic peptide)
CC   linked to the MHC molecule, where (I) is capable of modulating the
CC   activity of a T cell. Also included are a DNA construct coding for the
CC   complex, where the MHC molecule is a class II MHC (e.g. mouse I-Ad or I-
CC   As, or human HLA-DR1 (human leukocyte antigen-DR1)), a multivalent MHC
CC   fusion complex comprising two or more linked complexes, identifying a
CC   peptide that can modulate the activity of T cells (involving introducing
CC   into host cells cloning vectors that each contain the fusion complex DNA,
CC   culturing the host cells under conditions suitable for expression of the
CC   MHC fusion complex, and selecting host cells that express MHC fusion
CC   complex that modulate the activity of T cells), a single recombinant
CC   expression vector comprising DNA that codes for the alpha and beta chains
CC   of the fusion complex MHC protein, a single recombinant expression vector
CC   comprising DNA that codes for a T cell costimulatory factor and the alpha
CC   and beta chains of the MHC fusion complex. The DNA constructs can contain
CC   heterologous leader peptide sequences and Kozak sequence for efficient
CC   expression of the fusion complex. Also included are inducing an immune
CC   response in a mammal (including vaccinating a mammal against a targeted
CC   disorder, by administering DNA sequence comprising a fusion complex, or
CC   DNA sequence coding for a fusion complex which is a single chain fusion
CC   molecule) and suppressing an immune response in a mammal by administering
CC   to the mammal a DNA sequence comprising an expression vector, encoding a
CC   full length MHC molecule that contains a transmembrane domain, and a
CC   presenting peptide that is a T cell receptor (TCR) antagonist or partial
CC   agonist and is covalently linked to the MHC protein, or DNA sequence
CC   coding for the fusion complex which is a single chain fusion molecule.
CC   The methods are useful for identifying a peptide that can modulate the
CC   activity of T cells, inducing an immune response in a mammal (including
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CC   vaccinating a mammal against a targeted disorder) and for suppressing an
CC   immune response in a mammal. The disorders include an autoimmune disorder
CC   such as multiple sclerosis, insulin-dependent diabetes mellitus,
CC   rheumatoid arthritis, myasthenia gravis or chronic allergies. The present
CC   sequence encodes a mouse MHC class II I-Ad fusion complex of the
CC   invention
XX
SQ   Sequence 1382 BP; 320 A; 373 C; 405 G; 284 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              8.31e-101      Length:          1382
Score:                  1145.00        Matches:         227
Percent Similarity:     87.2%          Conservative:    4
Best Local Similarity:  85.7%          Mismatches:      24
Query Match:            72.8%          Indels:          10
DB:                     8              Gaps:            3

US-10-048-116B-6_COPY_1_300 (1-300) x ACA60744 (1-1382)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              |||||||||   |||         :::         :::       |||
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              |||      :::|||          ||||||||||||||||                |||
Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC--------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              |||||||||||||||||||||||||||||||||          :::
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy        261 GlyGlyGlyGlySer 265
              |||||||||||||||
```

```
Db        756 GGCGGTGGTGGTTCC 770

RESULT 10
AAT17586
ID   AAT17586 standard; DNA; 1385 BP.
XX
AC   AAT17586;
XX
DT   26-SEP-1996  (first entry)
XX
DE   Vector SSC1-derived single chain gene encoding MHC fusion complex.
XX
KW   MHC; major histocompatibility complex; PCR; polymerase chain reaction;
KW   T cell activity modulator; antagonist; immune disorder; allergy;
KW   multiple sclerosis; insulin-dependent diabetes mellitus;
KW   rheumatoid arthritis; myasthenia gravis; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             6. .1385
FT                   /*tag=  a
FT   sig_peptide     6. .86
FT                   /*tag=  b
FT                   /label= I-Ad_beta_chain_leader
FT                   /note= "murine MHC class II I-Ad gene beta chain leader
FT                   sequence"
FT   misc_feature    87. .137
FT                   /*tag=  c
FT                   /label= OVA_323-339
FT                   /note= "chicken ovalbumin residues 323-339"
FT   misc_feature    138. .167
FT                   /*tag=  d
FT                   /note= "10 residue linker peptide"
FT   misc_feature    168. .452
FT                   /*tag=  e
FT                   /label= I-Ad_beta1
FT                   /note= "murine MHC class II I-Ad gene beta-1 domain"
FT   misc_feature    453. .734
FT                   /*tag=  f
FT                   /label= I-Ad_beta2
FT                   /note= "murine MHC class II I-Ad gene beta-2 domain"
FT   misc_feature    735. .806
FT                   /*tag=  g
FT                   /note= "24 residue peptide linker"
FT   misc_feature    807. .1067
FT                   /*tag=  h
FT                   /label= I-Ad_alpha1
FT                   /note= "murine MHC class II I-Ad gene alpha-2 domain"
FT   misc_feature    1068. .1352
FT                   /*tag=  i
FT                   /label= I-Ad_alpha2
FT                   /note= "murine MHC class II I-Ad gene alpha-2 domain"
FT   misc_feature    1353. .1382
FT                   /*tag=  j
FT                   /note= "6xHis tag"
XX
PN   WO9604314-A1.
XX
PD   15-FEB-1996.
XX
PF   31-JUL-1995;   95WO-US009816.
XX
PR   29-JUL-1994;   94US-00283302.
PR   01-FEB-1995;   95US-00382454.
XX
PA   (DADE-) DADE INT INC.
XX
PI   Wong HC,  Rhode PR,  Weidanz JA,  Grammer S,  Edwards AC;
PI   Chavaillaz P,  Jiao J;
XX
DR   WPI; 1996-129343/13.
DR   P-PSDB; AAR98905.
```

```
XX
PT   Major histocompatability complex fusion complex for modulating T cell
PT   activity - used in the treatment of immune disorders, e.g. multiple
PT   sclerosis, IDDM and rheumatoid arthritis.
XX
PS   Example 17; Fig 27; 210pp; English.
XX
CC   AAT17586 encodes a murine MHC fusion complex capable of modulating T cell
CC   activity encoded by the vector SSC1. The MHC fusion complex comprises at
CC   least one MHC molecule containing a peptide-binding groove and a
CC   presenting peptide covalently linked to the MHC molecule and opt. a
CC   transmembrane domain. DNA encoding a MHC fusion complex may be cloned
CC   into a host cell to express the complex. The transformed cells may then
CC   be used to identify peptides that modulate, pref. antagonise, T cell
CC   activity. DNA encoding a MHC fusion complex or a single chain fusion
CC   molecule may be used to vaccinate a mammal against a targeted disorder.
CC   The fusion complexes may be used to suppress an immune response in an
CC   animal suffering from an immune disorder e.g. multiple sclerosis, insulin
CC   -dependent diabetes mellitus, rheumatoid arthritis, myasthenia gravis or
CC   chronic allergies. The complexes may also be used in the treatment of
CC   livestock and pets such as cats and dogs. The MHC fusion complexes can be
CC   produced such that they contain a single antigenic peptide including one
CC   of known structure, additionally a wide range of peptides can be
CC   presented for T cell interaction
XX
SQ   Sequence 1385 BP; 316 A; 384 C; 398 G; 287 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                8.33e-101      Length:          1385
Score:                    1145.00        Matches:         227
Percent Similarity:       87.2%          Conservative:    4
Best Local Similarity:    85.7%          Mismatches:      24
Query Match:              72.8%          Indels:          10
DB:                       2              Gaps:            3

US-10-048-116B-6_COPY_1_300 (1-300) x AAT17586 (1-1385)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
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Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              |||||||||   |||         :::           :::          |||
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              |||      :::|||          |||||||||||||||                 |||
Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC--------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTCGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              ||||||||||||||||||||||||||||||||  :::
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy        261 GlyGlyGlyGlySer 265
              |||||||||||||||
Db        756 GGCGGTGGTGGTTCC 770

RESULT 11
AAT86987
ID   AAT86987 standard; DNA; 1385 BP.
XX
AC   AAT86987;
XX
DT   27-MAR-1998  (first entry)
XX
DE   SSC1 single chain gene.
XX
KW   Construction; major histocompatibility complex; MHC; fusion complex;
KW   SSC1 single chain gene; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             6. .1385
FT                   /*tag=  a
XX
PN   WO9728191-A1.
XX
PD   07-AUG-1997.
XX
PF   30-JAN-1997;   97WO-US001617.
XX
PR   31-JAN-1996;   96US-00596387.
XX
PA   (DADE-) DADE INT INC.
XX
PI   Rhode PR,  Jiao J,  Burkhardt M,  Wong HC;
XX
DR   WPI; 1997-402555/37.
DR   P-PSDB; AAW29212.
XX
PT   Single chain major histocompatibility complex comprising linked alpha and
PT   beta chains - useful for suppressing an immune response to an auto:immune
PT   disease, e.g. multiple sclerosis, rheumatoid arthritis, diabetes
PT   mellitus, etc.
XX
PS   Example 17; Page 135-137; 217pp; English.
XX
CC   The present sequence was used in the construction of major
CC   histocompatibility complex (MHC) fusion complexes
XX
SQ   Sequence 1385 BP; 316 A; 383 C; 399 G; 287 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                8.33e-101      Length:          1385
Score:                    1145.00        Matches:         227
Percent Similarity:       87.2%          Conservative:    4
Best Local Similarity:    85.7%          Mismatches:      24
Query Match:              72.8%          Indels:          10
DB:                       2              Gaps:            3
```

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US-10-048-116B-6_COPY_1_300 (1-300) x AAT86987 (1-1385)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              |||||||||   |||         :::         :::         |||
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              |||      :::|||          ||||||||||||||                  |||
Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC---------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGluProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              ||||||||||||||||||||||||||||||||         :::
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy        261 GlyGlyGlyGlySer 265
              |||||||||||||||
Db        756 GGCGGTGGTGGTTCC 770

RESULT 12
ACA60742
ID   ACA60742 standard; DNA; 1385 BP.
XX
AC   ACA60742;
XX
DT   16-JUN-2003  (first entry)
XX
DE   Mouse MHC I-Ad/Ova 323-339 synthetic gene SSC1.
XX
KW   MHC; major histocompatibility complex; gene therapy; fusion complex;
KW   peptide-binding groove; T cell modulation; class II MHC; vaccine;
KW   autoimmune disorder; multiple sclerosis; rheumatoid arthritis;
KW   insulin-dependent diabetes mellitus; myasthenia gravis; immunogen;
KW   chronic allergy; mouse; ds; I-Ad; gene.
XX
OS   Mus sp.
OS   Synthetic.
XX
PN   US2002198144-A1.
XX
PD   26-DEC-2002.
XX
PF   06-JUL-2001; 2001US-00900379.
XX
PR   29-JUL-1994;   94US-00283302.
PR   01-FEB-1995;   95US-00382454.
PR   17-JAN-1997;   97US-00776084.
XX
PA   (DADE-) DADE INT INC.
XX
PI   Wong HC,  Rhode PR,  Weidanz JA,  Grammer S,  Edwards AC;
PI   Chavaillaz P,  Jiao JJJ;
XX
DR   WPI; 2003-341126/32.
DR   P-PSDB; ABU72106.
XX
PT   Novel major histocompatibility complex fusion complex having presenting
PT   peptide covalently linked to MHC molecule containing peptide-binding
PT   groove, used for suppressing immune response in multiple sclerosis,
PT   allergies.
XX
PS   Example 17; Fig 27; 126pp; English.
XX
CC   The invention relates to a major histocompatibility complex (MHC) fusion
CC   complex (I) comprising an MHC molecule that contains a peptide-binding
CC   groove, and a presenting peptide covalently (e.g. an antigenic peptide)
CC   linked to the MHC molecule, where (I) is capable of modulating the
CC   activity of a T cell. Also included are a DNA construct coding for the
CC   complex, where the MHC molecule is a class II MHC (e.g. mouse I-Ad or I-
CC   As, or human HLA-DR1 (human leukocyte antigen-DR1)), a multivalent MHC
CC   fusion complex comprising two or more linked complexes, identifying a
CC   peptide that can modulate the activity of T cells (involving introducing
CC   into host cells cloning vectors that each contain the fusion complex DNA,
CC   culturing the host cells under conditions suitable for expression of the
CC   MHC fusion complex, and selecting host cells that express MHC fusion
CC   complex that modulate the activity of T cells), a single recombinant
CC   expression vector comprising DNA that codes for the alpha and beta chains
CC   of the fusion complex MHC protein, a single recombinant expression vector
CC   comprising DNA that codes for a T cell costimulatory factor and the alpha
CC   and beta chains of the MHC fusion complex. The DNA constructs can contain
CC   heterologous leader peptide sequences and Kozak sequence for efficient
CC   expression of the fusion complex. Also included are inducing an immune
CC   response in a mammal (including vaccinating a mammal against a targeted
CC   disorder, by administering DNA sequence comprising a fusion complex, or
CC   DNA sequence coding for a fusion complex which is a single chain fusion
CC   molecule) and suppressing an immune response in a mammal by administering
CC   to the mammal a DNA sequence comprising an expression vector, encoding a
CC   full length MHC molecule that contains a transmembrane domain, and a
CC   presenting peptide that is a T cell receptor (TCR) antagonist or partial
CC   agonist and is covalently linked to the MHC protein, or DNA sequence
CC   coding for the fusion complex which is a single chain fusion molecule.
CC   The methods are useful for identifying a peptide that can modulate the
CC   activity of T cells, inducing an immune response in a mammal (including
CC   vaccinating a mammal against a targeted disorder) and for suppressing an
CC   immune response in a mammal. The disorders include an autoimmune disorder
CC   such as multiple sclerosis, insulin-dependent diabetes mellitus,
CC   rheumatoid arthritis, myasthenia gravis or chronic allergies. The present
CC   sequence encodes a mouse MHC class II I-Ad fusion complex of the
CC   invention
XX
SQ   Sequence 1385 BP; 316 A; 383 C; 399 G; 287 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              8.33e-101       Length:         1385
Score:                  1145.00         Matches:        227
Percent Similarity:     87.2%           Conservative:   4
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Best Local Similarity:  85.7%          Mismatches:     24
Query Match:            72.8%          Indels:         10
DB:                     8              Gaps:           3

US-10-048-116B-6_COPY_1_300 (1-300) x ACA60742 (1-1385)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
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Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              |||||||||   |||       :::           :::         |||
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              |||      :::|||          ||||||||||||||||                 |||
Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC--------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              ||||||||||||||||||||||||||||||    :::
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy        261 GlyGlyGlyGlySer 265
              |||||||||||||||
Db        756 GGCGGTGGTGGTTCC 770

RESULT 13
AAT17587
ID   AAT17587 standard; DNA; 1508 BP.
XX
AC   AAT17587;
XX
DT   26-SEP-1996  (first entry)
XX
DE   Vector SCT1-derived single chain gene encoding MHC fusion complex.
XX
KW   MHC; major histocompatibility complex; PCR; polymerase chain reaction;
KW   T cell activity modulator; antagonist; immune disorder; allergy;
KW   multiple sclerosis; insulin-dependent diabetes mellitus;
KW   rheumatoid arthritis; myasthenia gravis; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             6. .1508
FT                   /*tag=  a
FT   sig_peptide     6. .86
FT                   /*tag=  b
FT                   /label= I-Ad_beta_chain_leader
FT                   /note= "murine MHC class II I-Ad gene beta chain leader
FT                   sequence"
FT   misc_feature    87. .137
FT                   /*tag=  c
FT                   /label= OVA_323-339
FT                   /note= "chicken ovalbumin residues 323-339"
FT   misc_feature    138. .167
FT                   /*tag=  d
FT                   /note= "10 residue linker peptide"
FT   misc_feature    168. .452
FT                   /*tag=  e
FT                   /label= I-Ad_beta1
FT                   /note= "murine MHC class II I-Ad gene beta-1 domain"
FT   misc_feature    453. .734
FT                   /*tag=  f
FT                   /label= I-Ad_beta2
FT                   /note= "murine MHC class II I-Ad gene beta-2 domain"
FT   misc_feature    735. .806
FT                   /*tag=  g
FT                   /note= "24 residue peptide linker"
FT   misc_feature    807. .1067
FT                   /*tag=  h
FT                   /label= I-Ad_alpha1
FT                   /note= "murine MHC class II I-Ad gene alpha-2 domain"
FT   misc_feature    1068. .1352
FT                   /*tag=  i
FT                   /label= I-Ad_alpha2
FT                   /note= "murine MHC class II I-Ad gene alpha-2 domain"
FT   misc_feature    1353. .1505
FT                   /*tag=  j
FT                   /label= I-Ad_alpha-TM
FT                   /note= "murine MHC class II I-Ad gene alpha-transmembrane
FT                   domain"
XX
PN   WO9604314-A1.
XX
PD   15-FEB-1996.
XX
PF   31-JUL-1995;    95WO-US009816.
XX
PR   29-JUL-1994;    94US-00283302.
PR   01-FEB-1995;    95US-00382454.
XX
PA   (DADE-) DADE INT INC.
XX
PI   Wong HC,  Rhode PR,  Weidanz JA,  Grammer S,  Edwards AC;
PI   Chavaillaz P,  Jiao J;
XX
DR   WPI; 1996-129343/13.
DR   P-PSDB; AAR98906.
XX
PT   Major histocompatability complex fusion complex for modulating T cell
PT   activity - used in the treatment of immune disorders, e.g. multiple
PT   sclerosis, IDDM and rheumatoid arthritis.
XX
PS   Example 17; Fig 28; 210pp; English.
XX
CC   AAT17587 encodes a murine MHC fusion complex capable of modulating T cell
CC   activity encoded by the vector SCT1. The MHC fusion complex comprises at
CC   least one MHC molecule containing a peptide-binding groove and a
CC   presenting peptide covalently linked to the MHC molecule and opt. a
```

```
CC   transmembrane domain. DNA encoding a MHC fusion complex may be cloned
CC   into a host cell to express the complex. The transformed cells may then
CC   be used to identify peptides that modulate, pref. antagonise, T cell
CC   activity. DNA encoding a MHC fusion complex or a single chain fusion
CC   molecule may be used to vaccinate a mammal against a targeted disorder.
CC   The fusion complexes may be used to suppress an immune response in an
CC   animal suffering from an immune disorder e.g. multiple sclerosis, insulin
CC   -dependent diabetes mellitus, rheumatoid arthritis, myasthenia gravis or
CC   chronic allergies. The complexes may also be used in the treatment of
CC   livestock and pets such as cats and dogs. The MHC fusion complexes can be
CC   produced such that they contain a single antigenic peptide including one
CC   of known structure, additionally a wide range of peptides can be
CC   presented for T cell interaction
XX
SQ   Sequence 1508 BP; 337 A; 414 C; 440 G; 317 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              9.35e-101      Length:         1508
Score:                  1145.00        Matches:        227
Percent Similarity:     87.2%          Conservative:   4
Best Local Similarity:  85.7%          Mismatches:     24
Query Match:            72.8%          Indels:         10
DB:                     2              Gaps:           3

US-10-048-116B-6_COPY_1_300 (1-300) x AAT17587 (1-1508)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              |||||||||   |||         :::         :::         |||
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              |||      :::|||          ||||||||||||||                  |||
Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC---------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTCGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy        261 GlyGlyGlyGlySer 265
              |||||||||||||||
Db        756 GGCGGTGGTGGTTCC 770

RESULT 14
AAT86988
ID   AAT86988 standard; DNA; 1508 BP.
XX
AC   AAT86988;
XX
DT   27-MAR-1998  (first entry)
XX
DE   SCT1 single chain gene.
XX
KW   Construction; major histocompatibility complex; MHC; fusion complex;
KW   SCT1 single chain gene; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             6. .1508
FT                   /*tag=  a
XX
PN   WO9728191-A1.
XX
PD   07-AUG-1997.
XX
PF   30-JAN-1997;   97WO-US001617.
XX
PR   31-JAN-1996;   96US-00596387.
XX
PA   (DADE-) DADE INT INC.
XX
PI   Rhode PR,  Jiao J,  Burkhardt M,  Wong HC;
XX
DR   WPI; 1997-402555/37.
DR   P-PSDB; AAW29213.
XX
PT   Single chain major histocompatibility complex comprising linked alpha and
PT   beta chains - useful for suppressing an immune response to an auto:immune
PT   disease, e.g. multiple sclerosis, rheumatoid arthritis, diabetes
PT   mellitus, etc.
XX
PS   Example 17; Page 137-139; 217pp; English.
XX
CC   The present sequence was used in the construction of major
CC   histocompatibility complex (MHC) fusion complexes
XX
SQ   Sequence 1508 BP; 337 A; 413 C; 441 G; 317 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              9.35e-101      Length:         1508
Score:                  1145.00        Matches:        227
Percent Similarity:     87.2%          Conservative:   4
Best Local Similarity:  85.7%          Mismatches:     24
Query Match:            72.8%          Indels:         10
DB:                     2              Gaps:           3

US-10-048-116B-6_COPY_1_300 (1-300) x AAT86988 (1-1508)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              |||||||||   |||         :::         :::         |||
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119
```

```
Qy          41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
               |||      :::|||         |||||||||||||||                 |||
Db         120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC--------------GGCGGA 164

Qy          61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
               ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy          81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy         101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy         121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy         141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy         161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy         181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy         201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy         221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy         241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
               ||||||||||||||||||||||||||||||         :::
Db         705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy         261 GlyGlyGlyGlySer 265
               |||||||||||||||
Db         756 GGCGGTGGTGGTTCC 770
```

RESULT 15
AAX89069
ID AAX89069 standard; DNA; 1508 BP.
XX
AC AAX89069;
XX
DT 14-SEP-1999 (first entry)
XX
DE Single chain IAd/OVA 323-229 MHC fusion protein encoding DNA.
XX
KW Major histocompatibility complex; MHC; single chain MHC; sc-MHC; Ig;
KW peptide binding groove; immunoglobulin; T cell receptor; immune response;
KW immune-related disorder; antigenic peptide; fusion protein; ss.
XX
OS Synthetic.
XX
PN WO9921572-A1.
XX
PD 06-MAY-1999.
XX
PF 13-OCT-1998; 98WO-US021520.
XX
PR 29-OCT-1997; 97US-00960190.
XX
PA (SUNO-) SUNOL MOLECULAR CORP.
XX
PI Rhode PR, Acevedo J, Burkhardt M, Jiao J, Wong HC;
XX
DR WPI; 1999-418411/35.
DR P-PSDB; AAY27111.
XX
PT Single chain major histocompatibility complex class I complexes.
XX
PS Example 1; Fig 1; 148pp; English.
XX
CC The invention relates to new single chain major histocompatibility
CC complex (sc-MHC) class II complexes that comprise a peptide binding
CC groove, and a modified class II beta 2 chain or covalently linked
CC immunoglobulin (Ig) light chain constant (C1) region. The MHC complexes
CC are useful for detection and analysis of peptide ligands, pathogenic T-
CC cells, for functional, cellular and molecular assays. They can be used to
CC identify and isolate T cell receptor and/or MHC agonists and antagonists.
CC They can be used in vivo to compete with pathogenic antigen presenting
CC cells involved in immune-related disorders. They can also be used to
CC raise antibodies and to screen immune cells. It is also use in a method
CC of suppressing an immune response in mammals. The sc-MHC complexes
CC comprising modified class II beta 2 chains and/or Ig-C1 regions are
CC soluble and provide enhanced yield. These MHC complexes also can contain
CC single antigenic peptides readily isolated from expressing cells in
CC significant quantities. The polyspecific MHC complexes also provide a
CC means to detect cells expressing multiple target structures with a single
CC complex. The present sequence represents a DNA encoding a single chain
CC IAd/OVA 323-229 MHC fusion protein
XX
SQ Sequence 1508 BP; 337 A; 413 C; 441 G; 317 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	9.35e-101	Length:	1508
Score:	1145.00	Matches:	227
Percent Similarity:	87.2%	Conservative:	4
Best Local Similarity:	85.7%	Mismatches:	24
Query Match:	72.8%	Indels:	10
DB:	2	Gaps:	3

US-10-048-116B-6_COPY_1_300 (1-300) x AAX89069 (1-1508)

```
Qy           1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy          21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
               |||||||||   |||        :::        :::        |||
Db          66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy          41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
               |||      :::|||         |||||||||||||||                 |||
Db         120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC--------------GGCGGA 164

Qy          61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
               ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy          81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy         101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy         121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy         141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464
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```
Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              ||||||||||||||||||||||||||||||         :::
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy        261 GlyGlyGlyGlySer 265
              |||||||||||||||
Db        756 GGCGGTGGTGGTTCC 770
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Search completed: June 30, 2006, 01:48:14
Job time : 528.277 secs

OM nucleic - nucleic search, using sw model

Run on: June 29, 2006, 23:14:09 ; Search time 5748 Seconds
(without alignments)
10212.897 Million cell updates/sec

Title: US-10-048-116B-7
Perfect score: 918
Sequence: 1 atggctctgcagatccccag.....agcatcatcatcatcatcat 918

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_env:*
2: gb_pat:*
3: gb_ph:*
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5: gb_pr:*
6: gb_ro:*
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8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	918	100.0	921	2	AX081281	AX081281 Sequence
2	696.2	75.8	893	2	AR047947	AR047947 Sequence
3	637.6	69.5	1013	2	AR047957	AR047957 Sequence
4	607.8	66.2	1382	2	AR033964	AR033964 Sequence
5	607.8	66.2	1382	2	AR175097	AR175097 Sequence
6	607.8	66.2	1382	2	CS079301	CS079301 Sequence
7	607.8	66.2	1382	2	AX032545	AX032545 Sequence
8	607.8	66.2	1385	2	AR033962	AR033962 Sequence
9	607.8	66.2	1385	2	AR175095	AR175095 Sequence
10	607.8	66.2	1385	2	CS079299	CS079299 Sequence
11	607.8	66.2	1385	2	AX032543	AX032543 Sequence
12	607.8	66.2	1508	2	AR033963	AR033963 Sequence
13	607.8	66.2	1508	2	AR152030	AR152030 Sequence
14	607.8	66.2	1508	2	AR175096	AR175096 Sequence
15	607.8	66.2	1508	2	CS079300	CS079300 Sequence
16	607.8	66.2	1508	2	AX032544	AX032544 Sequence
17	604.6	65.9	1508	2	BD138632	BD138632 Soluble M
18	598.6	65.2	4724	2	AR199666	AR199666 Sequence
19	592.2	64.5	1251	6	BC010322	BC010322 Mus muscu
20	569.8	62.1	798	6	MUSMHIABQ	M13537 Mouse MHC c
21	561.8	61.2	798	2	CQ777552	CQ777552 Sequence
22	556.4	60.6	1070	6	AF015280	AF015280 Mus muscu
23	542	59.0	702	2	AR106257	AR106257 Sequence
24	542	59.0	702	2	AR229609	AR229609 Sequence
25	542	59.0	702	2	AR363024	AR363024 Sequence
26	541.4	59.0	888	6	MUSMHABNO	M15848 Mouse MHC c
27	541.4	59.0	1204	6	BC008168	BC008168 Mus muscu
28	539.6	58.8	578	6	AY303784	AY303784 Mus muscu
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32	525.4	57.2	792	6	AF119252	AF119252 Mus muscu
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35	522.2	56.9	777	6	AF065913	AF065913 Mus muscu
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38	522.2	56.9	792	6	MUSMHIH2	M66213 Mouse MHC c
39	522.2	56.9	1162	6	BC057998	BC057998 Mus muscu
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ALIGNMENTS

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LOCUS AX081281 921 bp DNA linear PAT 27-FEB-2001
DEFINITION Sequence 2 from Patent WO0109194.
ACCESSION AX081281
VERSION AX081281.1 GI:13170131
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Glaichenhaus,N. and Malherbe,L.
TITLE Recombinant proteins and molecular complexes derived therefrom, analogous to molecules involved in immune responses
JOURNAL Patent: WO 0109194-A 2 08-FEB-2001;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
FEATURES Location/Qualifiers
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/note="Ligation de fragments d'ADNc"
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/db_xref="GI:13170132"
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SDVGEYRAVTELGRPDAEYWNSQPEILERTRAEVDTACRHNYEGPETSTSLRRLEQPN
VAISLSRTEALNHHNTLVCSVTDFYPAKIKVRWFRNGQEETVGVSSTQLIRNGDWTFQ
VLVMLEMTPHQGEVYTCHVEHPSLKSPITVEWRAQSESARSKGGGGSTTAPSAQLKKK
LQALKKKNAQLKWKLQALKKKLAQHHHHHH"
ORIGIN

Query Match 100.0%; Score 918; DB 2; Length 921;
Best Local Similarity 100.0%; Pred. No. 4.8e-256;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 60

```
Db          1 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 60

Qy         61 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120
Db         61 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120

Qy        121 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 180
Db        121 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 180

Qy        181 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 240
Db        181 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 240

Qy        241 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 300
Db        241 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 300

Qy        301 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 360
Db        301 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 360

Qy        361 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 420
Db        361 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 420

Qy        421 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 480
Db        421 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 480

Qy        481 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 540
Db        481 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 540

Qy        541 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 600
Db        541 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 600

Qy        601 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 660
Db        601 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 660

Qy        661 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 720
Db        661 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 720

Qy        721 AGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCCGAGTCTGCCCGGAGCAAG 780
Db        721 AGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCCGAGTCTGCCCGGAGCAAG 780

Qy        781 GGAGGTGGAGGATCCACTACAGCTCCATCAGCTCAGTTGAAAAAGAAATTGCAAGCACTG 840
Db        781 GGAGGTGGAGGATCCACTACAGCTCCATCAGCTCAGTTGAAAAAGAAATTGCAAGCACTG 840

Qy        841 AAGAAAAAGAACGCTCAGCTGAAGTGGAAACTTCAAGCCCTCAAGAAGAAACTCGCCCAG 900
Db        841 AAGAAAAAGAACGCTCAGCTGAAGTGGAAACTTCAAGCCCTCAAGAAGAAACTCGCCCAG 900

Qy        901 CATCATCATCATCATCAT 918
Db        901 CATCATCATCATCATCAT 918


RESULT 2
AR047947
LOCUS       AR047947                893 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 25 from patent US 5820866.
ACCESSION   AR047947
VERSION     AR047947.1  GI:5970290
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 893)
  AUTHORS   Kappler,J.W. and Marrack,P.
  TITLE     Product and process for T cell regulation
  JOURNAL   Patent: US 5820866-A 25 13-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .893
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match           75.8%;  Score 696.2;  DB 2;  Length 893;
  Best Local Similarity   94.6%;  Pred. No. 2.6e-191;
  Matches  748;  Conservative    0;  Mismatches   28;  Indels   15;  Gaps    2;

Qy          1 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 60
Db         61 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 120

Qy         61 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120
Db        121 AGCAGCCCCGGGACTGAGGGCGGAAACTCC-----GTACATGCTGCCCATGCTGAGATCA 175

Qy        121 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 180
Db        176 ATGAGGCTGGCAG----------AGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 225

Qy        181 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 240
Db        226 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 285

Qy        241 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 300
Db        286 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 345

Qy        301 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 360
Db        346 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 405

Qy        361 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 420
Db        406 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 465

Qy        421 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 480
Db        466 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 525

Qy        481 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 540
Db        526 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 585

Qy        541 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 600
Db        586 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 645

Qy        601 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 660
Db        646 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 705

Qy        661 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 720
Db        706 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 765

Qy        721 AGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCCGAGTCTGCCCGGAGCAAG 780
Db        766 AGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCCGAGTCTGCCCGGAGCAAG 825

Qy        781 GGAGGTGGAGG 791
Db        826 TAAGCATGCGG 836


RESULT 3
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AR047957
LOCUS       AR047957                1013 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 38 from patent US 5820866.
ACCESSION   AR047957
VERSION     AR047957.1  GI:5970300
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1013)
  AUTHORS   Kappler,J.W. and Marrack,P.
  TITLE     Product and process for T cell regulation
  JOURNAL   Patent: US 5820866-A 38 13-OCT-1998;
FEATURES             Location/Qualifiers
     source          1..1013
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             69.5%;  Score 637.6;  DB 2;  Length 1013;
  Best Local Similarity   89.5%;  Pred. No. 3.3e-174;
  Matches  698;  Conservative    0;  Mismatches   79;  Indels    3;  Gaps    1;

Qy          1 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 60
Db         63 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCGGCTGCTGTGGTGGTGCTGATGGTGCTG 122

Qy         61 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120
Db        123 AGCAGCCCAGGGACTGAGGGCGGAGACTCCGAAGCTAGCTTTGAGGCTCAGGGTGCACTG 182

Qy        121 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGCTCACTAGTGCCCCGAGGCTCTGGA 180
Db        183 GCCAACATTGCTGTCGACAAGGCTGGAGGTGGTGGATC---CGGTGGAGGGGGAAGTGGA 239

Qy        181 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 240
Db        240 GGTGGAGGGTCTGAAAGGCATTTCGTGTACCAGTTCATGGGCGAGTGCTACTTCACCAAC 299

Qy        241 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 300
Db        300 GGGACGCAGCGCATACGATATGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 359

Qy        301 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 360
Db        360 TACGACAGCGACGTGGGCGAGCACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 419

Qy        361 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 420
Db        420 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGTGTGC 479

Qy        421 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 480
Db        480 AGACACAACTACGAGGGGCCGGAGACCCACACCTCCCTGCGGCGGCTTGAACAGCCCAAT 539

Qy        481 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 540
Db        540 GTCGTCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGCTCA 599

Qy        541 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 600
Db        600 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCCGGAATGGCCAGGAGGAG 659

Qy        601 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 660
Db        660 ACGGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 719

Qy        661 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 720
Db        720 GTCATGCTGGAGATGACCCCTCGGCGGGGAGAGGTCTACACCTGTCACGTGGAGCATCCC 779

Qy        721 AGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCCGAGTCTGCCCGGAGCAAG 780
Db        780 AGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCTGAGTCTGCCTGGAGCAAG 839

RESULT 4
AR033964
LOCUS       AR033964                1382 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 123 from patent US 5869270.
ACCESSION   AR033964
VERSION     AR033964.1  GI:5949569
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1382)
  AUTHORS   Rhode,P.R., Jiao,J.-A., Burkhardt,M. and Wong,H.C.
  TITLE     Single chain MHC complexes and uses thereof
  JOURNAL   Patent: US 5869270-A 123 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1..1382
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             66.2%;  Score 607.8;  DB 2;  Length 1382;
  Best Local Similarity   89.6%;  Pred. No. 1.7e-165;
  Matches  673;  Conservative    0;  Mismatches   57;  Indels   21;  Gaps    1;

Qy          1 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 60
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         61 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120
Db         66 AGCAGCCCAAGGAC--------------------CTTAAGTATCTCTCAGGCTGTTCAC 104

Qy        121 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGCTCACTAGTGCCCCGAGGCTCTGGA 180
Db        105 GCTGCTCACGCTGAAATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGCGGCGGA 164

Qy        181 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 240
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy        241 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 300
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        301 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 360
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        361 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 420
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        421 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 480
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        481 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 540
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        541 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 600
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        601 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 660
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        661 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 720
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Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        721 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 751
              |||||||||||||||||||||||||||||||
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 735


RESULT 5
AR175097
LOCUS       AR175097               1382 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 123 from patent US 6309645.
ACCESSION   AR175097
VERSION     AR175097.1  GI:17916396
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1382)
  AUTHORS   Rhode,P.R., Jiao,J.-A., Burkhardt,M. and Wong,H.C.
  TITLE     MHC molecules and uses thereof
  JOURNAL   Patent: US 6309645-A 123 30-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .1382
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match           66.2%;  Score 607.8;  DB 2;  Length 1382;
  Best Local Similarity   89.6%;  Pred. No. 1.7e-165;
  Matches  673;  Conservative    0;  Mismatches   57;  Indels   21;  Gaps    1;

Qy          1 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         61 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120
              ||||||||  ||||                     |||       || | ||     |
Db         66 AGCAGCCCAAGGAC--------------------CTTAAGTATCTCTCAGGCTGTTCAC 104

Qy        121 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 180
                  |     | | | |   || |  ||| | |        || |  | || ||   |||
Db        105 GCTGCTCACGCTGAAATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGCGGCGGA 164

Qy        181 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 240
              || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy        241 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        301 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        361 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        421 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        481 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        541 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 600
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        601 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        661 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 720
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        721 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 751
              |||||||||||||||||||||||||||||||
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 735


RESULT 6
CS079301
LOCUS       CS079301               1382 bp    DNA     linear   PAT 06-MAY-2005
DEFINITION  Sequence 123 from Patent EP1526141.
ACCESSION   CS079301
VERSION     CS079301.1  GI:63093743
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1
  AUTHORS   Rhode,P.R., Jiao,J.A., Burkhardt,M. and Wong,H.C.
  TITLE     MHC complexes and uses thereof
  JOURNAL   Patent: EP 1526141-A 123 27-APR-2005;
            Altor BioScience Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .1382
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match           66.2%;  Score 607.8;  DB 2;  Length 1382;
  Best Local Similarity   89.6%;  Pred. No. 1.7e-165;
  Matches  673;  Conservative    0;  Mismatches   57;  Indels   21;  Gaps    1;

Qy          1 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         61 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120
              ||||||||  ||||                     |||       || | ||     |
Db         66 AGCAGCCCAAGGAC--------------------CTTAAGTATCTCTCAGGCTGTTCAC 104

Qy        121 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 180
                  |     | | | |   || |  ||| | |        || |  | || ||   |||
Db        105 GCTGCTCACGCTGAAATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGCGGCGGA 164

Qy        181 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 240
              || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy        241 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        301 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        361 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        421 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        481 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524
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Qy        541 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        601 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        661 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        721 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 751
              |||||||||||||||||||||||||||||||
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 735
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RESULT 7
AX032545
LOCUS AX032545 1382 bp DNA linear PAT 20-SEP-2000
DEFINITION Sequence 123 from Patent EP0997477.
ACCESSION AX032545
VERSION AX032545.1 GI:10279486
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
unclassified sequences.
REFERENCE 1
AUTHORS Chavaillaz,P.A., Edwards,A.C., Grammer,S., Jiao,J.A., Rhode,P.R., Weidanz,J.A. and Wong,H.C.
TITLE Mhc complexes and uses thereof
JOURNAL Patent: EP 0997477-A 123 03-MAY-2000; SUNOL MOLECULAR CORP (US)
FEATURES Location/Qualifiers
source 1. .1382
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
ORIGIN

Query Match 66.2%; Score 607.8; DB 2; Length 1382;
Best Local Similarity 89.6%; Pred. No. 1.7e-165;
Matches 673; Conservative 0; Mismatches 57; Indels 21; Gaps 1;

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Qy          1 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         61 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120
              |||||||  ||||          |||      || | ||     |
Db         66 AGCAGCCCAAGGAC--------------------CTTAAGTATCTCTCAGGCTGTTCAC 104

Qy        121 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 180
              |    | |  | |   || |  ||| | |       || |  | || ||   |||
Db        105 GCTGCTCACGCTGAAATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGCGGCGGA 164

Qy        181 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 240
              || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy        241 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 300
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Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        301 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        361 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        421 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 480
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Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        481 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        541 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        601 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        661 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        721 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 751
              |||||||||||||||||||||||||||||||
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 735
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RESULT 8
AR033962
LOCUS AR033962 1385 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 121 from patent US 5869270.
ACCESSION AR033962
VERSION AR033962.1 GI:5949567
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1385)
AUTHORS Rhode,P.R., Jiao,J.-A., Burkhardt,M. and Wong,H.C.
TITLE Single chain MHC complexes and uses thereof
JOURNAL Patent: US 5869270-A 121 09-FEB-1999;
FEATURES Location/Qualifiers
source 1. .1385
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Query Match 66.2%; Score 607.8; DB 2; Length 1385;
Best Local Similarity 89.6%; Pred. No. 1.7e-165;
Matches 673; Conservative 0; Mismatches 57; Indels 21; Gaps 1;

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Qy          1 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         61 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120
              ||||||||  ||||                          |||        || | ||     |
Db         66 AGCAGCCCAAGGAC--------------------CTTAAGTATCTCTCAGGCTGTTCAC 104

Qy        121 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 180
              |    | |  | |   || |  ||| | |       || |  | || ||   |||
Db        105 GCTGCTCACGCTGAAATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGCGGCGGA 164

Qy        181 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 240
              || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy        241 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        301 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        361 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 420
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Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        421 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 480

Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        481 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 540

Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        541 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 600

Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        601 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 660

Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        661 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 720

Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        721 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 751

Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 735


RESULT 9
AR175095
LOCUS       AR175095               1385 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 121 from patent US 6309645.
ACCESSION   AR175095
VERSION     AR175095.1  GI:17916394
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1385)
  AUTHORS   Rhode,P.R., Jiao,J.-A., Burkhardt,M. and Wong,H.C.
  TITLE     MHC molecules and uses thereof
  JOURNAL   Patent: US 6309645-A 121 30-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .1385
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match           66.2%;  Score 607.8;  DB 2;  Length 1385;
  Best Local Similarity   89.6%;  Pred. No. 1.7e-165;
  Matches  673;  Conservative    0;  Mismatches   57;  Indels   21;  Gaps    1;

Qy          1 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 60

Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         61 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120

Db         66 AGCAGCCCAAGGAC--------------------CTTAAGTATCTCTCAGGCTGTTCAC 104

Qy        121 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 180

Db        105 GCTGCTCACGCTGAAATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGCGGCGGA 164

Qy        181 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 240

Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy        241 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 300

Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        301 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 360

Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        361 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 420

Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        421 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 480

Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        481 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 540

Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        541 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 600

Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        601 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 660

Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        661 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 720

Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        721 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 751

Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 735


RESULT 10
CS079299
LOCUS       CS079299               1385 bp    DNA     linear   PAT 06-MAY-2005
DEFINITION  Sequence 121 from Patent EP1526141.
ACCESSION   CS079299
VERSION     CS079299.1  GI:63093741
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1
  AUTHORS   Rhode,P.R., Jiao,J.A., Burkhardt,M. and Wong,H.C.
  TITLE     MHC complexes and uses thereof
  JOURNAL   Patent: EP 1526141-A 121 27-APR-2005;
            Altor BioScience Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .1385
                     /organism="unidentified"
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                     /db_xref="taxon:32644"
ORIGIN

  Query Match           66.2%;  Score 607.8;  DB 2;  Length 1385;
  Best Local Similarity   89.6%;  Pred. No. 1.7e-165;
  Matches  673;  Conservative    0;  Mismatches   57;  Indels   21;  Gaps    1;

Qy          1 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 60

Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         61 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120

Db         66 AGCAGCCCAAGGAC--------------------CTTAAGTATCTCTCAGGCTGTTCAC 104

Qy        121 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 180

Db        105 GCTGCTCACGCTGAAATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGCGGCGGA 164

Qy        181 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 240

Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224
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Qy        241 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        301 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        361 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        421 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        481 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        541 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        601 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        661 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        721 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 751
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Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 735
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RESULT 11
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LOCUS       AX032543               1385 bp    DNA     linear   PAT 20-SEP-2000
DEFINITION  Sequence 121 from Patent EP0997477.
ACCESSION   AX032543
VERSION     AX032543.1  GI:10279484
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1
  AUTHORS   Chavaillaz,P.A., Edwards,A.C., Grammer,S., Jiao,J.A., Rhode,P.R.,
            Weidanz,J.A. and Wong,H.C.
  TITLE     Mhc complexes and uses thereof
  JOURNAL   Patent: EP 0997477-A 121 03-MAY-2000;
            SUNOL MOLECULAR CORP (US)
FEATURES             Location/Qualifiers
     source          1. .1385
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             66.2%;  Score 607.8;  DB 2;  Length 1385;
  Best Local Similarity   89.6%;  Pred. No. 1.7e-165;
  Matches  673;  Conservative    0;  Mismatches   57;  Indels   21;  Gaps    1;

Qy          1 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         61 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120
              ||||||||  ||||                  |||       || | ||      |
Db         66 AGCAGCCCAAGGAC--------------------CTTAAGTATCTCTCAGGCTGTTCAC 104
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Qy        121 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 180
              |      | | | |   || |  ||| | |        || |  | || ||   |||
Db        105 GCTGCTCACGCTGAAATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGCGGCGGA 164

Qy        181 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 240
              ||  |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy        241 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        301 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        361 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        421 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        481 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 540
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Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        541 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        601 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        661 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        721 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 751
              ||||||||||||||||||||||||||||||
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 735
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RESULT 12
AR033963
LOCUS       AR033963               1508 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 122 from patent US 5869270.
ACCESSION   AR033963
VERSION     AR033963.1  GI:5949568
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1508)
  AUTHORS   Rhode,P.R., Jiao,J.-A., Burkhardt,M. and Wong,H.C.
  TITLE     Single chain MHC complexes and uses thereof
  JOURNAL   Patent: US 5869270-A 122 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .1508
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             66.2%;  Score 607.8;  DB 2;  Length 1508;
  Best Local Similarity   89.6%;  Pred. No. 1.8e-165;
  Matches  673;  Conservative    0;  Mismatches   57;  Indels   21;  Gaps    1;

Qy          1 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65
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Qy         61 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120
              ||||||||  ||||                 |||        || | ||      |
Db         66 AGCAGCCCAAGGAC--------------------CTTAAGTATCTCTCAGGCTGTTCAC 104

Qy        121 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 180
                  |     | |  | |   || |  ||| | |       || |  | || ||   |||
Db        105 GCTGCTCACGCTGAAATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGCGGCGGA 164

Qy        181 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 240
              || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy        241 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        301 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        361 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        421 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        481 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        541 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        601 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        661 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 720
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Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        721 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 751
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Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 735
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RESULT 13
AR152030
LOCUS       AR152030               1508 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 24 from patent US 6232445.
ACCESSION   AR152030
VERSION     AR152030.1  GI:15118080
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1508)
  AUTHORS   Rhode,P.R., Acevedo,J., Burkhardt,M., Jiao,J.-a. and Wong,H.C.
  TITLE     Soluble MHC complexes and methods of use thereof
  JOURNAL   Patent: US 6232445-A 24 15-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .1508
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            66.2%;  Score 607.8;  DB 2;  Length 1508;
  Best Local Similarity  89.6%;  Pred. No. 1.8e-165;
  Matches  673;  Conservative    0;  Mismatches   57;  Indels   21;  Gaps    1;
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```
Qy          1 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         61 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120
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Qy        121 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 180
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Db        105 GCTGCTCACGCTGAAATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGCGGCGGA 164

Qy        181 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 240
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Qy        241 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 300
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Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        301 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 360
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Qy        361 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 420
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Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        421 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 480
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Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        481 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 540
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Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        541 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 600
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Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        601 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 660
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RESULT 14
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LOCUS       AR175096               1508 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 122 from patent US 6309645.
ACCESSION   AR175096
VERSION     AR175096.1  GI:17916395
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1508)
  AUTHORS   Rhode,P.R., Jiao,J.-A., Burkhardt,M. and Wong,H.C.
  TITLE     MHC molecules and uses thereof
  JOURNAL   Patent: US 6309645-A 122 30-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .1508
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                     /mol_type="unassigned DNA"
ORIGIN
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  Query Match           66.2%;  Score 607.8;  DB 2;  Length 1508;
  Best Local Similarity  89.6%;  Pred. No. 1.8e-165;
  Matches  673;  Conservative    0;  Mismatches   57;  Indels   21;  Gaps    1;

Qy          1 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 60
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Qy        121 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 180
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Db        105 GCTGCTCACGCTGAAATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGCGGCGGA 164

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Qy        241 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 300
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Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        301 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 360
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Qy        421 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 480
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Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        481 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 540
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Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        541 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 600
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Qy        721 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 751
              ||||||||||||||||||||||||||||||
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 735


RESULT 15
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LOCUS       CS079300               1508 bp    DNA     linear   PAT 06-MAY-2005
DEFINITION  Sequence 122 from Patent EP1526141.
ACCESSION   CS079300
VERSION     CS079300.1  GI:63093742
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1
  AUTHORS   Rhode,P.R., Jiao,J.A., Burkhardt,M. and Wong,H.C.
  TITLE     MHC complexes and uses thereof
  JOURNAL   Patent: EP 1526141-A 122 27-APR-2005;
            Altor BioScience Corporation (US)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match           66.2%;  Score 607.8;  DB 2;  Length 1508;
  Best Local Similarity  89.6%;  Pred. No. 1.8e-165;
  Matches  673;  Conservative    0;  Mismatches   57;  Indels   21;  Gaps    1;

Qy          1 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 60
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Qy         61 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120
              ||||||||  ||||                  |||       || | ||     |
Db         66 AGCAGCCCAAGGAC--------------------CTTAAGTATCTCTCAGGCTGTTCAC 104

Qy        121 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 180
                 |     | |  | |   || |  ||| | |       || |  | || ||   |||
Db        105 GCTGCTCACGCTGAAATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGCGGCGGA 164

Qy        181 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 240
              || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy        241 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 300
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Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        301 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 360
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Qy        361 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 420
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Qy        421 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        481 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 540
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Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        541 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 600
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Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        601 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 660
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Qy        661 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 720
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Qy        721 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 751
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Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 735


Search completed: June 30, 2006, 00:52:42
Job time : 5753 secs
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GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: June 29, 2006, 23:09:40 ; Search time 625 Seconds
(without alignments)
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Perfect score: 918
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: geneseqn1980s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	918	100.0	921	5	AAF55099	Aaf55099 DNA encod
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3	665.2	72.5	945	12	ADQ31225	Adq31225 I-Ab(beta
4	634	69.1	1013	2	AAT04269	Aat04269 Hybrid IA
5	628.6	68.5	915	12	ADQ31228	Adq31228 I-Ab(beta
6	607.8	66.2	1382	2	AAT86989	Aat86989 SCE1 sing
7	607.8	66.2	1382	8	ACA60744	Aca60744 Mouse MHC
8	607.8	66.2	1385	2	AAT86987	Aat86987 SSC1 sing
9	607.8	66.2	1385	8	ACA60742	Aca60742 Mouse MHC
10	607.8	66.2	1508	2	AAT86988	Aat86988 SCT1 sing
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14	606.2	66.0	1385	2	AAT17586	Aat17586 Vector SS
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20	542	59.0	702	2	AAQ03170	Aaq03170 Sequence
21	542	59.0	702	2	AAT06286	Aat06286 I-Ab-beta
22	542	59.0	702	2	AAQ56920	Aaq56920 Mouse I-A
23	535.6	58.3	702	2	AAQ35055	Aaq35055 IAB beta
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27	497.2	54.2	1686	4	ABI99031	Abi99031 MBP 1-14
28	497.2	54.2	1701	4	ABI99028	Abi99028 IAS MBP 1
29	497.2	54.2	2059	4	ABI99032	Abi99032 MBP 1-14
30	497.2	54.2	2346	4	ABI99027	Abi99027 IAS MBP 1
31	496	54.0	1680	4	ABI99021	Abi99021 I-As MBP.
32	496	54.0	1707	4	ABI99030	Abi99030 IAS MBP 9
33	496	54.0	2053	4	ABI99029	Abi99029 IAS MBP 9
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ALIGNMENTS

RESULT 1
AAF55099
ID AAF55099 standard; DNA; 921 BP.
XX
AC AAF55099;
XX
DT 15-MAY-2001 (first entry)
XX
DE DNA encoding a fusion protein comprising a beta chain of MHC.
XX
KW Recombinant protein; alpha chain; beta chain; MHC; immunoglobulin;
KW major histocompatibility complex; Fc region; antigen; T lymphocyte;
KW immunostimulant; vaccine; infection; tumour; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1. .921
FT /*tag= a
XX
PN WO200109194-A1.
XX
PD 08-FEB-2001.
XX
PF 28-JUL-2000; 2000WO-FR002193.
XX
PR 29-JUL-1999; 99FR-00009862.
XX
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
PI Glaichenhaus N, Malherbe L;
XX
DR WPI; 2001-182944/18.
DR P-PSDB; AAB67481.
XX
PT New soluble recombinant protein, useful e.g. as immunostimulant,
PT comprises dimeric major histocompatibility complex molecule fused to
PT immunoglobulin Fc region.
XX
PS Example 1; Page 34-35; 43pp; French.
XX

```
CC   The specification describes soluble recombinant proteins that comprise at
CC   least a dimer formed from the alpha and beta-chains of MHC (major
CC   histocompatibility complex) Class I and II molecules in which at least
CC   one chain has, attached to its C-terminus, at least part of the Fc region
CC   of an immunoglobulin. The recombinant proteins, when linked to an
CC   antigenic peptide, are used to count and/or purify antigen-reactive T
CC   lymphocytes and to characterize their phenotype, e.g. in preclinical
CC   evaluation of vaccines. They are also used as immunostimulants,
CC   particularly for vaccine development (against infections and tumours), to
CC   count and determine phenotype of autoreactive T cells in subjects with,
CC   or at risk of developing, autoimmune diseases, e.g. for staging or
CC   evaluating treatments, and (to purify and/or enrich Ag-reactive T cells
CC   from cell cultures or patient samples, for use in subsequent curative or
CC   preventative cellular therapy. The present sequence encodes a recombinant
CC   protein of the invention, comprising a beta chain of MHC molecules
XX
SQ   Sequence 921 BP; 214 A; 265 C; 286 G; 156 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 918;  DB 5;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-203;
  Matches  918;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 60

Qy         61 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120
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Db         61 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120

Qy        121 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 180
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Qy        181 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 240
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Qy        241 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 300
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Db        361 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 420

Qy        421 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 480

Qy        481 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 540

Qy        541 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 600

Qy        601 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 660

Qy        661 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 720

Qy        721 AGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCCGAGTCTGCCCGGAGCAAG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCCGAGTCTGCCCGGAGCAAG 780

Qy        781 GGAGGTGGAGGATCCACTACAGCTCCATCAGCTCAGTTGAAAAAGAAATTGCAAGCACTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGAGGTGGAGGATCCACTACAGCTCCATCAGCTCAGTTGAAAAAGAAATTGCAAGCACTG 840

Qy        841 AAGAAAAAGAACGCTCAGCTGAAGTGGAAACTTCAAGCCCTCAAGAAGAAACTCGCCCAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAAAAAGAACGCTCAGCTGAAGTGGAAACTTCAAGCCCTCAAGAAGAAACTCGCCCAG 900

Qy        901 CATCATCATCATCATCAT 918
              ||||||||||||||||||
Db        901 CATCATCATCATCATCAT 918


RESULT 2
AAT04262
ID   AAT04262 standard; DNA; 893 BP.
XX
AC   AAT04262;
XX
DT   16-APR-1996  (first entry)
XX
DE   Hybrid IA beta chain gene.
XX
KW   Polymerase chain reaction; PCR; primer; amplify;
KW   major histocompatability complex; MHC; T-cell receptor; TCR;
KW   autoimmune disease; immunodeficiency disease; immune response;
KW   immunoproliferation disease; graft-host rejection; therapy; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   primer_bind     1. .16
FT                   /*tag= a
FT                   /note= "probable primer binding site (primer #233)"
FT   primer_bind     complement(45. .74)
FT                   /*tag= b
FT                   /note= "binding site for primer #261 (see AAT04260)"
FT   CDS             61. .828
FT                   /*tag= c
FT                   /product= "hybrid IA beta chain"
FT   sig_peptide     61. .141
FT                   /*tag= d
FT                   /note= "leader region"
FT   primer_bind     complement(119. .172)
FT                   /*tag= e
FT                   /note= "binding site for primer #331 (see AAT04261)"
FT   primer_bind     complement(158. .212)
FT                   /*tag= f
FT                   /note= "primer #332 binding site"
FT   primer_bind     complement(199. .250)
FT                   /*tag= g
FT                   /note= "primer #333 (see AAT04263) binding site"
FT   misc_feature    371. .389
FT                   /*tag= h
FT                   /note= "probable primer binding site (primer #270)"
FT   mat_peptide     511. .825
FT                   /*tag= i
FT                   /product= "IA beta chain beta 2 region"
FT   primer_bind     521. .550
FT                   /*tag= j
FT                   /note= "probable primer binding site (primer #271)"
FT   primer_bind     532. .554
FT                   /*tag= k
FT                   /note= "probable primer binding site (primer #272)"
FT   primer_bind     808. .836
FT                   /*tag= l
FT                   /note= "probable primer binding site (primer #259)"
FT   primer_bind     877. .893
FT                   /*tag= m
FT                   /note= "probable primer binding site (primer #232)"
XX
PN   WO9523814-A1.
```

XX
PD 08-SEP-1995.
XX
PF 03-MAR-1995; 95WO-US002689.
XX
PR 04-MAR-1994; 94US-00207481.
XX
PA (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
XX
PI Kappler JW, Marrack P;
XX
DR WPI; 1995-320543/41.
DR P-PSDB; AAR82533.
XX
PT Peptide-MHC complex comprising antigenic peptide, linker and MHC segment
PT - useful as reagents for the treatment of diseases including auto-immune
PT diseases, immuno-stimulatory diseases or graft-host rejection.
XX
PS Example 1; Page 53; 94pp; English.
XX
CC This sequence represents a hybrid IA beta chain gene, containing the
CC chicken ovalbumin peptide (cOVA). This sequence was used in the
CC construction of a hybrid IA alpha beta dimer. The encoded protein (pIAd-
CC OVA) was found to be more stable than the IA alpha beta dimer. The
CC stability was decreased by the addition of a MHC groove specific binding
CC peptide (e.g. see AAR82527, AAR82528 and AAR82531), compared to an
CC increase seen on the addition of a MHC binding peptide to IE k/d-MCC.
CC These complexes may be used to regulate an immune response. The complexes
CC are capable of being recognised by a TCR alone or in combination with
CC additional MHC proteins. These complexes are useful for therapeutic
CC purposes and experimental purposes. They can also be used as reagents for
CC the treatment of diseases including autoimmune diseases, immunodeficiency
CC diseases, immunoproliferation diseases, and graft-host rejection
XX
SQ Sequence 893 BP; 204 A; 239 C; 275 G; 175 T; 0 U; 0 Other;

Query Match 75.8%; Score 696.2; DB 2; Length 893;
Best Local Similarity 94.6%; Pred. No. 1.9e-151;
Matches 748; Conservative 0; Mismatches 28; Indels 15; Gaps 2;

```
Qy          1 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 120

Qy         61 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120
              |||||||||||||||||||||||||||||||      | |  || | |  ||  |    |
Db        121 AGCAGCCCCGGGACTGAGGGCGGAAACTCC-----GTACATGCTGCCCATGCTGAGATCA 175

Qy        121 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 180
              ||   | || | |           ||||||||||||||||||||||||||||||||||
Db        176 ATGAGGCTGGCAG----------AGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 225

Qy        181 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 285

Qy        241 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 345

Qy        301 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 405

Qy        361 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 465

Qy        421 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 525

Qy        481 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        526 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 585

Qy        541 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 645

Qy        601 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 705

Qy        661 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        706 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 765

Qy        721 AGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCCGAGTCTGCCCGGAGCAAG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        766 AGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCCGAGTCTGCCCGGAGCAAG 825

Qy        781 GGAGGTGGAGG 791
                ||   | ||
Db        826 TAAGCATGCGG 836
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RESULT 3
ADQ31225
ID ADQ31225 standard; cDNA; 945 BP.
XX
AC ADQ31225;
XX
DT 07-OCT-2004 (first entry)
XX
DE I-Ab(beta)-Cholera toxin B subunit-leucine zipper (LZ)-BirA fusion cDNA.
XX
KW class II major histocompatibility complex; MHC; CD4+ T-cell detection;
KW flow cytometry; mucous membrane invasive antigen;
KW I-Ab(beta)-cholera toxin B subunit-leucine zipper-BirA fusion; CTB; ss;
KW gene.
XX
OS Vibrio cholerae.
OS Unidentified.
XX
FH Key Location/Qualifiers
FT CDS 1. .945
FT /*tag= a
FT /product= "I-Ab(beta)-Cholera toxin B subunit (CTB)-
FT leucine zipper (LZ)-BirA fusion cDNA"
XX
PN JP2004196789-A.
XX
PD 15-JUL-2004.
XX
PF 03-DEC-2003; 2003JP-00404367.
XX
PR 03-DEC-2002; 2002JP-00351818.
XX
PA (SENT-) SENTAN KAGAKU GIJUTSU INCUBATION CENT KK.
XX
DR WPI; 2004-546819/53.
DR P-PSDB; ADQ31224.
XX
PT Peptide-Class II major histocompatibility complex (MHC) composite, useful
PT for detecting antigen specific CD4+ T-cell, comprises antigen peptide
PT containing epitope of mucous membrane invasive protein, and extracellular
PT region of MHC.
XX
PS Example 1; SEQ ID NO 10; 30pp; Japanese.
XX
CC The invention relates to a novel class II major histocompatibility
CC complex (MHC) antigenic peptide composite comprising a peptide containing
CC the T-cell antigenic determinant of a mucous membrane invasive protein
CC and the extracellular region of a class II MHC molecule or at least part
CC of the extracellular region of the class II MHC molecule having an amino

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CC   acid sequence comprising one or more deletions, substitutions or
CC   additions. The molecule of the invention may be useful for detecting an
CC   antigen-specific CD4+ T-cell by flow cytometry and for presenting a
CC   microorganism-derived mucous membrane invasive protein as an antigen. The
CC   method of the invention enables efficient detection of antigen-specific
CC   activation of CD4+ T-cells in the mucous membrane. The current sequence
CC   is that of the class II major histocompatibility complex-related I-
CC   Ab(alpha)-Cholera toxin B subunit (CTB)-leucine zipper (LZ)-BirA fusion
CC   cDNA of the invention.
XX
SQ   Sequence 945 BP; 230 A; 256 C; 294 G; 165 T; 0 U; 0 Other;

  Query Match             72.5%;  Score 665.2;  DB 12;  Length 945;
  Best Local Similarity   86.6%;  Pred. No. 3e-144;
  Matches  759;  Conservative    0;  Mismatches  108;  Indels    9;  Gaps    2;

Qy         43 GTGGTGCTGATGGTGCTGAGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCG 102
              |||   |||||||||||||||  |||   | ||  ||  ||| |||||  |   |
Db         49 GTGACACTGATGGTGCTGAGCTCCCCACTGGCTTTGGCTGGAGACTCCTGCGTGTGGAAC 108

Qy        103 CCGTCGCTGGAGCACCCGATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTA 162
                |  | |||| |||||| ||     | |||     | |||||||||| || ||
Db        109 AATAAGACGCCGCACGCGATCGCGGCCATCAGCATGGCGAACGGAGGTGGTGGGTCCGGT 168

Qy        163 GTGCCCCGAGGCTCTGGAGGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGC 222
              |      || |  |||||||||||| || ||||||||||||||  |||||||| ||||
Db        169 GGAGGGGGAAG---TGGAGGTGGAGGGTCTGAAAGGCATTTCGTGTACCAGTTCATGGGC 225

Qy        223 GAGTGCTACTACACCAACGGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAAC 282
              ||||||||||| ||||||||||||||||||||||||    ||||||||||||||||||||
Db        226 GAGTGCTACTTCACCAACGGGACGCAGCGCATACGATATGTGACCAGATACATCTACAAC 285

Qy        283 CGGGAGGAGTACGTGCGCTACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTG 342
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        286 CGGGAGGAGTACGTGCGCTACGACAGCGACGTGGGCGAGCACCGCGCGGTGACCGAGCTG 345

Qy        343 GGGCGGCCAGACGCCGAGTACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCC 402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 GGGCGGCCAGACGCCGAGTACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCC 405

Qy        403 GAGGTGGACACGGCGTGCAGACACAACTACGAGGGGCCGGAGACCGAGCACCTCCCTGCGG 462
              ||| |||||||| ||||||||||||||||||||||||||||  ||||||||||||||||||
Db        406 GAGCTGGACACGGTGTGCAGACACAACTACGAGGGGCCGGAGACCCACACCTCCCTGCGG 465

Qy        463 CGGCTTGAACAGCCCAATGTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCAC 522
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        466 CGGCTTGAACAGCCCAATGTCGTCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCAC 525

Qy        523 AACACTCTGGTCTGTTCGGTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTC 582
              |||||||||||||| || ||||||||||||||||||||||||||||||||||||||||||
Db        526 AACACTCTGGTCTGCTCAGTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTC 585

Qy        583 AGGAATGGCCAGGAGGAGACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGAC 642
               |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        586 CGGAATGGCCAGGAGGAGACGGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGAC 645

Qy        643 TGGACCTTCCAGGTCCTGGTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACC 702
              |||||||||||||||||||||||||||||||||||  | ||||||||||||||||||
Db        646 TGGACCTTCCAGGTCCTGGTCATGCTGGAGATGACCCCTCGGCGGGGAGAGGTCTACACC 705

Qy        703 TGCCATGTGGAGCATCCCAGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCC 762
              || || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        706 TGTCACGTGGAGCATCCCAGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCG 765

Qy        763 GAGTCTGCCCGGAGCAAGGGAGGTGGAGGATCCACTACAGCTCCATCAGCTCAGTTGAAA 822
              | | ||      ||      | ||||||||||||||||||||||||||||||||||||||
Db        766 TCAGCAGACC------TGGTTCCGCGCGGATCCACTACAGCTCCATCAGCTCAGTTGAAA 819

Qy        823 AAGAAATTGCAAGCACTGAAGAAAAAGAACGCTCAGCTGAAGTGGAAACTTCAAGCCCTC 882
              |||||| |||| ||||| ||||||||||||||||||||||||||||||||||||||||||
Db        820 AAGAAACTGCAGGCACTTAAGAAAAAGAACGCTCAGCTGAAGTGGAAACTTCAAGCCCTC 879

Qy        883 AAGAAGAAACTCGCCCAGCATCATCATCATCATCAT 918
                  ||||||||||||||||||  ||||||  ||    ||
Db        880 AAGAAGAAACTCGCCCAGCTGCATCATATTCTGGAT 915


RESULT 4
AAT04269
ID   AAT04269 standard; DNA; 1013 BP.
XX
AC   AAT04269;
XX
DT   16-APR-1996  (first entry)
XX
DE   Hybrid IA beta chain gene.
XX
KW   Major histocompatability complex; MHC; T-cell receptor; TCR;
KW   autoimmune disease; immunodeficiency disease; immune response;
KW   immunoproliferation disease; graft-host rejection; therapy; B cell;
KW   M12.C3; pM12-IAb-Ea; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   primer_bind     1. .18
FT                   /*tag= a
FT                   /note= "probable primer binding site (primer #76)"
FT   primer_bind     complement(40. .74)
FT                   /*tag= b
FT                   /note= "binding site for primer #362 (see AAT04270)"
FT   CDS             63. .959
FT                   /*tag= c
FT                   /product= "hybrid IA beta chain"
FT   sig_peptide     63. .143
FT                   /*tag= d
FT                   /note= "leader region"
FT   primer_bind     complement(140. .191)
FT                   /*tag= e
FT                   /note= "binding site for primer #363 (see AAT04271)"
FT   primer_bind     complement(177. .226)
FT                   /*tag= f
FT                   /note= "primer #364 binding site"
FT   primer_bind     complement(212. .266)
FT                   /*tag= g
FT                   /note= "primer #365 (see AAT04272) binding site"
FT   primer_bind     385. .403
FT                   /*tag= h
FT                   /note= "probable primer binding site (primer #270)"
FT   mat_peptide     531. .959
FT                   /*tag= i
FT                   /product= "IA beta chain beta 2 region"
FT   primer_bind     535. .564
FT                   /*tag= j
FT                   /note= "probable primer binding site (primer #271)"
FT   primer_bind     544. .568
FT                   /*tag= k
FT                   /note= "probable primer binding site (primer #272)"
FT   primer_bind     823. .850
FT                   /*tag= l
FT                   /note= "probable primer binding site (primer #259)"
FT   primer_bind     942. .976
FT                   /*tag= m
FT                   /note= "probable primer binding site (primer #366)"
FT   primer_bind     1000. .1013
FT                   /*tag= n
FT                   /note= "probable primer binding site (primer #59)"
XX
PN   WO9523814-A1.
XX
PD   08-SEP-1995.
XX
PF   03-MAR-1995;   95WO-US002689.
XX
PR   04-MAR-1994;   94US-00207481.
XX
```

PA (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
XX
PI Kappler JW, Marrack P;
XX
DR WPI; 1995-320543/41.
DR P-PSDB; AAR82538.
XX
PT Peptide-MHC complex comprising antigenic peptide, linker and MHC segment
PT - useful as reagents for the treatment of diseases including auto-immune
PT diseases, immuno-stimulatory diseases or graft-host rejection.
XX
PS Example 2; Page 65; 94pp; English.
XX
CC This sequence represents a hybrid IA beta chain gene. This sequence
CC contains a fragment of the IE alpha chain (residues 56-73), as well as a
CC linker and cleavage site. This sequence was transfected into a B cell
CC line (M12.C3) using plasmid pM12-IAb-Ea. It was found that the encoded
CC sequence was expressed in these cells. Complexes such as this may be used
CC to regulate an immune response. The complexes are capable of being
CC recognised by a TCR alone or in combination with additional MHC proteins.
CC These complexes are useful for therapeutic purposes and experimental
CC purposes. They can also be used as reagents for the treatment of diseases
CC including autoimmune diseases, immunodeficiency diseases,
CC immunoproliferation diseases, and graft-host rejection
XX
SQ Sequence 1013 BP; 220 A; 272 C; 327 G; 192 T; 0 U; 2 Other;

Query Match 69.1%; Score 634; DB 2; Length 1013;
Best Local Similarity 89.1%; Pred. No. 5.1e-137;
Matches 695; Conservative 1; Mismatches 81; Indels 3; Gaps 1;

```
Qy          1 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 60
              ||||||||||||||||||||||||||||||| |||||||||||||||| |||||||||
Db         63 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCGGCTGCTGTGGTGGTGCTCATGGTGCTG 122

Qy         61 AGCAGCCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120
              |||||||| |||||||||||||||| |||||         ||    | | | ||     | |
Db        123 AGCAGCCCAGGGACTGAGGGCGGAGACTCCGAAGCTAGCTTTGAGGCTCAGGGTGCACTG 182

Qy        121 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 180
                |    | | | |  ||  |||||||| || ||    |     | ||   ||||
Db        183 GCCAACATTGCTGTCGACAAGGCTGGAGGTGGTGGATC---CGGTGGAGGGGGAAGTGGA 239

Qy        181 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 240
              |||||||| || ||||||||||||||  |||||||| |||||||||||||| |||||||
Db        240 GGTGGAGGGTCTGAAAGGCATTTCGTGTACCAGTTCATGGGCGAGTGCTACTTCACCAAC 299

Qy        241 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 300
              ||||||||||||||||    ||||||||||||||||||||||||||||||||||||||
Db        300 GGGACGCAGCGCATACGATATGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 359

Qy        301 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 360
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        360 TACGACAGCGACGTGGGCGAGCACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 419

Qy        361 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db        420 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGTGTGC 479

Qy        421 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 480
              |||||||||||||||||||||||||  |||||||||||||||||||||||||||||||||
Db        480 AGACACAACTACGAGGGGCCGGAGACCCACACCTCCCTGCGGCGGCTTGAACAGCCCAAT 539

Qy        481 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 540
              |||| |||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        540 GTCGTCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGCTCA 599

Qy        541 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 600
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        600 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCCGGAATGGCCAGGAGGAG 659

Qy        601 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 660
              || ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        660 ACGGTGGGGCTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 719

Qy        661 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 720
              |||||||||||||||||||| | |||||||||||:||||| || ||||||||||||
Db        720 GTCATGCTGGAGATGACCCCTCGGCGGGGAGAGGTCTAYACCTGTCACGTGGAGCATCCC 779

Qy        721 AGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCCGAGTCTGCCCGGAGCAAG 780
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||| ||||||||
Db        780 AGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCTGAGTCTGCCTGGAGCAAG 839
```

RESULT 5
ADQ31228
ID ADQ31228 standard; cDNA; 915 BP.
XX
AC ADQ31228;
XX
DT 07-OCT-2004 (first entry)
XX
DE I-Ab(beta)-E. coli heat-labile toxin B subunit-LZ-BirA fusion cDNA.
XX
KW class II major histocompatibility complex; MHC; CD4+ T-cell detection;
KW flow cytometry; mucous membrane invasive antigen;
KW I-Ab(beta)-heat-labile toxin B subunit-leucine zipper-BirA fusion; LTB;
KW ss; gene.
XX
OS Escherichia coli.
OS Unidentified.
XX
FH Key Location/Qualifiers
FT CDS 1. .915
FT /*tag= a
FT /product= "I-Ab(beta)-Escherichia coli heat-labile toxin
FT B subunit (LTB)-leucine zipper (LZ)-BirA fusion protein"
XX
PN JP2004196789-A.
XX
PD 15-JUL-2004.
XX
PF 03-DEC-2003; 2003JP-00404367.
XX
PR 03-DEC-2002; 2002JP-00351818.
XX
PA (SENT-) SENTAN KAGAKU GIJUTSU INCUBATION CENT KK.
XX
DR WPI; 2004-546819/53.
DR P-PSDB; ADQ31227.
XX
PT Peptide-Class II major histocompatibility complex (MHC) composite, useful
PT for detecting antigen specific CD4+ T-cell, comprises antigen peptide
PT containing epitope of mucous membrane invasive protein, and extracellular
PT region of MHC.
XX
PS Example 3; SEQ ID NO 13; 30pp; Japanese.
XX
CC The invention relates to a novel class II major histocompatibility
CC complex (MHC) antigenic peptide composite comprising a peptide containing
CC the T-cell antigenic determinant of a mucous membrane invasive protein
CC and the extracellular region of a class II MHC molecule or at least part
CC of the extracellular region of the class II MHC molecule having an amino
CC acid sequence comprising one or more deletions, substitutions or
CC additions. The molecule of the invention may be useful for detecting an
CC antigen-specific CD4+ T-cell by flow cytometry and for presenting a
CC microorganism-derived mucous membrane invasive protein as an antigen. The
CC method of the invention enables efficient detection of antigen-specific
CC activation of CD4+ T-cells in the mucous membrane. The current sequence
CC is that of the class II major histocompatibility complex-related I-
CC Ab(alpha)-Escherichia coli heat-labile toxin B subunit (LTB)-leucine
CC zipper (LZ)-BirA fusion cDNA of the invention.
XX
SQ Sequence 915 BP; 228 A; 242 C; 271 G; 174 T; 0 U; 0 Other;

Query Match 68.5%; Score 628.6; DB 12; Length 915;

```
  Best Local Similarity   91.9%;  Pred. No. 8.9e-136;
  Matches  677;  Conservative    0;  Mismatches   54;  Indels    6;  Gaps    1;

Qy        182 GTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAACG 241
              | || ||    ||||||||||||||  |||||||| ||||||||||||| ||||||||
Db        155 GAGGTGGTAGTGAAAGGCATTTCGTGTACCAGTTCATGGGCGAGTGCTACTTCACCAACG 214

Qy        242 GGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGCT 301
              ||||||||||||||    ||||||||||||||||||||||||||||||||||||||||
Db        215 GGACGCAGCGCATACGATATGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGCT 274

Qy        302 ACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAGT 361
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        275 ACGACAGCGACGTGGGCGAGCACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAGT 334

Qy        362 ACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGCA 421
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||| |||||
Db        335 ACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGCTGGACACGGTGTGCA 394

Qy        422 GACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAATG 481
              |||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db        395 GACACAACTACGAGGGGCCGGAGACCCACACCTCCCTGCGGCGGCTTGAACAGCCCAATG 454

Qy        482 TCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCGG 541
              ||| |||||||||||||||||||||||||||||||||||||||||||||||||||| || |
Db        455 TCGTCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGCTCAG 514

Qy        542 TGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAGA 601
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        515 TGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCCGGAATGGCCAGGAGGAGA 574

Qy        602 CAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTGG 661
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        575 CGGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTGG 634

Qy        662 TCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCCA 721
              |||||||||||||||||||  | |||||||||||||||||| || ||||||||||||||
Db        635 TCATGCTGGAGATGACCCCTCGGCGGGGAGAGGTCTACACCTGTCACGTGGAGCATCCCA 694

Qy        722 GCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCCGAGTCTGCCCGGAGCAAGG 781
              |||||||||||||||||||||||||||||||||||||||     | | ||       ||
Db        695 GCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCGTCAGCAGACC------TGG 748

Qy        782 GAGGTGGAGGATCCACTACAGCTCCATCAGCTCAGTTGAAAAAGAAATTGCAAGCACTGA 841
              | ||||||||||||||||||||||||||||||||||||||||||| |||| ||||| |
Db        749 TTCCGCGCGGATCCACTACAGCTCCATCAGCTCAGTTGAAAAAGAAACTGCAGGCACTTA 808

Qy        842 AGAAAAAGAACGCTCAGCTGAAGTGGAAACTTCAAGCCCTCAAGAAGAAACTCGCCCAGC 901
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        809 AGAAAAAGAACGCTCAGCTGAAGTGGAAACTTCAAGCCCTCAAGAAGAAACTCGCCCAGC 868

Qy        902 ATCATCATCATCATCAT 918
                ||||||  ||   ||
Db        869 TGCATCATATTCTGGAT 885


RESULT 6
AAT86989
ID   AAT86989 standard; DNA; 1382 BP.
XX
AC   AAT86989;
XX
DT   27-MAR-1998  (first entry)
XX
DE   SCE1 single chain gene.
XX
KW   Construction; major histocompatibility complex; MHC; fusion complex;
KW   SCE1 single chain gene; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             6. .1382
FT                   /*tag=  a
XX
PN   WO9728191-A1.
XX
PD   07-AUG-1997.
XX
PF   30-JAN-1997;   97WO-US001617.
XX
PR   31-JAN-1996;   96US-00596387.
XX
PA   (DADE-) DADE INT INC.
XX
PI   Rhode PR,  Jiao J,  Burkhardt M,  Wong HC;
XX
DR   WPI; 1997-402555/37.
DR   P-PSDB; AAW29214.
XX
PT   Single chain major histocompatibility complex comprising linked alpha and
PT   beta chains - useful for suppressing an immune response to an auto:immune
PT   disease, e.g. multiple sclerosis, rheumatoid arthritis, diabetes
PT   mellitus, etc.
XX
PS   Example 17; Page 140-141; 217pp; English.
XX
CC   The present sequence was used in the construction of major
CC   histocompatibility complex (MHC) fusion complexes
XX
SQ   Sequence 1382 BP; 320 A; 373 C; 405 G; 284 T; 0 U; 0 Other;

  Query Match             66.2%;  Score 607.8;  DB 2;  Length 1382;
  Best Local Similarity   89.6%;  Pred. No. 6.5e-131;
  Matches  673;  Conservative    0;  Mismatches   57;  Indels   21;  Gaps    1;

Qy          1 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         61 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120
              ||||||||  ||||                    |||          || | ||      |
Db         66 AGCAGCCCAAGGAC--------------------CTTAAGTATCTCTCAGGCTGTTCAC 104

Qy        121 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 180
                 |      | | | |   || |  ||| | |       || |  | || ||   |||
Db        105 GCTGCTCACGCTGAAATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGCGGCGGA 164

Qy        181 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 240
              || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy        241 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        301 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        361 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        421 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        481 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        541 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584
```

```
Qy        601 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        661 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        721 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 751
              |||||||||||||||||||||||||||||
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 735
```

RESULT 7
ACA60744
ID ACA60744 standard; DNA; 1382 BP.
XX
AC ACA60744;
XX
DT 16-JUN-2003 (first entry)
XX
DE Mouse MHC I-Ad/Ova 323-339 synthetic gene SCE1.
XX
KW MHC; major histocompatibility complex; gene therapy; fusion complex;
KW peptide-binding groove; T cell modulation; class II MHC; vaccine;
KW autoimmune disorder; multiple sclerosis; rheumatoid arthritis;
KW insulin-dependent diabetes mellitus; myasthenia gravis; immunogen;
KW chronic allergy; mouse; ds; I-Ad; gene.
XX
OS Mus sp.
OS Synthetic.
XX
PN US2002198144-A1.
XX
PD 26-DEC-2002.
XX
PF 06-JUL-2001; 2001US-00900379.
XX
PR 29-JUL-1994; 94US-00283302.
PR 01-FEB-1995; 95US-00382454.
PR 17-JAN-1997; 97US-00776084.
XX
PA (DADE-) DADE INT INC.
XX
PI Wong HC, Rhode PR, Weidanz JA, Grammer S, Edwards AC;
PI Chavaillaz P, Jiao JJJ;
XX
DR WPI; 2003-341126/32.
DR P-PSDB; ABU72108.
XX
PT Novel major histocompatibility complex fusion complex having presenting
PT peptide covalently linked to MHC molecule containing peptide-binding
PT groove, used for suppressing immune response in multiple sclerosis,
PT allergies.
XX
PS Example 17; Fig 29; 126pp; English.
XX
CC The invention relates to a major histocompatibility complex (MHC) fusion
CC complex (I) comprising an MHC molecule that contains a peptide-binding
CC groove, and a presenting peptide covalently (e.g. an antigenic peptide)
CC linked to the MHC molecule, where (I) is capable of modulating the
CC activity of a T cell. Also included are a DNA construct coding for the
CC complex, where the MHC molecule is a class II MHC (e.g. mouse I-Ad or I-
CC As, or human HLA-DR1 (human leukocyte antigen-DR1)), a multivalent MHC
CC fusion complex comprising two or more linked complexes, identifying a
CC peptide that can modulate the activity of T cells (involving introducing
CC into host cells cloning vectors that each contain the fusion complex DNA,
CC culturing the host cells under conditions suitable for expression of the
CC MHC fusion complex, and selecting host cells that express MHC fusion
CC complex that modulate the activity of T cells), a single recombinant
CC expression vector comprising DNA that codes for the alpha and beta chains
CC of the fusion complex MHC protein, a single recombinant expression vector
CC comprising DNA that codes for a T cell costimulatory factor and the alpha
CC and beta chains of the MHC fusion complex. The DNA constructs can contain
CC heterologous leader peptide sequences and Kozak sequence for efficient
CC expression of the fusion complex. Also included are inducing an immune
CC response in a mammal (including vaccinating a mammal against a targeted
CC disorder, by administering DNA sequence comprising a fusion complex, or
CC DNA sequence coding for a fusion complex which is a single chain fusion
CC molecule) and suppressing an immune response in a mammal by administering
CC to the mammal a DNA sequence comprising an expression vector, encoding a
CC full length MHC molecule that contains a transmembrane domain, and a
CC presenting peptide that is a T cell receptor (TCR) antagonist or partial
CC agonist and is covalently linked to the MHC protein, or DNA sequence
CC coding for the fusion complex which is a single chain fusion molecule.
CC The methods are useful for identifying a peptide that can modulate the
CC activity of T cells, inducing an immune response in a mammal (including
CC vaccinating a mammal against a targeted disorder) and for suppressing an
CC immune response in a mammal. The disorders include an autoimmune disorder
CC such as multiple sclerosis, insulin-dependent diabetes mellitus,
CC rheumatoid arthritis, myasthenia gravis or chronic allergies. The present
CC sequence encodes a mouse MHC class II I-Ad fusion complex of the
CC invention
XX
SQ Sequence 1382 BP; 320 A; 373 C; 405 G; 284 T; 0 U; 0 Other;

Query Match 66.2%; Score 607.8; DB 8; Length 1382;
Best Local Similarity 89.6%; Pred. No. 6.5e-131;
Matches 673; Conservative 0; Mismatches 57; Indels 21; Gaps 1;

```
Qy          1 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         61 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120
              |||||||  ||||                        |||       || | ||     |
Db         66 AGCAGCCCAAGGAC--------------------CTTAAGTATCTCTCAGGCTGTTCAC 104

Qy        121 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 180
                |    | |  | |   || |  ||| | |        || |  | || ||   |||
Db        105 GCTGCTCACGCTGAAATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGCGGCGGA 164

Qy        181 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 240
              || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy        241 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        301 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        361 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        421 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        481 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        541 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 600
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        601 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        661 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 720
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        721 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 751
              ||||||||||||||||||||||||||||||
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 735


RESULT 8
AAT86987
ID   AAT86987 standard; DNA; 1385 BP.
XX
AC   AAT86987;
XX
DT   27-MAR-1998  (first entry)
XX
DE   SSC1 single chain gene.
XX
KW   Construction; major histocompatibility complex; MHC; fusion complex;
KW   SSC1 single chain gene; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             6. .1385
FT                   /*tag=  a
XX
PN   WO9728191-A1.
XX
PD   07-AUG-1997.
XX
PF   30-JAN-1997;   97WO-US001617.
XX
PR   31-JAN-1996;   96US-00596387.
XX
PA   (DADE-) DADE INT INC.
XX
PI   Rhode PR,  Jiao J,  Burkhardt M,  Wong HC;
XX
DR   WPI; 1997-402555/37.
DR   P-PSDB; AAW29212.
XX
PT   Single chain major histocompatibility complex comprising linked alpha and
PT   beta chains - useful for suppressing an immune response to an auto:immune
PT   disease, e.g. multiple sclerosis, rheumatoid arthritis, diabetes
PT   mellitus, etc.
XX
PS   Example 17; Page 135-137; 217pp; English.
XX
CC   The present sequence was used in the construction of major
CC   histocompatibility complex (MHC) fusion complexes
XX
SQ   Sequence 1385 BP; 316 A; 383 C; 399 G; 287 T; 0 U; 0 Other;

  Query Match             66.2%;  Score 607.8;  DB 2;  Length 1385;
  Best Local Similarity   89.6%;  Pred. No. 6.5e-131;
  Matches  673;  Conservative    0;  Mismatches   57;  Indels   21;  Gaps    1;

Qy          1 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         61 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120
              ||||||||  ||||                     |||       || | ||     |
Db         66 AGCAGCCCAAGGAC--------------------CTTAAGTATCTCTCAGGCTGTTCAC 104

Qy        121 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 180
                 |      | |  | |   || |  ||| | |       || |  | || ||   |||
Db        105 GCTGCTCACGCTGAAATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGCGGCGGA 164

Qy        181 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 240
              || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy        241 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        301 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        361 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        421 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        481 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        541 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        601 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        661 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        721 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 751
              ||||||||||||||||||||||||||||||
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 735


RESULT 9
ACA60742
ID   ACA60742 standard; DNA; 1385 BP.
XX
AC   ACA60742;
XX
DT   16-JUN-2003  (first entry)
XX
DE   Mouse MHC I-Ad/Ova 323-339 synthetic gene SSC1.
XX
KW   MHC; major histocompatibility complex; gene therapy; fusion complex;
KW   peptide-binding groove; T cell modulation; class II MHC; vaccine;
KW   autoimmune disorder; multiple sclerosis; rheumatoid arthritis;
KW   insulin-dependent diabetes mellitus; myasthenia gravis; immunogen;
KW   chronic allergy; mouse; ds; I-Ad; gene.
XX
OS   Mus sp.
OS   Synthetic.
XX
PN   US2002198144-A1.
XX
PD   26-DEC-2002.
XX
PF   06-JUL-2001; 2001US-00900379.
XX
PR   29-JUL-1994;   94US-00283302.
PR   01-FEB-1995;   95US-00382454.
PR   17-JAN-1997;   97US-00776084.
XX
PA   (DADE-) DADE INT INC.
XX
PI   Wong HC,  Rhode PR,  Weidanz JA,  Grammer S,  Edwards AC;
PI   Chavaillaz P,  Jiao JJJ;
XX
DR   WPI; 2003-341126/32.
DR   P-PSDB; ABU72106.
```

XX
PT Novel major histocompatibility complex fusion complex having presenting
PT peptide covalently linked to MHC molecule containing peptide-binding
PT groove, used for suppressing immune response in multiple sclerosis,
PT allergies.
XX
PS Example 17; Fig 27; 126pp; English.
XX
CC The invention relates to a major histocompatibility complex (MHC) fusion
CC complex (I) comprising an MHC molecule that contains a peptide-binding
CC groove, and a presenting peptide covalently (e.g. an antigenic peptide)
CC linked to the MHC molecule, where (I) is capable of modulating the
CC activity of a T cell. Also included are a DNA construct coding for the
CC complex, where the MHC molecule is a class II MHC (e.g. mouse I-Ad or I-
CC As, or human HLA-DR1 (human leukocyte antigen-DR1)), a multivalent MHC
CC fusion complex comprising two or more linked complexes, identifying a
CC peptide that can modulate the activity of T cells (involving introducing
CC into host cells cloning vectors that each contain the fusion complex DNA,
CC culturing the host cells under conditions suitable for expression of the
CC MHC fusion complex, and selecting host cells that express MHC fusion
CC complex that modulate the activity of T cells), a single recombinant
CC expression vector comprising DNA that codes for the alpha and beta chains
CC of the fusion complex MHC protein, a single recombinant expression vector
CC comprising DNA that codes for a T cell costimulatory factor and the alpha
CC and beta chains of the MHC fusion complex. The DNA constructs can contain
CC heterologous leader peptide sequences and Kozak sequence for efficient
CC expression of the fusion complex. Also included are inducing an immune
CC response in a mammal (including vaccinating a mammal against a targeted
CC disorder, by administering DNA sequence comprising a fusion complex, or
CC DNA sequence coding for a fusion complex which is a single chain fusion
CC molecule) and suppressing an immune response in a mammal by administering
CC to the mammal a DNA sequence comprising an expression vector, encoding a
CC full length MHC molecule that contains a transmembrane domain, and a
CC presenting peptide that is a T cell receptor (TCR) antagonist or partial
CC agonist and is covalently linked to the MHC protein, or DNA sequence
CC coding for the fusion complex which is a single chain fusion molecule.
CC The methods are useful for identifying a peptide that can modulate the
CC activity of T cells, inducing an immune response in a mammal (including
CC vaccinating a mammal against a targeted disorder) and for suppressing an
CC immune response in a mammal. The disorders include an autoimmune disorder
CC such as multiple sclerosis, insulin-dependent diabetes mellitus,
CC rheumatoid arthritis, myasthenia gravis or chronic allergies. The present
CC sequence encodes a mouse MHC class II I-Ad fusion complex of the
CC invention
XX
SQ Sequence 1385 BP; 316 A; 383 C; 399 G; 287 T; 0 U; 0 Other;

Query Match 66.2%; Score 607.8; DB 8; Length 1385;
Best Local Similarity 89.6%; Pred. No. 6.5e-131;
Matches 673; Conservative 0; Mismatches 57; Indels 21; Gaps 1;

```
Qy          1 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         61 AGCAGCCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120
              ||||||||  ||||                    |||       || | ||     |
Db         66 AGCAGCCCAAGGAC--------------------CTTAAGTATCTCTCAGGCTGTTCAC 104

Qy        121 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 180
                 |      | | | |   || |  ||| | |       || |  | || ||   |||
Db        105 GCTGCTCACGCTGAAATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGCGGCGGA 164

Qy        181 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 240
              || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy        241 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        301 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        361 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        421 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        481 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        541 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        601 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        661 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        721 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 751
              ||||||||||||||||||||||||||||||
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 735
```

RESULT 10
AAT86988
ID AAT86988 standard; DNA; 1508 BP.
XX
AC AAT86988;
XX
DT 27-MAR-1998 (first entry)
XX
DE SCT1 single chain gene.
XX
KW Construction; major histocompatibility complex; MHC; fusion complex;
KW SCT1 single chain gene; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 6. .1508
FT /*tag= a
XX
PN WO9728191-A1.
XX
PD 07-AUG-1997.
XX
PF 30-JAN-1997; 97WO-US001617.
XX
PR 31-JAN-1996; 96US-00596387.
XX
PA (DADE-) DADE INT INC.
XX
PI Rhode PR, Jiao J, Burkhardt M, Wong HC;
XX
DR WPI; 1997-402555/37.
DR P-PSDB; AAW29213.
XX
PT Single chain major histocompatibility complex comprising linked alpha and
PT beta chains - useful for suppressing an immune response to an auto:immune
PT disease, e.g. multiple sclerosis, rheumatoid arthritis, diabetes
PT mellitus, etc.
XX
PS Example 17; Page 137-139; 217pp; English.
XX
CC The present sequence was used in the construction of major

```
CC   histocompatibility complex (MHC) fusion complexes
XX
SQ   Sequence 1508 BP; 337 A; 413 C; 441 G; 317 T; 0 U; 0 Other;

  Query Match             66.2%;  Score 607.8;  DB 2;  Length 1508;
  Best Local Similarity   89.6%;  Pred. No. 6.7e-131;
  Matches  673;  Conservative    0;  Mismatches   57;  Indels   21;  Gaps    1;

Qy          1 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         61 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120
              ||||||||  ||||                    |||        || | ||     |
Db         66 AGCAGCCCAAGGAC--------------------CTTAAGTATCTCTCAGGCTGTTCAC 104

Qy        121 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 180
                |      | |  | |   || |  ||| | |      || |  | || ||   |||
Db        105 GCTGCTCACGCTGAAATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGCGGCGGA 164

Qy        181 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 240
              || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy        241 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        301 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        361 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        421 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        481 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        541 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        601 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        661 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        721 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 751
              ||||||||||||||||||||||||||||||
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 735


RESULT 11
AAX89069
ID   AAX89069 standard; DNA; 1508 BP.
XX
AC   AAX89069;
XX
DT   14-SEP-1999  (first entry)
XX
DE   Single chain IAd/OVA 323-229 MHC fusion protein encoding DNA.
XX
KW   Major histocompatibility complex; MHC; single chain MHC; sc-MHC; Ig;
KW   peptide binding groove; immunoglobulin; T cell receptor; immune response;
KW   immune-related disorder; antigenic peptide; fusion protein; ss.
XX
OS   Synthetic.
XX
PN   WO9921572-A1.
XX
PD   06-MAY-1999.
XX
PF   13-OCT-1998;   98WO-US021520.
XX
PR   29-OCT-1997;   97US-00960190.
XX
PA   (SUNO-) SUNOL MOLECULAR CORP.
XX
PI   Rhode PR,  Acevedo J,  Burkhardt M,  Jiao J,  Wong HC;
XX
DR   WPI; 1999-418411/35.
DR   P-PSDB; AAY27111.
XX
PT   Single chain major histocompatibility complex class I complexes.
XX
PS   Example 1; Fig 1; 148pp; English.
XX
CC   The invention relates to new single chain major histocompatibility
CC   complex (sc-MHC) class II complexes that comprise a peptide binding
CC   groove, and a modified class II beta 2 chain or covalently linked
CC   immunoglobulin (Ig) light chain constant (C1) region. The MHC complexes
CC   are useful for detection and analysis of peptide ligands, pathogenic T-
CC   cells, for functional, cellular and molecular assays. They can be used to
CC   identify and isolate T cell receptor and/or MHC agonists and antagonists.
CC   They can be used in vivo to compete with pathogenic antigen presenting
CC   cells involved in immune-related disorders. They can also be used to
CC   raise antibodies and to screen immune cells. It is also use in a method
CC   of suppressing an immune response in mammals. The sc-MHC complexes
CC   comprising modified class II beta 2 chains and/or Ig-C1 regions are
CC   soluble and provide enhanced yield. These MHC complexes also can contain
CC   single antigenic peptides readily isolated from expressing cells in
CC   significant quantities. The polyspecific MHC complexes also provide a
CC   means to detect cells expressing multiple target structures with a single
CC   complex. The present sequence represents a DNA encoding a single chain
CC   IAd/OVA 323-229 MHC fusion protein
XX
SQ   Sequence 1508 BP; 337 A; 413 C; 441 G; 317 T; 0 U; 0 Other;

  Query Match             66.2%;  Score 607.8;  DB 2;  Length 1508;
  Best Local Similarity   89.6%;  Pred. No. 6.7e-131;
  Matches  673;  Conservative    0;  Mismatches   57;  Indels   21;  Gaps    1;

Qy          1 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         61 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120
              ||||||||  ||||                    |||        || | ||     |
Db         66 AGCAGCCCAAGGAC--------------------CTTAAGTATCTCTCAGGCTGTTCAC 104

Qy        121 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 180
                |      | |  | |   || |  ||| | |      || |  | || ||   |||
Db        105 GCTGCTCACGCTGAAATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGCGGCGGA 164

Qy        181 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 240
              || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy        241 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        301 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        361 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 420
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        421 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        481 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        541 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        601 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        661 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        721 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 751
                ||||||||||||||||||||||||||||||
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 735
```

RESULT 12
ACA60743
ID ACA60743 standard; DNA; 1508 BP.
XX
AC ACA60743;
XX
DT 16-JUN-2003 (first entry)
XX
DE Mouse MHC I-Ad/Ova 323-339 synthetic gene SCT1.
XX
KW MHC; major histocompatibility complex; gene therapy; fusion complex;
KW peptide-binding groove; T cell modulation; class II MHC; vaccine;
KW autoimmune disorder; multiple sclerosis; rheumatoid arthritis;
KW insulin-dependent diabetes mellitus; myasthenia gravis; immunogen;
KW chronic allergy; mouse; ds; I-Ad; gene.
XX
OS Mus sp.
OS Synthetic.
XX
PN US2002198144-A1.
XX
PD 26-DEC-2002.
XX
PF 06-JUL-2001; 2001US-00900379.
XX
PR 29-JUL-1994; 94US-00283302.
PR 01-FEB-1995; 95US-00382454.
PR 17-JAN-1997; 97US-00776084.
XX
PA (DADE-) DADE INT INC.
XX
PI Wong HC, Rhode PR, Weidanz JA, Grammer S, Edwards AC;
PI Chavaillaz P, Jiao JJJ;
XX
DR WPI; 2003-341126/32.
DR P-PSDB; ABU72107.
XX
PT Novel major histocompatibility complex fusion complex having presenting
PT peptide covalently linked to MHC molecule containing peptide-binding
PT groove, used for suppressing immune response in multiple sclerosis,
PT allergies.
XX
PS Example 17; Fig 28; 126pp; English.
XX
CC The invention relates to a major histocompatibility complex (MHC) fusion
CC complex (I) comprising an MHC molecule that contains a peptide-binding
CC groove, and a presenting peptide covalently (e.g. an antigenic peptide)
CC linked to the MHC molecule, where (I) is capable of modulating the
CC activity of a T cell. Also included are a DNA construct coding for the
CC complex, where the MHC molecule is a class II MHC (e.g. mouse I-Ad or I-
CC As, or human HLA-DR1 (human leukocyte antigen-DR1)), a multivalent MHC
CC fusion complex comprising two or more linked complexes, identifying a
CC peptide that can modulate the activity of T cells (involving introducing
CC into host cells cloning vectors that each contain the fusion complex DNA,
CC culturing the host cells under conditions suitable for expression of the
CC MHC fusion complex, and selecting host cells that express MHC fusion
CC complex that modulate the activity of T cells), a single recombinant
CC expression vector comprising DNA that codes for the alpha and beta chains
CC of the fusion complex MHC protein, a single recombinant expression vector
CC comprising DNA that codes for a T cell costimulatory factor and the alpha
CC and beta chains of the MHC fusion complex. The DNA constructs can contain
CC heterologous leader peptide sequences and Kozak sequence for efficient
CC expression of the fusion complex. Also included are inducing an immune
CC response in a mammal (including vaccinating a mammal against a targeted
CC disorder, by administering DNA sequence comprising a fusion complex, or
CC DNA sequence coding for a fusion complex which is a single chain fusion
CC molecule) and suppressing an immune response in a mammal by administering
CC to the mammal a DNA sequence comprising an expression vector, encoding a
CC full length MHC molecule that contains a transmembrane domain, and a
CC presenting peptide that is a T cell receptor (TCR) antagonist or partial
CC agonist and is covalently linked to the MHC protein, or DNA sequence
CC coding for the fusion complex which is a single chain fusion molecule.
CC The methods are useful for identifying a peptide that can modulate the
CC activity of T cells, inducing an immune response in a mammal (including
CC vaccinating a mammal against a targeted disorder) and for suppressing an
CC immune response in a mammal. The disorders include an autoimmune disorder
CC such as multiple sclerosis, insulin-dependent diabetes mellitus,
CC rheumatoid arthritis, myasthenia gravis or chronic allergies. The present
CC sequence encodes a mouse MHC class II I-Ad fusion complex of the
CC invention
XX
SQ Sequence 1508 BP; 337 A; 413 C; 441 G; 317 T; 0 U; 0 Other;

Query Match 66.2%; Score 607.8; DB 8; Length 1508;
Best Local Similarity 89.6%; Pred. No. 6.7e-131;
Matches 673; Conservative 0; Mismatches 57; Indels 21; Gaps 1;

```
Qy          1 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         61 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120
              ||||||||  ||||                        |||       || | ||     |
Db         66 AGCAGCCCAAGGAC--------------------CTTAAGTATCTCTCAGGCTGTTCAC 104

Qy        121 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 180
                 |      | |  | |   || |  ||| | |        || |  | || ||  |||
Db        105 GCTGCTCACGCTGAAATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGCGGCGGA 164

Qy        181 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 240
              || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy        241 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        301 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        361 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        421 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 480
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Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464
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Qy        481 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 540
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Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        541 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 600
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Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        601 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 660
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Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        661 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 720
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Qy        721 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 751
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Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 735
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RESULT 13
AAT17588
ID   AAT17588 standard; DNA; 1382 BP.
XX
AC   AAT17588;
XX
DT   26-SEP-1996  (first entry)
XX
DE   Vector SCE1-derived single chain gene encoding MHC fusion complex.
XX
KW   MHC; major histocompatibility complex; PCR; polymerase chain reaction;
KW   T cell activity modulator; antagonist; immune disorder; allergy;
KW   multiple sclerosis; insulin-dependent diabetes mellitus;
KW   rheumatoid arthritis; myasthenia gravis; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             6. .1382
FT                   /*tag=  a
FT   sig_peptide     6. .86
FT                   /*tag=  b
FT                   /label= I-Ad_beta_chain_leader
FT                   /note= "murine MHC class II I-Ad gene beta chain leader
FT                   sequence"
FT   misc_feature    87. .137
FT                   /*tag=  c
FT                   /label= OVA_323-339
FT                   /note= "chicken ovalbumin residues 323-339"
FT   misc_feature    138. .167
FT                   /*tag=  d
FT                   /note= "10 residue linker peptide"
FT   misc_feature    168. .452
FT                   /*tag=  e
FT                   /label= I-Ad_beta1
FT                   /note= "murine MHC class II I-Ad gene beta-1 domain"
FT   misc_feature    453. .734
FT                   /*tag=  f
FT                   /label= I-Ad_beta2
FT                   /note= "murine MHC class II I-Ad gene beta-2 domain"
FT   misc_feature    735. .806
FT                   /*tag=  g
FT                   /note= "24 residue peptide linker"
FT   misc_feature    807. .1067
FT                   /*tag=  h
FT                   /label= I-Ad_alpha1
FT                   /note= "murine MHC class II I-Ad gene alpha-2 domain"
FT   misc_feature    1068. .1352
FT                   /*tag=  i
FT                   /label= I-Ad_alpha2
FT                   /note= "murine MHC class II I-Ad gene alpha-2 domain"
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FT                   /*tag=  j
FT                   /note= "EE tag"
XX
PN   WO9604314-A1.
XX
PD   15-FEB-1996.
XX
PF   31-JUL-1995;   95WO-US009816.
XX
PR   29-JUL-1994;   94US-00283302.
PR   01-FEB-1995;   95US-00382454.
XX
PA   (DADE-) DADE INT INC.
XX
PI   Wong HC,  Rhode PR,  Weidanz JA,  Grammer S,  Edwards AC;
PI   Chavaillaz P,  Jiao J;
XX
DR   WPI; 1996-129343/13.
DR   P-PSDB; AAR98907.
XX
PT   Major histocompatability complex fusion complex for modulating T cell
PT   activity - used in the treatment of immune disorders, e.g. multiple
PT   sclerosis, IDDM and rheumatoid arthritis.
XX
PS   Example 17; Fig 29; 210pp; English.
XX
CC   AAT17588 encodes a murine MHC fusion complex capable of modulating T cell
CC   activity encoded by the vector SCE1. The MHC fusion complex comprises at
CC   least one MHC molecule containing a peptide-binding groove and a
CC   presenting peptide covalently linked to the MHC molecule and opt. a
CC   transmembrane domain. DNA encoding a MHC fusion complex may be cloned
CC   into a host cell to express the complex. The transformed cells may then
CC   be used to identify peptides that modulate, pref. antagonise, T cell
CC   activity. DNA encoding a MHC fusion complex or a single chain fusion
CC   molecule may be used to vaccinate a mammal against a targeted disorder.
CC   The fusion complexes may be used to suppress an immune response in an
CC   animal suffering from an immune disorder e.g. multiple sclerosis, insulin
CC   -dependent diabetes mellitus, rheumatoid arthritis, myasthenia gravis or
CC   chronic allergies. The complexes may also be used in the treatment of
CC   livestock and pets such as cats and dogs. The MHC fusion complexes can be
CC   produced such that they contain a single antigenic peptide including one
CC   of known structure, additionally a wide range of peptides can be
CC   presented for T cell interaction
XX
SQ   Sequence 1382 BP; 320 A; 374 C; 404 G; 284 T; 0 U; 0 Other;
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  Best Local Similarity   89.5%;  Pred. No. 1.5e-130;
  Matches  672;  Conservative    0;  Mismatches   58;  Indels   21;  Gaps    1;

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Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         61 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120
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Db         66 AGCAGCCCAAGGAC--------------------CTTAAGTATCTCTCAGGCTGTTCAC 104

Qy        121 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 180
                 |      | |  | |   || |  ||| | |      || |  | || ||   |||
Db        105 GCTGCTCACGCTGAAATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGCGGCGGA 164

Qy        181 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 240
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Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy        241 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 300
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Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        301 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 360
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Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTCGGGCGGCCAGACGCCGAG 344

Qy        361 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 420
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Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        421 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        481 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        541 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        601 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        661 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        721 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 751
              ||||||||||||||||||||||||||||||
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 735
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RESULT 14
AAT17586
ID AAT17586 standard; DNA; 1385 BP.
XX
AC AAT17586;
XX
DT 26-SEP-1996 (first entry)
XX
DE Vector SSC1-derived single chain gene encoding MHC fusion complex.
XX
KW MHC; major histocompatibility complex; PCR; polymerase chain reaction;
KW T cell activity modulator; antagonist; immune disorder; allergy;
KW multiple sclerosis; insulin-dependent diabetes mellitus;
KW rheumatoid arthritis; myasthenia gravis; ds.
XX
OS Synthetic.
XX

FH	Key	Location/Qualifiers
FT	CDS	6. .1385
FT		/*tag= a
FT	sig_peptide	6. .86
FT		/*tag= b
FT		/label= I-Ad_beta_chain_leader
FT		/note= "murine MHC class II I-Ad gene beta chain leader sequence"
FT	misc_feature	87. .137
FT		/*tag= c
FT		/label= OVA_323-339
FT		/note= "chicken ovalbumin residues 323-339"
FT	misc_feature	138. .167
FT		/*tag= d
FT		/note= "10 residue linker peptide"
FT	misc_feature	168. .452
FT		/*tag= e
FT		/label= I-Ad_beta1
FT		/note= "murine MHC class II I-Ad gene beta-1 domain"
FT	misc_feature	453. .734
FT		/*tag= f
FT		/label= I-Ad_beta2
FT		/note= "murine MHC class II I-Ad gene beta-2 domain"
FT	misc_feature	735. .806
FT		/*tag= g
FT		/note= "24 residue peptide linker"
FT	misc_feature	807. .1067
FT		/*tag= h
FT		/label= I-Ad_alpha1
FT		/note= "murine MHC class II I-Ad gene alpha-2 domain"
FT	misc_feature	1068. .1352
FT		/*tag= i
FT		/label= I-Ad_alpha2
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XX
PN WO9604314-A1.
XX
PD 15-FEB-1996.
XX
PF 31-JUL-1995; 95WO-US009816.
XX
PR 29-JUL-1994; 94US-00283302.
PR 01-FEB-1995; 95US-00382454.
XX
PA (DADE-) DADE INT INC.
XX
PI Wong HC, Rhode PR, Weidanz JA, Grammer S, Edwards AC;
PI Chavaillaz P, Jiao J;
XX
DR WPI; 1996-129343/13.
DR P-PSDB; AAR98905.
XX
PT Major histocompatability complex fusion complex for modulating T cell
PT activity - used in the treatment of immune disorders, e.g. multiple
PT sclerosis, IDDM and rheumatoid arthritis.
XX
PS Example 17; Fig 27; 210pp; English.
XX
CC AAT17586 encodes a murine MHC fusion complex capable of modulating T cell
CC activity encoded by the vector SSC1. The MHC fusion complex comprises at
CC least one MHC molecule containing a peptide-binding groove and a
CC presenting peptide covalently linked to the MHC molecule and opt. a
CC transmembrane domain. DNA encoding a MHC fusion complex may be cloned
CC into a host cell to express the complex. The transformed cells may then
CC be used to identify peptides that modulate, pref. antagonise, T cell
CC activity. DNA encoding a MHC fusion complex or a single chain fusion
CC molecule may be used to vaccinate a mammal against a targeted disorder.
CC The fusion complexes may be used to suppress an immune response in an
CC animal suffering from an immune disorder e.g. multiple sclerosis, insulin
CC -dependent diabetes mellitus, rheumatoid arthritis, myasthenia gravis or
CC chronic allergies. The complexes may also be used in the treatment of
CC livestock and pets such as cats and dogs. The MHC fusion complexes can be
CC produced such that they contain a single antigenic peptide including one
CC of known structure, additionally a wide range of peptides can be
CC presented for T cell interaction
XX
SQ Sequence 1385 BP; 316 A; 384 C; 398 G; 287 T; 0 U; 0 Other;

Query Match 66.0%; Score 606.2; DB 2; Length 1385;
Best Local Similarity 89.5%; Pred. No. 1.5e-130;
Matches 672; Conservative 0; Mismatches 58; Indels 21; Gaps 1;

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Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         61 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120
              ||||||||  ||||                          |||        || | ||     |
Db         66 AGCAGCCCAAGGAC----------------------CTTAAGTATCTCTCAGGCTGTTCAC 104

Qy        121 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 180
                |     | |  | |   || |  ||| | |       || |  | || ||   |||
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Qy        181 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 240
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Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy        241 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 300
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Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        301 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 360
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Qy        361 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 420
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Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        421 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 480
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Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

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Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        601 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 660
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Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        661 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 720
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Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        721 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 751
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Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 735
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RESULT 15
AAT17587
ID   AAT17587 standard; DNA; 1508 BP.
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AC   AAT17587;
XX
DT   26-SEP-1996  (first entry)
XX
DE   Vector SCT1-derived single chain gene encoding MHC fusion complex.
XX
KW   MHC; major histocompatibility complex; PCR; polymerase chain reaction;
KW   T cell activity modulator; antagonist; immune disorder; allergy;
KW   multiple sclerosis; insulin-dependent diabetes mellitus;
KW   rheumatoid arthritis; myasthenia gravis; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             6. .1508
FT                   /*tag=  a
FT   sig_peptide     6. .86
FT                   /*tag=  b
FT                   /label= I-Ad_beta_chain_leader
FT                   /note= "murine MHC class II I-Ad gene beta chain leader
FT                   sequence"
FT   misc_feature    87. .137
FT                   /*tag=  c
FT                   /label= OVA_323-339
FT                   /note= "chicken ovalbumin residues 323-339"
FT   misc_feature    138. .167
FT                   /*tag=  d
FT                   /note= "10 residue linker peptide"
FT   misc_feature    168. .452
FT                   /*tag=  e
FT                   /label= I-Ad_beta1
FT                   /note= "murine MHC class II I-Ad gene beta-1 domain"
FT   misc_feature    453. .734
FT                   /*tag=  f
FT                   /label= I-Ad_beta2
FT                   /note= "murine MHC class II I-Ad gene beta-2 domain"
FT   misc_feature    735. .806
FT                   /*tag=  g
FT                   /note= "24 residue peptide linker"
FT   misc_feature    807. .1067
FT                   /*tag=  h
FT                   /label= I-Ad_alpha1
FT                   /note= "murine MHC class II I-Ad gene alpha-2 domain"
FT   misc_feature    1068. .1352
FT                   /*tag=  i
FT                   /label= I-Ad_alpha2
FT                   /note= "murine MHC class II I-Ad gene alpha-2 domain"
FT   misc_feature    1353. .1505
FT                   /*tag=  j
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FT                   domain"
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PN   WO9604314-A1.
XX
PD   15-FEB-1996.
XX
PF   31-JUL-1995;   95WO-US009816.
XX
PR   29-JUL-1994;   94US-00283302.
PR   01-FEB-1995;   95US-00382454.
XX
PA   (DADE-) DADE INT INC.
XX
PI   Wong HC,  Rhode PR,  Weidanz JA,  Grammer S,  Edwards AC;
PI   Chavaillaz P,  Jiao J;
XX
DR   WPI; 1996-129343/13.
DR   P-PSDB; AAR98906.
XX
PT   Major histocompatability complex fusion complex for modulating T cell
PT   activity - used in the treatment of immune disorders, e.g. multiple
PT   sclerosis, IDDM and rheumatoid arthritis.
XX
PS   Example 17; Fig 28; 210pp; English.
XX
CC   AAT17587 encodes a murine MHC fusion complex capable of modulating T cell
CC   activity encoded by the vector SCT1. The MHC fusion complex comprises at
CC   least one MHC molecule containing a peptide-binding groove and a
CC   presenting peptide covalently linked to the MHC molecule and opt. a
CC   transmembrane domain. DNA encoding a MHC fusion complex may be cloned
CC   into a host cell to express the complex. The transformed cells may then
CC   be used to identify peptides that modulate, pref. antagonise, T cell
CC   activity. DNA encoding a MHC fusion complex or a single chain fusion
CC   molecule may be used to vaccinate a mammal against a targeted disorder.
CC   The fusion complexes may be used to suppress an immune response in an
CC   animal suffering from an immune disorder e.g. multiple sclerosis, insulin
CC   -dependent diabetes mellitus, rheumatoid arthritis, myasthenia gravis or
CC   chronic allergies. The complexes may also be used in the treatment of
CC   livestock and pets such as cats and dogs. The MHC fusion complexes can be
CC   produced such that they contain a single antigenic peptide including one
CC   of known structure, additionally a wide range of peptides can be
CC   presented for T cell interaction
XX
SQ   Sequence 1508 BP; 337 A; 414 C; 440 G; 317 T; 0 U; 0 Other;

  Query Match           66.0%;  Score 606.2;  DB 2;  Length 1508;
  Best Local Similarity  89.5%;  Pred. No. 1.6e-130;
  Matches  672;  Conservative    0;  Mismatches   58;  Indels   21;  Gaps    1;

Qy          1 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 60
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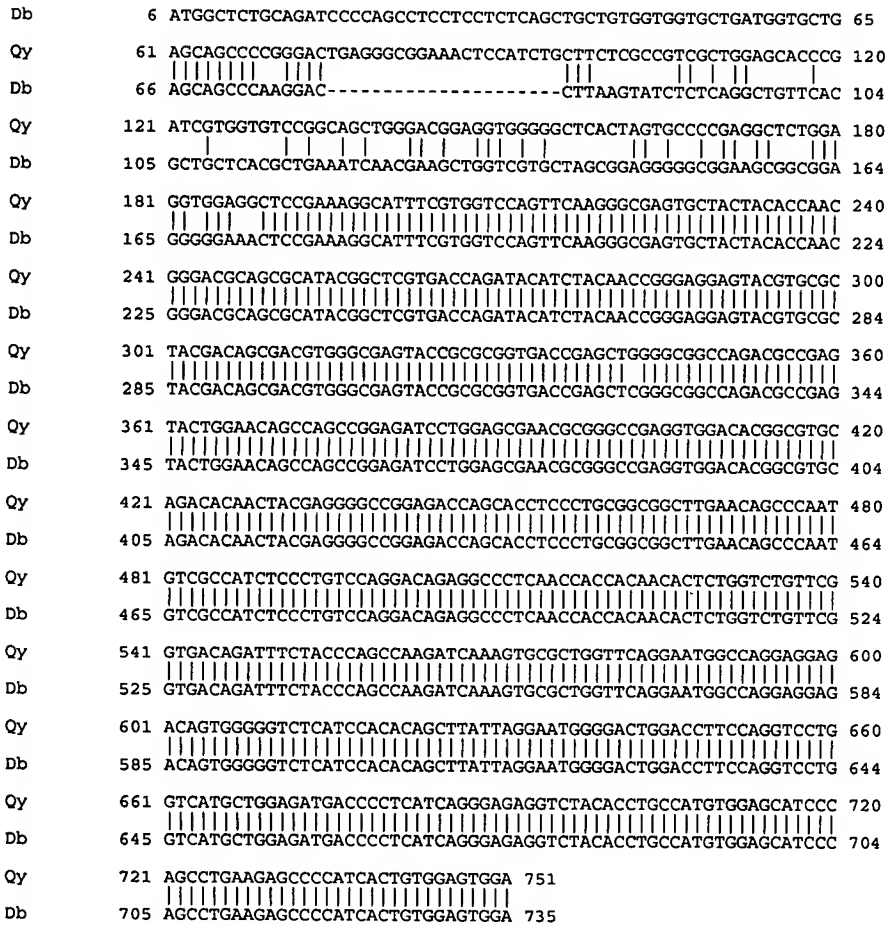

Search completed: June 30, 2006, 02:47:27
Job time : 630 secs

GenCore version 5.1.9

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 30, 2006, 01:28:47 ; Search time 6493.66 Seconds
(without alignments)
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Perfect score: 1620
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
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5: gb_pr:*
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7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1620	100.0	921	2	AX081281	AX081281 Sequence
2	1255.5	77.5	893	2	AR047947	AR047947 Sequence
3	1161.5	71.7	4724	2	AR199666	AR199666 Sequence
4	1154	71.2	1013	2	AR047957	AR047957 Sequence
5	1145	70.7	1382	2	AR033964	AR033964 Sequence
6	1145	70.7	1382	2	AR175097	AR175097 Sequence
7	1145	70.7	1382	2	CS079301	CS079301 Sequence
8	1145	70.7	1382	2	AX032545	AX032545 Sequence
9	1145	70.7	1385	2	AR033962	AR033962 Sequence
10	1145	70.7	1385	2	AR175095	AR175095 Sequence
11	1145	70.7	1385	2	CS079299	CS079299 Sequence
12	1145	70.7	1385	2	AX032543	AX032543 Sequence
13	1145	70.7	1508	2	AR033963	AR033963 Sequence
14	1145	70.7	1508	2	AR152030	AR152030 Sequence
15	1145	70.7	1508	2	AR175096	AR175096 Sequence
16	1145	70.7	1508	2	CS079300	CS079300 Sequence
17	1145	70.7	1508	2	AX032544	AX032544 Sequence
18	1136	70.1	1508	2	BD138632	BD138632 Soluble M
19	1131.5	69.8	1251	6	BC010322	BC010322 Mus muscu
20	1102.5	68.1	798	6	MUSMHIABQ	M13537 Mouse MHC c
21	1096.5	67.7	798	2	CQ777552	CQ777552 Sequence
22	1054.5	65.1	888	6	MUSMHABNO	M15848 Mouse MHC c
23	1054.5	65.1	1204	6	BC008168	BC008168 Mus muscu
24	1050.5	64.8	792	6	AY452202	AY452202 Mus muscu
25	1042.5	64.4	777	6	AF065913	AF065913 Mus muscu
26	1042.5	64.4	792	6	AF293060	AF293060 Mus muscu
27	1042.5	64.4	792	6	MUSMHIH2	M66213 Mouse MHC c
28	1042.5	64.4	1162	6	BC057998	BC057998 Mus muscu
29	1041.5	64.3	792	6	MUSMHIABS	M13540 Mouse MHC c
30	1036.5	64.0	792	6	AF119251	AF119251 Mus muscu
31	1036.5	64.0	792	6	AF119252	AF119252 Mus muscu
32	1033.5	63.8	750	6	AF065912	AF065912 Mus muscu
33	1030.5	63.6	1078	6	AF293061	AF293061 Mus muscu
34	1028.5	63.5	792	6	MUSMHIABK	M13538 Mouse MHC c
35	1016.5	62.7	792	6	MUSMHIABU	M13539 Mouse MHC c
36	998.5	61.6	1070	6	AF015280	AF015280 Mus muscu
37	993.5	61.3	760	6	MUSMHIABF	M13541 Mouse MHC c
38	979.5	60.5	702	2	AR106257	AR106257 Sequence
39	979.5	60.5	702	2	AR229609	AR229609 Sequence
40	979.5	60.5	702	2	AR363024	AR363024 Sequence
41	972	60.0	575	6	AY303785	AY303785 Mus muscu
42	972	60.0	578	6	AY303784	AY303784 Mus muscu
43	972	60.0	1243	2	AX490802	AX490802 Sequence
44	964.5	59.5	792	6	AY626181	AY626181 Rattus no
45	964.5	59.5	792	6	AY626184	AY626184 Rattus no

ALIGNMENTS

RESULT 1
AX081281
LOCUS AX081281 921 bp DNA linear PAT 27-FEB-2001
DEFINITION Sequence 2 from Patent WO0109194.
ACCESSION AX081281
VERSION AX081281.1 GI:13170131
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Glaichenhaus,N. and Malherbe,L.
TITLE Recombinant proteins and molecular complexes derived therefrom, analogous to molecules involved in immune responses
JOURNAL Patent: WO 0109194-A 2 08-FEB-2001;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
FEATURES Location/Qualifiers
source 1. .921
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Ligation de fragments d'ADNc"
CDS 1. .921
/note="unnamed protein product"
/codon_start=1
/transl_table=11
/protein_id="CAC33123.1"

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                     /db_xref="GI:13170132"
                     /translation="MALQIPSLLLSAAVVVLMVLSSPGTEGGNSICFSPSLEHPIVVS
                     GSWDGGGGSLVPRGSGGGGSERHFVVQFKGECYYTNGTQRIRLVTRYIYNREEYVRYD
                     SDVGEYRAVTELGRPDAEYWNSQPEILERTRAEVDTACRHNYEGPETSTSLRRLEQPN
                     VAISLSRTEALNHHNTLVCSVTDFYPAKIKVRWFRNGQEETVGVSSTQLIRNGDWTFQ
                     VLVMLEMTPHQGEVYTCHVEHPSLKSPITVEWRAQSESARSKGGGGSTTAPSAQLKKK
                     LQALKKKNAQLKWKLQALKKKLAQHHHHHH"
ORIGIN

Alignment Scores:
Pred. No.:              8.59e-161       Length:         921
Score:                  1620.00         Matches:        306
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     2               Gaps:           0

US-10-048-116B-6 (1-306) x AX081281 (1-921)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 60

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 180

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 240

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 300

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 360

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 420

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 480

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 540

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 600

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 660

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 720

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCCGAGTCTGCCCGGAGCAAG 780

Qy        261 GlyGlyGlyGlySerThrThrAlaProSerAlaGlnLeuLysLysLysLeuGlnAlaLeu 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGAGGTGGAGGATCCACTACAGCTCCATCAGCTCAGTTGAAAAAGAAATTGCAAGCACTG 840

Qy        281 LysLysLysAsnAlaGlnLeuLysTrpLysLeuGlnAlaLeuLysLysLysLeuAlaGln 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAAAAAGAACGCTCAGCTGAAGTGGAAACTTCAAGCCCTCAAGAAGAAACTCGCCCAG 900

Qy        301 HisHisHisHisHisHis 306
              ||||||||||||||||||
Db        901 CATCATCATCATCATCAT 918

RESULT 2
AR047947
LOCUS       AR047947                 893 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 25 from patent US 5820866.
ACCESSION   AR047947
VERSION     AR047947.1  GI:5970290
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 893)
  AUTHORS   Kappler,J.W. and Marrack,P.
  TITLE     Product and process for T cell regulation
  JOURNAL   Patent: US 5820866-A 25 13-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .893
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              2.4e-122        Length:         893
Score:                  1255.50         Matches:        242
Percent Similarity:     95.4%           Conservative:   6
Best Local Similarity:  93.1%           Mismatches:     7
Query Match:            77.5%           Indels:         5
DB:                     2               Gaps:           1

US-10-048-116B-6 (1-306) x AR047947 (1-893)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 120

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              ||||||||||||||||||||||||||||||:::      :::   :::
Db        121 AGCAGCCCCGGGACTGAGGGCGGAAACTCCGTACATGCTGCCCATGCT------------ 168

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
                    ::::::   :::      ||||||||||||||||||||||||||||||||||||||
Db        169 ---GAGATCAATGAGGCTGGCAGAGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 225

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 285

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 345

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 405

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 465

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 525

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
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Db        526 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 585

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200

Db        586 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 645

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220

Db        646 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 705

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240

Db        706 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 765

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260

Db        766 AGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCCGAGTCTGCCCGGAGCAAG 825
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RESULT 3
AR199666
LOCUS AR199666 4724 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 8 from patent US 6355479.
ACCESSION AR199666
VERSION AR199666.1 GI:20249740
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 4724)
AUTHORS Webb,S.R., Winqvist,O., Karlsson,L., Jackson,M.R. and Peterson,P.A.
TITLE MHC class II antigen-presenting systems and methods for activating CD4+ T cells
JOURNAL Patent: US 6355479-A 8 12-MAR-2002;
FEATURES Location/Qualifiers
source 1. .4724
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Alignment Scores:

Pred. No.:	1.64e-111	Length:	4724
Score:	1161.50	Matches:	228
Percent Similarity:	85.8%	Conservative:	1
Best Local Similarity:	85.4%	Mismatches:	1
Query Match:	71.7%	Indels:	37
DB:	2	Gaps:	2

US-10-048-116B-6 (1-306) x AR199666 (1-4724)

```
Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20

Db        451 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 510

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40

Db        511 AGCAGCCCAGGGACTGAGGGCGGAAAC------------------------------ 537

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60

Db        537 ------------------------------------------------------------ 537

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80

Db        538 ---------TCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 588

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100

Db        589 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 648

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120

Db        649 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 708

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140

Db        709 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 768

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160

Db        769 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 828

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180

Db        829 ATCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 888

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200

Db        889 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 948

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220

Db        949 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 1008

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240

Db       1009 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 1068

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260

Db       1069 AGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCCGAGTCTGCCCGGAGCAAG 1128

Qy        261 ---------GlyGlyGlyGly 264

Db       1129 ATGTTGAGCGGCATCGGGGGC 1149
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RESULT 4
AR047957
LOCUS AR047957 1013 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 38 from patent US 5820866.
ACCESSION AR047957
VERSION AR047957.1 GI:5970300
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1013)
AUTHORS Kappler,J.W. and Marrack,P.
TITLE Product and process for T cell regulation
JOURNAL Patent: US 5820866-A 38 13-OCT-1998;
FEATURES Location/Qualifiers
source 1. .1013
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Alignment Scores:

Pred. No.:	1.44e-111	Length:	1013
Score:	1154.00	Matches:	231
Percent Similarity:	86.8%	Conservative:	5
Best Local Similarity:	84.9%	Mismatches:	22
Query Match:	71.2%	Indels:	14
DB:	2	Gaps:	4

US-10-048-116B-6 (1-306) x AR047957 (1-1013)

```
Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20

Db         63 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCGGCTGCTGTGGTGGTGCTGATGGTGCTG 122

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40

Db        123 AGCAGCCCAGGGACTGAGGGCGGAGACTCC---------GAAGCTAGCTTTGAGGCTCAG 173

Qy         41 ---------------IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuVal 55
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Db        174 GGTGCACTGGCCAACATTGCTGTCGACAAGGCTGGAGGTGGTGGATCCGGTGGA------ 227

Qy         56 ProArgGlySerGlyGlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGlu 75
              ||||||||||||||||||||||||||||||||||||||||||||||   ||||||   ||||||
Db        228 ---GGGGGAAGTGGAGGTGGAGGGTCTGAAAGGCATTTCGTGTACCAGTTCATGGGCGAG 284

Qy         76 CysTyrTyrThrAsnGlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArg 95
              ||||||:::||||||||||||||||||||||||||||   ||||||||||||||||||||||
Db        285 TGCTACTTCACCAACGGGACGCAGCGCATACGATATGTGACCAGATACATCTACAACCGG 344

Qy         96 GluGluTyrValArgTyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGly 115
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||||
Db        345 GAGGAGTACGTGCGCTACGACAGCGACGTGGGCGAGCACCGCGCGGTGACCGAGCTGGGG 404

Qy        116 ArgProAspAlaGluTyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGlu 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 CGGCCAGACGCCGAGTACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAG 464

Qy        136 ValAspThrAlaCysArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArg 155
              |||||||||   ||||||||||||||||||||||||||||||   ||||||||||||||||
Db        465 GTGGACACGGTGTGCAGACACAACTACGAGGGGCCGGAGACCCACACCTCCCTGCGGCGG 524

Qy        156 LeuGluGlnProAsnValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsn 175
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        525 CTTGAACAGCCCAATGTCGTCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAAC 584

Qy        176 ThrLeuValCysSerValThrAspPheTyrProAlaLysIleLysValArgTrpPheArg 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACTCTGGTCTGCTCAGTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCCGG 644

Qy        196 AsnGlyGlnGluGluThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrp 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 AATGGCCAGGAGGAGACGGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGG 704

Qy        216 ThrPheGlnValLeuValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCys 235
              ||||||||||||||||||||||||||||||||||||   :::||||||||||||||||||
Db        705 ACCTTCCAGGTCCTGGTCATGCTGGAGATGACCCCTCGGCGGGGAGAGGTCTACACCTGT 764

Qy        236 HisValGluHisProSerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGlu 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        765 CACGTGGAGCATCCCAGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCTGAG 824

Qy        256 SerAlaArgSerLys---------GlyGlyGlyGly 264
              ||||||   ||||||         |||   ||||||
Db        825 TCTGCCTGGAGCAAGATGTTGAGCGGCATCGGGGGC 860

RESULT 5
AR033964
LOCUS       AR033964               1382 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 123 from patent US 5869270.
ACCESSION   AR033964
VERSION     AR033964.1  GI:5949569
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1382)  .
  AUTHORS   Rhode,P.R., Jiao,J.-A., Burkhardt,M. and Wong,H.C.
  TITLE     Single chain MHC complexes and uses thereof
  JOURNAL   Patent: US 5869270-A 123 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .1382
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.91e-110      Length:         1382
Score:                  1145.00        Matches:        227
Percent Similarity:     87.2%          Conservative:   4
Best Local Similarity:  85.7%          Mismatches:     24
Query Match:            70.7%          Indels:         10
DB:                     2              Gaps:           3
```

```
US-10-048-116B-6 (1-306) x AR033964 (1-1382)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              |||||||||   |||        :::            :::            |||
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              |||      :::|||          ||||||||||||||                  |||
Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC--------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
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Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
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Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              ||||||||||||||||||||||||||||||||||||||||||||||         :::
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy        261 GlyGlyGlyGlySer 265
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Db        756 GGCGGTGGTGGTTCC 770

RESULT 6
AR175097
LOCUS       AR175097               1382 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 123 from patent US 6309645.
ACCESSION   AR175097
VERSION     AR175097.1  GI:17916396
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1382)
  AUTHORS   Rhode,P.R., Jiao,J.-A., Burkhardt,M. and Wong,H.C.
  TITLE     MHC molecules and uses thereof
  JOURNAL   Patent: US 6309645-A 123 30-OCT-2001;
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FEATURES             Location/Qualifiers
     source          1. .1382
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                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:                1.91e-110      Length:          1382
Score:                    1145.00        Matches:         227
Percent Similarity:       87.2%          Conservative:    4
Best Local Similarity:    85.7%          Mismatches:      24
Query Match:              70.7%          Indels:          10
DB:                       2              Gaps:            3

US-10-048-116B-6 (1-306) x AR175097 (1-1382)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              |||||||||   |||         :::         :::         |||
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              |||      :::|||       |||||||||||||||                  |||
Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC--------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
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Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
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Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
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Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
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Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
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Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              ||||||||||||||||||||||||||||||||  :::
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy        261 GlyGlyGlyGlySer 265
              |||||||||||||||
Db        756 GGCGGTGGTGGTTCC 770

RESULT 7

CS079301
LOCUS       CS079301                1382 bp    DNA     linear   PAT 06-MAY-2005
DEFINITION  Sequence 123 from Patent EP1526141.
ACCESSION   CS079301
VERSION     CS079301.1  GI:63093743
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1
  AUTHORS   Rhode,P.R., Jiao,J.A., Burkhardt,M. and Wong,H.C.
  TITLE     MHC complexes and uses thereof
  JOURNAL   Patent: EP 1526141-A 123 27-APR-2005;
            Altor BioScience Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .1382
                     /organism="unidentified"
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                     /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:                1.91e-110      Length:          1382
Score:                    1145.00        Matches:         227
Percent Similarity:       87.2%          Conservative:    4
Best Local Similarity:    85.7%          Mismatches:      24
Query Match:              70.7%          Indels:          10
DB:                       2              Gaps:            3

US-10-048-116B-6 (1-306) x CS079301 (1-1382)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              |||||||||   |||         :::         :::         |||
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              |||      :::|||       |||||||||||||||                  |||
Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC--------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
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Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
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Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
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Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
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Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              |||||||||||||||||||||||||||||||||||||          :::
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy        261 GlyGlyGlyGlySer 265
              |||||||||||||||
Db        756 GGCGGTGGTGGTTCC 770

RESULT 8
AX032545
LOCUS       AX032545               1382 bp    DNA     linear   PAT 20-SEP-2000
DEFINITION  Sequence 123 from Patent EP0997477.
ACCESSION   AX032545
VERSION     AX032545.1  GI:10279486
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1
  AUTHORS   Chavaillaz,P.A., Edwards,A.C., Grammer,S., Jiao,J.A., Rhode,P.R.,
            Weidanz,J.A. and Wong,H.C.
  TITLE     Mhc complexes and uses thereof
  JOURNAL   Patent: EP 0997477-A 123 03-MAY-2000;
            SUNOL MOLECULAR CORP (US)
FEATURES             Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.:              1.91e-110      Length:         1382
Score:                  1145.00        Matches:        227
Percent Similarity:     87.2%          Conservative:   4
Best Local Similarity:  85.7%          Mismatches:     24
Query Match:            70.7%          Indels:         10
DB:                     2              Gaps:           3

US-10-048-116B-6 (1-306) x AX032545 (1-1382)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
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Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              |||||||||   |||         :::           :::         |||
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              |||      :::|||          ||||||||||||||                 |||
Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC--------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
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Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
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Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
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Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
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Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
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Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy        261 GlyGlyGlyGlySer 265
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Db        756 GGCGGTGGTGGTTCC 770

RESULT 9
AR033962
LOCUS       AR033962               1385 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 121 from patent US 5869270.
ACCESSION   AR033962
VERSION     AR033962.1  GI:5949567
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1385)
  AUTHORS   Rhode,P.R., Jiao,J.-A., Burkhardt,M. and Wong,H.C.
  TITLE     Single chain MHC complexes and uses thereof
  JOURNAL   Patent: US 5869270-A 121 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .1385
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.91e-110      Length:         1385
Score:                  1145.00        Matches:        227
Percent Similarity:     87.2%          Conservative:   4
Best Local Similarity:  85.7%          Mismatches:     24
Query Match:            70.7%          Indels:         10
DB:                     2              Gaps:           3

US-10-048-116B-6 (1-306) x AR033962 (1-1385)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
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Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              |||||||||   |||         :::           :::         |||
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              |||      :::|||          ||||||||||||||                 |||
Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC--------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
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Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100

Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120

Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140

Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160

Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180

Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200

Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220

Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240

Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260

Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy        261 GlyGlyGlyGlySer 265

Db        756 GGCGGTGGTGGTTCC 770
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RESULT 10
AR175095
LOCUS       AR175095               1385 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 121 from patent US 6309645.
ACCESSION   AR175095
VERSION     AR175095.1  GI:17916394
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1385)
  AUTHORS   Rhode,P.R., Jiao,J.-A., Burkhardt,M. and Wong,H.C.
  TITLE     MHC molecules and uses thereof
  JOURNAL   Patent: US 6309645-A 121 30-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .1385
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.91e-110       Length:         1385
Score:                  1145.00         Matches:        227
Percent Similarity:     87.2%           Conservative:   4
Best Local Similarity:  85.7%           Mismatches:     24
Query Match:            70.7%           Indels:         10
DB:                     2               Gaps:           3

US-10-048-116B-6 (1-306) x AR175095 (1-1385)
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Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20

Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40

Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60

Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC--------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80

Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100

Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120

Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140

Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160

Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180

Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200

Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220

Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240

Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260

Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy        261 GlyGlyGlyGlySer 265

Db        756 GGCGGTGGTGGTTCC 770
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RESULT 11
CS079299
LOCUS       CS079299               1385 bp    DNA     linear   PAT 06-MAY-2005
DEFINITION  Sequence 121 from Patent EP1526141.
ACCESSION   CS079299
VERSION     CS079299.1  GI:63093741
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1
  AUTHORS   Rhode,P.R., Jiao,J.A., Burkhardt,M. and Wong,H.C.
  TITLE     MHC complexes and uses thereof
  JOURNAL   Patent: EP 1526141-A 121 27-APR-2005;
            Altor BioScience Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .1385
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                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:              1.91e-110      Length:         1385
Score:                  1145.00        Matches:        227
Percent Similarity:     87.2%          Conservative:   4
Best Local Similarity:  85.7%          Mismatches:     24
Query Match:            70.7%          Indels:         10
DB:                     2              Gaps:           3

US-10-048-116B-6 (1-306) x CS079299 (1-1385)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              |||||||||   |||        :::          :::          |||
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              |||      :::|||          ||||||||||||||                  |||
Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC--------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              ||||||||||||||||||||||||||||||||  :::
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy        261 GlyGlyGlyGlySer 265
              |||||||||||||||
Db        756 GGCGGTGGTGGTTCC 770

RESULT 12
AX032543
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LOCUS       AX032543               1385 bp    DNA     linear   PAT 20-SEP-2000
DEFINITION  Sequence 121 from Patent EP0997477.
ACCESSION   AX032543
VERSION     AX032543.1  GI:10279484
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1
  AUTHORS   Chavaillaz,P.A., Edwards,A.C., Grammer,S., Jiao,J.A., Rhode,P.R.,
            Weidanz,J.A. and Wong,H.C.
  TITLE     Mhc complexes and uses thereof
  JOURNAL   Patent: EP 0997477-A 121 03-MAY-2000;
            SUNOL MOLECULAR CORP (US)
FEATURES             Location/Qualifiers
     source          1. .1385
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:              1.91e-110      Length:         1385
Score:                  1145.00        Matches:        227
Percent Similarity:     87.2%          Conservative:   4
Best Local Similarity:  85.7%          Mismatches:     24
Query Match:            70.7%          Indels:         10
DB:                     2              Gaps:           3

US-10-048-116B-6 (1-306) x AX032543 (1-1385)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              |||||||||   |||        :::          :::          |||
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              |||      :::|||          ||||||||||||||                  |||
Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC--------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              ||||||||||||||||||||||||||||||||          :::
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy        261 GlyGlyGlyGlySer 265
              |||||||||||||||
Db        756 GGCGGTGGTGGTTCC 770

RESULT 13
AR033963
LOCUS       AR033963               1508 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 122 from patent US 5869270.
ACCESSION   AR033963
VERSION     AR033963.1  GI:5949568
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1508)
  AUTHORS   Rhode,P.R., Jiao,J.-A., Burkhardt,M. and Wong,H.C.
  TITLE     Single chain MHC complexes and uses thereof
  JOURNAL   Patent: US 5869270-A 122 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .1508
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:                2.13e-110      Length:          1508
Score:                    1145.00        Matches:         227
Percent Similarity:       87.2%          Conservative:    4
Best Local Similarity:    85.7%          Mismatches:      24
Query Match:              70.7%          Indels:          10
DB:                       2              Gaps:            3

US-10-048-116B-6 (1-306) x AR033963 (1-1508)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              |||||||||   |||         :::           :::         |||
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              |||      :::|||         ||||||||||||||                 |||
Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC---------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              ||||||||||||||||||||||||||||||||          :::
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy        261 GlyGlyGlyGlySer 265
              |||||||||||||||
Db        756 GGCGGTGGTGGTTCC 770

RESULT 14
AR152030
LOCUS       AR152030               1508 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 24 from patent US 6232445.
ACCESSION   AR152030
VERSION     AR152030.1  GI:15118080
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1508)
  AUTHORS   Rhode,P.R., Acevedo,J., Burkhardt,M., Jiao,J.-a. and Wong,H.C.
  TITLE     Soluble MHC complexes and methods of use thereof
  JOURNAL   Patent: US 6232445-A 24 15-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .1508
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:                2.13e-110      Length:          1508
Score:                    1145.00        Matches:         227
Percent Similarity:       87.2%          Conservative:    4
Best Local Similarity:    85.7%          Mismatches:      24
Query Match:              70.7%          Indels:          10
DB:                       2              Gaps:            3

US-10-048-116B-6 (1-306) x AR152030 (1-1508)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              |||||||||   |||         :::           :::         |||
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              |||      :::|||         ||||||||||||||                 |||
Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC---------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224
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Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              ||||||||||||||||||||||||||||||||              :::
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy        261 GlyGlyGlyGlySer 265
              |||||||||||||||
Db        756 GGCGGTGGTGGTTCC 770
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RESULT 15
AR175096
LOCUS       AR175096               1508 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 122 from patent US 6309645.
ACCESSION   AR175096
VERSION     AR175096.1  GI:17916395
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1508)
  AUTHORS   Rhode,P.R., Jiao,J.-A., Burkhardt,M. and Wong,H.C.
  TITLE     MHC molecules and uses thereof
  JOURNAL   Patent: US 6309645-A 122 30-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .1508
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              2.13e-110      Length:         1508
Score:                  1145.00        Matches:        227
Percent Similarity:     87.2%          Conservative:   4
Best Local Similarity:  85.7%          Mismatches:     24
Query Match:            70.7%          Indels:         10
DB:                     2              Gaps:           3

US-10-048-116B-6 (1-306) x AR175096 (1-1508)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65
```

```
Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              |||||||||   |||          :::          :::          |||
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              |||      :::|||          |||||||||||||||                  |||
Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC---------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              ||||||||||||||||||||||||||||||||              :::
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy        261 GlyGlyGlyGlySer 265
              |||||||||||||||
Db        756 GGCGGTGGTGGTTCC 770
```

```
Search completed: June 30, 2006, 05:17:54
Job time : 6500.66 secs
```

GenCore version 5.1.9

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 30, 2006, 01:23:04 ; Search time 532.723 Seconds
(without alignments)
6007.369 Million cell updates/sec

Title: US-10-048-116B-6
Perfect score: 1620
Sequence: 1 MALQIPSLLLSAAVVVLMVL.....LKWKLQALKKKLAQHHHHHH 306

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10048116/runat_29062006_093309_10102/app_query.fasta_1
-DB=N_Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss05p
-USER=US10048116_@CGN_1_1_1423_@runat_29062006_093309_10102 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1620	100.0	921	5	AAF55099	Aaf55099 DNA encod
2	1255.5	77.5	893	2	AAT04262	Aat04262 Hybrid IA
3	1235	76.2	945	12	ADQ31225	Adq31225 I-Ab(beta
4	1219	75.2	915	12	ADQ31228	Adq31228 I-Ab(beta
5	1161.5	71.7	4724	2	AAV12068	Aav12068 Murine IA
6	1151	71.0	1013	2	AAT04269	Aat04269 Hybrid IA
7	1145	70.7	1382	2	AAT17588	Aat17588 Vector SC
8	1145	70.7	1382	2	AAT86989	Aat86989 SCE1 sing
9	1145	70.7	1382	8	ACA60744	Aca60744 Mouse MHC
10	1145	70.7	1385	2	AAT17586	Aat17586 Vector SS
11	1145	70.7	1385	2	AAT86987	Aat86987 SSC1 sing
12	1145	70.7	1385	8	ACA60742	Aca60742 Mouse MHC
13	1145	70.7	1508	2	AAT17587	Aat17587 Vector SC
14	1145	70.7	1508	2	AAT86988	Aat86988 SCT1 sing
15	1145	70.7	1508	2	AAX89069	Aax89069 Single ch
16	1145	70.7	1508	8	ACA60743	Aca60743 Mouse MHC
17	1096.5	67.7	798	12	ADJ75986	Adj75986 Marker ge
18	1096.5	67.7	798	14	ADX26090	Adx26090 Novel cel
19	1093	67.5	1085	4	ABI99040	Abi99040 Murine pC
20	1049.5	64.8	1698	4	ABI99038	Abi99038 Murine pC
21	1044.5	64.5	1662	4	ABI99039	Abi99039 Murine pC
22	979.5	60.5	702	2	AAQ03170	Aaq03170 Sequence
23	979.5	60.5	702	2	AAT06286	Aat06286 I-Ab-beta
24	979.5	60.5	702	2	AAQ56920	Aaq56920 Mouse I-A
25	972	60.0	1243	6	ABN84048	Abn84048 Single ch
26	963.5	59.5	702	2	AAQ35055	Aaq35055 IAB beta
27	957	59.1	1686	4	ABI99031	Abi99031 MBP 1-14
28	957	59.1	1701	4	ABI99028	Abi99028 IAS MBP 1
29	957	59.1	2059	4	ABI99032	Abi99032 MBP 1-14
30	957	59.1	2346	4	ABI99027	Abi99027 IAS MBP 1
31	952	58.8	1707	4	ABI99030	Abi99030 IAS MBP 9
32	949	58.6	1680	4	ABI99021	Abi99021 I-As MBP.
33	949	58.6	2053	4	ABI99029	Abi99029 IAS MBP 9
34	949	58.6	2343	4	ABI99033	Abi99033 MBP 90-10
35	871	53.8	1344	2	AAT60705	Aat60705 cDNA enco
36	854.5	52.7	1323	2	AAT60700	Aat60700 cDNA enco
37	844.5	52.1	861	14	AEC64482	Aec64482 DRB1-biot
38	839.5	51.8	1192	10	AAD63150	Aad63150 Human maj
39	839.5	51.8	1192	10	AAD62751	Aad62751 Human maj
40	839.5	51.8	1192	11	ADP88246	Adp88246 Lung canc
41	839.5	51.8	1192	13	ADR24869	Adr24869 Breast ca
42	833.5	51.5	941	12	ADO40822	Ado40822 DNA encod
43	829	51.2	562	6	ABK63510	Abk63510 Rat seque
44	829	51.2	562	10	ADB57995	Adb57995 Toxicity-
45	829	51.2	562	10	ABT41775	Abt41775 Toxicity

ALIGNMENTS

RESULT 1
AAF55099
ID AAF55099 standard; DNA; 921 BP.
XX
AC AAF55099;
XX
DT 15-MAY-2001 (first entry)
XX
DE DNA encoding a fusion protein comprising a beta chain of MHC.
XX
KW Recombinant protein; alpha chain; beta chain; MHC; immunoglobulin;
KW major histocompatibility complex; Fc region; antigen; T lymphocyte;
KW immunostimulant; vaccine; infection; tumour; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1. .921
FT /*tag= a
XX
PN WO200109194-A1.
XX
PD 08-FEB-2001.
XX
PF 28-JUL-2000; 2000WO-FR002193.
XX
PR 29-JUL-1999; 99FR-00009862.

```
XX
PA   (CNRS ) CNRS CENT NAT RECH SCI.
XX
PI   Glaichenhaus N,  Malherbe L;
XX
DR   WPI; 2001-182944/18.
DR   P-PSDB; AAB67481.
XX
PT   New soluble recombinant protein, useful e.g. as immunostimulant,
PT   comprises dimeric major histocompatibility complex molecule fused to
PT   immunoglobulin Fc region.
XX
PS   Example 1; Page 34-35; 43pp; French.
XX
CC   The specification describes soluble recombinant proteins that comprise at
CC   least a dimer formed from the alpha and beta-chains of MHC (major
CC   histocompatibility complex) Class I and II molecules in which at least
CC   one chain has, attached to its C-terminus, at least part of the Fc region
CC   of an immunoglobulin. The recombinant proteins, when linked to an
CC   antigenic peptide, are used to count and/or purify antigen-reactive T
CC   lymphocytes and to characterize their phenotype, e.g. in preclinical
CC   evaluation of vaccines. They are also used as immunostimulants,
CC   particularly for vaccine development (against infections and tumours), to
CC   count and determine phenotype of autoreactive T cells in subjects with,
CC   or at risk of developing, autoimmune diseases, e.g. for staging or
CC   evaluating treatments, and (to purify and/or enrich Ag-reactive T cells
CC   from cell cultures or patient samples, for use in subsequent curative or
CC   preventative cellular therapy. The present sequence encodes a recombinant
CC   protein of the invention, comprising a beta chain of MHC molecules
XX
SQ   Sequence 921 BP; 214 A; 265 C; 286 G; 156 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              6.68e-144       Length:         921
Score:                  1620.00         Matches:        306
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     5               Gaps:           0

US-10-048-116B-6 (1-306) x AAF55099 (1-921)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 60

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 180

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 240

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 300

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 360

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 420

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 480

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 540

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 600

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 660

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 720

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCCGAGTCTGCCCGGAGCAAG 780

Qy        261 GlyGlyGlyGlySerThrThrAlaProSerAlaGlnLeuLysLysLysLeuGlnAlaLeu 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGAGGTGGAGGATCCACTACAGCTCCATCAGCTCAGTTGAAAAAGAAATTGCAAGCACTG 840

Qy        281 LysLysLysAsnAlaGlnLeuLysTrpLysLeuGlnAlaLeuLysLysLysLeuAlaGln 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAAAAAGAACGCTCAGCTGAAGTGGAAACTTCAAGCCCTCAAGAAGAAACTCGCCCAG 900

Qy        301 HisHisHisHisHisHis 306
              ||||||||||||||||||
Db        901 CATCATCATCATCATCAT 918

RESULT 2
AAT04262
ID   AAT04262 standard; DNA; 893 BP.
XX
AC   AAT04262;
XX
DT   16-APR-1996  (first entry)
XX
DE   Hybrid IA beta chain gene.
XX
KW   Polymerase chain reaction; PCR; primer; amplify;
KW   major histocompatability complex; MHC; T-cell receptor; TCR;
KW   autoimmune disease; immunodeficiency disease; immune response;
KW   immunoproliferation disease; graft-host rejection; therapy; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   primer_bind     1. .16
FT                   /*tag=  a
FT                   /note= "probable primer binding site (primer #233)"
FT   primer_bind     complement(45. .74)
FT                   /*tag=  b
FT                   /note= "binding site for primer #261 (see AAT04260)"
FT   CDS             61. .828
FT                   /*tag=  c
FT                   /product= "hybrid IA beta chain"
FT   sig_peptide     61. .141
FT                   /*tag=  d
FT                   /note= "leader region"
FT   primer_bind     complement(119. .172)
FT                   /*tag=  e
FT                   /note= "binding site for primer #331 (see AAT04261)"
FT   primer_bind     complement(158. .212)
FT                   /*tag=  f
FT                   /note= "primer #332 binding site"
FT   primer_bind     complement(199. .250)
FT                   /*tag=  g
FT                   /note= "primer #333 (see AAT04263) binding site"
FT   misc_feature    371. .389
```

```
FT                   /*tag=  h
FT                   /note= "probable primer binding site (primer #270)"
FT   mat_peptide     511. .825
FT                   /*tag=  i
FT                   /product= "IA beta chain beta 2 region"
FT   primer_bind     521. .550
FT                   /*tag=  j
FT                   /note= "probable primer binding site (primer #271)"
FT   primer_bind     532. .554
FT                   /*tag=  k
FT                   /note= "probable primer binding site (primer #272)"
FT   primer_bind     808. .836
FT                   /*tag=  l
FT                   /note= "probable primer binding site (primer #259)"
FT   primer_bind     877. .893
FT                   /*tag=  m
FT                   /note= "probable primer binding site (primer #232)"
XX
PN   WO9523814-A1.
XX
PD   08-SEP-1995.
XX
PF   03-MAR-1995;   95WO-US002689.
XX
PR   04-MAR-1994;   94US-00207481.
XX
PA   (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
XX
PI   Kappler JW,  Marrack P;
XX
DR   WPI; 1995-320543/41.
DR   P-PSDB; AAR82533.
XX
PT   Peptide-MHC complex comprising antigenic peptide, linker and MHC segment
PT   - useful as reagents for the treatment of diseases including auto-immune
PT   diseases, immuno-stimulatory diseases or graft-host rejection.
XX
PS   Example 1; Page 53; 94pp; English.
XX
CC   This sequence represents a hybrid IA beta chain gene, containing the
CC   chicken ovalbumin peptide (cOVA). This sequence was used in the
CC   construction of a hybrid IA alpha beta dimer. The encoded protein (pIAd-
CC   OVA) was found to be more stable than the IA alpha beta dimer. The
CC   stability was decreased by the addition of a MHC groove specific binding
CC   peptide (e.g. see AAR82527, AAR82528 and AAR82531), compared to an
CC   increase seen on the addition of a MHC binding peptide to IE k/d-MCC.
CC   These complexes may be used to regulate an immune response. The complexes
CC   are capable of being recognised by a TCR alone or in combination with
CC   additional MHC proteins. These complexes are useful for therapeutic
CC   purposes and experimental purposes. They can also be used as reagents for
CC   the treatment of diseases including autoimmune diseases, immunodeficiency
CC   diseases, immunoproliferation diseases, and graft-host rejection
XX
SQ   Sequence 893 BP; 204 A; 239 C; 275 G; 175 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.39e-109      Length:         893
Score:                  1255.50        Matches:        242
Percent Similarity:     95.4%          Conservative:   6
Best Local Similarity:  93.1%          Mismatches:     7
Query Match:            77.5%          Indels:         5
DB:                     2              Gaps:           1

US-10-048-116B-6 (1-306) x AAT04262 (1-893)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 120

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              ||||||||||||||||||||||||||||:::      :::   :::
Db        121 AGCAGCCCCGGGACTGAGGGCGGAAACTCCGTACATGCTGCCCATGCT---------- 168

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
                          ::::::   :::       ||||||||||||||||||||||||||||||
Db        169 ---GAGATCAATGAGGCTGGCAGAGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 225

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 285

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 345

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 405

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 465

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 525

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        526 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 585

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 645

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 705

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        706 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 765

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        766 AGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCCGAGTCTGCCCGGAGCAAG 825

RESULT 3
ADQ31225
ID   ADQ31225 standard; cDNA; 945 BP.
XX
AC   ADQ31225;
XX
DT   07-OCT-2004  (first entry)
XX
DE   I-Ab(beta)-Cholera toxin B subunit-leucine zipper (LZ)-BirA fusion cDNA.
XX
KW   class II major histocompatibility complex; MHC; CD4+ T-cell detection;
KW   flow cytometry; mucous membrane invasive antigen;
KW   I-Ab(beta)-cholera toxin B subunit-leucine zipper-BirA fusion; CTB; ss;
KW   gene.
XX
OS   Vibrio cholerae.
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .945
FT                   /*tag=  a
FT                   /product= "I-Ab(beta)-Cholera toxin B subunit (CTB)-
FT                   leucine zipper (LZ)-BirA fusion cDNA"
XX
PN   JP2004196789-A.
XX
PD   15-JUL-2004.
XX
PF   03-DEC-2003; 2003JP-00404367.
```

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XX
PR   03-DEC-2002; 2002JP-00351818.
XX
PA   (SENT-) SENTAN KAGAKU GIJUTSU INCUBATION CENT KK.
XX
DR   WPI; 2004-546819/53.
DR   P-PSDB; ADQ31224.
XX
PT   Peptide-Class II major histocompatibility complex (MHC) composite, useful
PT   for detecting antigen specific CD4+ T-cell, comprises antigen peptide
PT   containing epitope of mucous membrane invasive protein, and extracellular
PT   region of MHC.
XX
PS   Example 1; SEQ ID NO 10; 30pp; Japanese.
XX
CC   The invention relates to a novel class II major histocompatibility
CC   complex (MHC) antigenic peptide composite comprising a peptide containing
CC   the T-cell antigenic determinant of a mucous membrane invasive protein
CC   and the extracellular region of a class II MHC molecule or at least part
CC   of the extracellular region of the class II MHC molecule having an amino
CC   acid sequence comprising one or more deletions, substitutions or
CC   additions. The molecule of the invention may be useful for detecting an
CC   antigen-specific CD4+ T-cell by flow cytometry and for presenting a
CC   microorganism-derived mucous membrane invasive protein as an antigen. The
CC   method of the invention enables efficient detection of antigen-specific
CC   activation of CD4+ T-cells in the mucous membrane. The current sequence
CC   is that of the class II major histocompatibility complex-related I-
CC   Ab(alpha)-Cholera toxin B subunit (CTB)-leucine zipper (LZ)-BirA fusion
CC   cDNA of the invention.
XX
SQ   Sequence 945 BP; 230 A; 256 C; 294 G; 165 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.27e-107      Length:          945
Score:                  1235.00        Matches:         244
Percent Similarity:     84.9%          Conservative:    14
Best Local Similarity:  80.3%          Mismatches:      42
Query Match:            76.2%          Indels:          4
DB:                     12             Gaps:            3

US-10-048-116B-6 (1-306) x ADQ31225 (1-945)

Qy          1 MetAlaLeuGlnIlePro---SerLeuLeuLeuSerAlaAlaValValValLeuMetVal 19
              :::   |||::::::|||           ::::::        |||   |||||||||
Db          4 GTGTGTCTGAAGCTCCCTGGAGGTTCCTACATGGCAAAGCTGACAGTGACACTGATGGTG 63

Qy         20 LeuSerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHis 39
              ||||||||||||           |||:::|||      ::::::           |||
Db         64 CTGAGCTCCCCACTGGCTTTGGCTGGAGACTCCTGCGTGTGGAACAATAAGACGCCGCAC 123

Qy         40 ProIleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySer 59
                |||                ::::||||||||||||||||                ||||||
Db        124 GCGATCGCGGCCATCAGCATGGCGAACGGAGGTGGTGGGTCC---GGTGGAGGGGGAAGT 180

Qy         60 GlyGlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThr 79
              ||||||||||||||||||||||||||||||   ||||||   ||||||||||||:::|||
Db        181 GGAGGTGGAGGGTCTGAAAGGCATTTCGTGTACCAGTTCATGGGCGAGTGCTACTTCACC 240

Qy         80 AsnGlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrVal 99
              ||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db        241 AACGGGACGCAGCGCATACGATATGTGACCAGATACATCTACAACCGGGAGGAGTACGTG 300

Qy        100 ArgTyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAla 119
              ||||||||||||||||||||||:::||||||||||||||||||||||||||||||||||
Db        301 CGCTACGACAGCGACGTGGGCGAGCACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCC 360

Qy        120 GluTyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAla 139
              ||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        361 GAGTACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGCTGGACACGGTG 420

Qy        140 CysArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnPro 159
              ||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        421 TGCAGACACAACTACGAGGGGCCGGAGACCCACACCTCCCTGCGGCGGCTTGAACAGCCC 480

Qy        160 AsnValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCys 179
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AATGTCGTCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGC 540

Qy        180 SerValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGlu 199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCAGTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCCGGAATGGCCAGGAG 600

Qy        200 GluThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnVal 219
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GAGACGGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTC 660

Qy        220 LeuValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHis 239
              ||||||||||||||||||||||||   :::||||||||||||||||||||||||||||
Db        661 CTGGTCATGCTGGAGATGACCCCTCGGCGGGGAGAGGTCTACACCTGTCACGTGGAGCAT 720

Qy        240 ProSerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSer 259
              ||||||||||||||||||||||||||||||||||||||||||||||||   :::
Db        721 CCCAGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCGTCAGCA------GAC 774

Qy        260 LysGlyGlyGlyGlySerThrThrAlaProSerAlaGlnLeuLysLysLysLeuGlnAla 279
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        775 CTGGTTCCGCGCGGATCCACTACAGCTCCATCAGCTCAGTTGAAAAAGAAACTGCAGGCA 834

Qy        280 LeuLysLysLysAsnAlaGlnLeuLysTrpLysLeuGlnAlaLeuLysLysLysLeuAla 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        835 CTTAAGAAAAAGAACGCTCAGCTGAAGTGGAAACTTCAAGCCCTCAAGAAGAAACTCGCC 894

Qy        300 GlnHisHisHis 303
              |||   ||||||
Db        895 CAGCTGCATCAT 906

RESULT 4
ADQ31228
ID   ADQ31228 standard; cDNA; 915 BP.
XX
AC   ADQ31228;
XX
DT   07-OCT-2004  (first entry)
XX
DE   I-Ab(beta)-E. coli heat-labile toxin B subunit-LZ-BirA fusion cDNA.
XX
KW   class II major histocompatibility complex; MHC; CD4+ T-cell detection;
KW   flow cytometry; mucous membrane invasive antigen;
KW   I-Ab(beta)-heat-labile toxin B subunit-leucine zipper-BirA fusion; LTB;
KW   ss; gene.
XX
OS   Escherichia coli.
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .915
FT                   /*tag= a
FT                   /product= "I-Ab(beta)-Escherichia coli heat-labile toxin
FT                   B subunit (LTB)-leucine zipper (LZ)-BirA fusion protein"
XX
PN   JP2004196789-A.
XX
PD   15-JUL-2004.
XX
PF   03-DEC-2003; 2003JP-00404367.
XX
PR   03-DEC-2002; 2002JP-00351818.
XX
PA   (SENT-) SENTAN KAGAKU GIJUTSU INCUBATION CENT KK.
XX
DR   WPI; 2004-546819/53.
DR   P-PSDB; ADQ31227.
XX
PT   Peptide-Class II major histocompatibility complex (MHC) composite, useful
PT   for detecting antigen specific CD4+ T-cell, comprises antigen peptide
PT   containing epitope of mucous membrane invasive protein, and extracellular
```

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PT   region of MHC.
XX
PS   Example 3; SEQ ID NO 13; 30pp; Japanese.
XX
CC   The invention relates to a novel class II major histocompatibility
CC   complex (MHC) antigenic peptide composite comprising a peptide containing
CC   the T-cell antigenic determinant of a mucous membrane invasive protein
CC   and the extracellular region of a class II MHC molecule or at least part
CC   of the extracellular region of the class II MHC molecule having an amino
CC   acid sequence comprising one or more deletions, substitutions or
CC   additions. The molecule of the invention may be useful for detecting an
CC   antigen-specific CD4+ T-cell by flow cytometry and for presenting a
CC   microorganism-derived mucous membrane invasive protein as an antigen. The
CC   method of the invention enables efficient detection of antigen-specific
CC   activation of CD4+ T-cells in the mucous membrane. The current sequence
CC   is that of the class II major histocompatibility complex-related I-
CC   Ab(alpha)-Escherichia coli heat-labile toxin B subunit (LTB)-leucine
CC   zipper (LZ)-BirA fusion cDNA of the invention.
XX
SQ   Sequence 915 BP; 228 A; 242 C; 271 G; 174 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                7.14e-106      Length:          915
Score:                    1219.00        Matches:         242
Percent Similarity:       84.9%          Conservative:    16
Best Local Similarity:    79.6%          Mismatches:      32
Query Match:              75.2%          Indels:          14
DB:                       12             Gaps:            5

US-10-048-116B-6 (1-306) x ADQ31228 (1-915)

Qy          1 MetAlaLeuGlnIlePro---SerLeuLeuLeuSerAlaAlaValValValLeuMetVal 19
              :::   |||::::::|||          ::::::         |||   |||||||||
Db          4 GTGTGTCTGAAGCTCCCTGGAGGTTCCTACATGGCAAAGCTGACAGTGACACTGATGGTG 63

Qy         20 LeuSerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHis 39
              ||||||||||||          |||:::|||
Db         64 CTGAGCTCCCCACTGGCTTTGGCTGGAGACTCC--------------GGTAAAAGAGAA 108

Qy         40 ProIleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySer 59
                 :::::::::      ::::::   ||||||||||||||||||||||||||
Db        109 ATGGTTATCATT------ACATTTAAGGGTGGTGGTGGTTCTTTAGTTCCTAGA------ 156

Qy         60 GlyGlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThr 79
              ||||||||||||||||||||||||   ||||||   ||||||||||||:::|||
Db        157 ------GGTGGTAGTGAAAGGCATTTCGTGTACCAGTTCATGGGCGAGTGCTACTTCACC 210

Qy         80 AsnGlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrVal 99
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db        211 AACGGGACGCAGCGCATACGATATGTGACCAGATACATCTACAACCGGGAGGAGTACGTG 270

Qy        100 ArgTyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAla 119
              ||||||||||||||||||||||:::||||||||||||||||||||||||||||||||||
Db        271 CGCTACGACAGCGACGTGGGCGAGCACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCC 330

Qy        120 GluTyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAla 139
              ||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        331 GAGTACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGCTGGACACGGTG 390

Qy        140 CysArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnPro 159
              ||||||||||||||||||||||||||   |||||||||||||||||||||||||||||||
Db        391 TGCAGACACAACTACGAGGGGCCGGAGACCCACACCTCCCTGCGGCGGCTTGAACAGCCC 450

Qy        160 AsnValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCys 179
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 AATGTCGTCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGC 510

Qy        180 SerValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGlu 199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 TCAGTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCCGGAATGGCCAGGAG 570

Qy        200 GluThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnVal 219
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        571 GAGACGGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTC 630

Qy        220 LeuValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHis 239
              ||||||||||||||||||||||||   :::||||||||||||||||||||||||||||||
Db        631 CTGGTCATGCTGGAGATGACCCCTCGGCGGGGAGAGGTCTACACCTGTCACGTGGAGCAT 690

Qy        240 ProSerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSer 259
              ||||||||||||||||||||||||||||||||||||||||||||||||||   :::
Db        691 CCCAGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCGTCAGCA------GAC 744

Qy        260 LysGlyGlyGlyGlySerThrThrAlaProSerAlaGlnLeuLysLysLysLeuGlnAla 279
                          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 CTGGTTCCGCGCGGATCCACTACAGCTCCATCAGCTCAGTTGAAAAAGAAACTGCAGGCA 804

Qy        280 LeuLysLysLysAsnAlaGlnLeuLysTrpLysLeuGlnAlaLeuLysLysLysLeuAla 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 CTTAAGAAAAAGAACGCTCAGCTGAAGTGGAAACTTCAAGCCCTCAAGAAGAAACTCGCC 864

Qy        300 GlnHisHisHis 303
              |||   ||||||
Db        865 CAGCTGCATCAT 876

RESULT 5
AAV12068
ID   AAV12068 standard; cDNA; 4724 BP.
XX
AC   AAV12068;
XX
DT   08-JUN-1998  (first entry)
XX
DE   Murine IAd beta chain cDNA.
XX
KW   Major histocompatibility class II antigen; MHC class II; T cell;
KW   T lymphocyte; Th1; Th2; activation; CD4+; antigen presenting cell; APC;
KW   autoimmune disease; diabetes; multiple sclerosis; autoimmune thyroiditis;
KW   systemic lupus erythromatosus; myasthenia gravis; Crohn's disease;
KW   inflammatory bowel disease; allergy; asthma; contact sensitivity;
KW   immunotherapy; therapy; IAd beta chain; mouse; ds; circular; cyclic.
XX
OS   Mus musculus.
XX
PN   WO9746256-A1.
XX
PD   11-DEC-1997.
XX
PF   22-MAY-1997;   97WO-US008697.
XX
PR   23-MAY-1996;   96US-0018175P.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Webb SR,  Winqvist O,  Karlsson L,  Jackson MR,  Peterson PA;
XX
DR   WPI; 1998-041895/04.
XX
PT   Synthetic antigen presenting cell for activating CD4+ T cells - useful to
PT   treat autoimmune disease, e.g. diabetes, multiple sclerosis, Crohn's
PT   disease and inflammatory bowel disease, or allergy, e.g. asthma and
PT   contact sensitivity.
XX
PS   Example 2; Page 94-96; 141pp; English.
XX
CC   This nucleotide sequence comprises a PCR product obtained by
CC   amplification of mouse splenocyte cDNA using primers (see AAV12065 and
CC   AAV12066) designed for the amplification of IAd beta chain full-length
CC   cDNA. IAd alpha chain cDNA (see AAV12067) has been similarly obtained.
CC   The IAd sequences were cloned into metallothionein promoter (see
CC   AAV12062)-driven vector pRmHa-3 prior to sequencing. Major
CC   histocompatibility complex (MHC) class II IAd heterodimers were expressed
CC   at the cell surface of transfected Drosophila Schneider 2 (ATCC CRL
CC   10974) cells. The invention relates to the preparation and use of
CC   synthetic antigen presenting matrices, in particular antigen presenting
CC   cells such as insect cells that have been transfected to produce MHC
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CC   antigen presenting molecules with one or more accessory molecules. The
CC   matrices are used to activate naive CD4+ T cells and to shift the ongoing
CC   activation state into a preferred differentiated population of Th1 or Th2
CC   cells. Applications include the treatment of autoimmune disease, e.g.
CC   diabetes, multiple sclerosis, autoimmune thyroiditis, systemic lupus
CC   erythematosus, myasthenia gravis, Crohn's disease and inflammatory bowel
CC   disease, or an allergy, e.g. asthma and contact sensitivity
XX
SQ   Sequence 4724 BP; 1196 A; 1194 C; 1200 G; 1134 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.85e-99        Length:         4724
Score:                  1161.50         Matches:        228
Percent Similarity:     85.8%           Conservative:   1
Best Local Similarity:  85.4%           Mismatches:     1
Query Match:            71.7%           Indels:         37
DB:                     2               Gaps:           2

US-10-048-116B-6 (1-306) x AAV12068 (1-4724)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 510

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              ||||||||||||||||||||||||||||
Db        511 AGCAGCCCAGGGACTGAGGGCGGAAAC------------------------------ 537

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60

Db        537 ------------------------------------------------------------ 537

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
                         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 ---------TCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 588

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        589 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 648

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        649 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 708

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        709 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 768

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        769 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 828

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              :::||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        829 ATCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 888

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        889 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 948

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        949 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 1008

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1009 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 1068

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1069 AGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCCGAGTCTGCCCGGAGCAAG 1128

Qy        261 ---------GlyGlyGlyGly 264
                          |||   ||||||
Db       1129 ATGTTGAGCGGCATCGGGGGC 1149

RESULT 6
AAT04269
ID   AAT04269 standard; DNA; 1013 BP.
XX
AC   AAT04269;
XX
DT   16-APR-1996  (first entry)
XX
DE   Hybrid IA beta chain gene.
XX
KW   Major histocompatability complex; MHC; T-cell receptor; TCR;
KW   autoimmune disease; immunodeficiency disease; immune response;
KW   immunoproliferation disease; graft-host rejection; therapy; B cell;
KW   M12.C3; pM12-IAb-Ea; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   primer_bind     1. .18
FT                   /*tag= a
FT                   /note= "probable primer binding site (primer #76)"
FT   primer_bind     complement(40. .74)
FT                   /*tag= b
FT                   /note= "binding site for primer #362 (see AAT04270)"
FT   CDS             63. .959
FT                   /*tag= c
FT                   /product= "hybrid IA beta chain"
FT   sig_peptide     63. .143
FT                   /*tag= d
FT                   /note= "leader region"
FT   primer_bind     complement(140. .191)
FT                   /*tag= e
FT                   /note= "binding site for primer #363 (see AAT04271)"
FT   primer_bind     complement(177. .226)
FT                   /*tag= f
FT                   /note= "primer #364 binding site"
FT   primer_bind     complement(212. .266)
FT                   /*tag= g
FT                   /note= "primer #365 (see AAT04272) binding site"
FT   primer_bind     385. .403
FT                   /*tag= h
FT                   /note= "probable primer binding site (primer #270)"
FT   mat_peptide     531. .959
FT                   /*tag= i
FT                   /product= "IA beta chain beta 2 region"
FT   primer_bind     535. .564
FT                   /*tag= j
FT                   /note= "probable primer binding site (primer #271)"
FT   primer_bind     544. .568
FT                   /*tag= k
FT                   /note= "probable primer binding site (primer #272)"
FT   primer_bind     823. .850
FT                   /*tag= l
FT                   /note= "probable primer binding site (primer #259)"
FT   primer_bind     942. .976
FT                   /*tag= m
FT                   /note= "probable primer binding site (primer #366)"
FT   primer_bind     1000. .1013
FT                   /*tag= n
FT                   /note= "probable primer binding site (primer #59)"
XX
PN   WO9523814-A1.
XX
PD   08-SEP-1995.
XX
PF   03-MAR-1995;   95WO-US002689.
XX
PR   04-MAR-1994;   94US-00207481.
XX
PA   (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
```

```
XX
PI   Kappler JW,  Marrack P;
XX
DR   WPI; 1995-320543/41.
DR   P-PSDB; AAR82538.
XX
PT   Peptide-MHC complex comprising antigenic peptide, linker and MHC segment
PT   - useful as reagents for the treatment of diseases including auto-immune
PT   diseases, immuno-stimulatory diseases or graft-host rejection.
XX
PS   Example 2; Page 65; 94pp; English.
XX
CC   This sequence represents a hybrid IA beta chain gene. This sequence
CC   contains a fragment of the IE alpha chain (residues 56-73), as well as a
CC   linker and cleavage site. This sequence was transfected into a B cell
CC   line (M12.C3) using plasmid pM12-IAb-Ea. It was found that the encoded
CC   sequence was expressed in these cells. Complexes such as this may be used
CC   to regulate an immune response. The complexes are capable of being
CC   recognised by a TCR alone or in combination with additional MHC proteins.
CC   These complexes are useful for therapeutic purposes and experimental
CC   purposes. They can also be used as reagents for the treatment of diseases
CC   including autoimmune diseases, immunodeficiency diseases,
CC   immunoproliferation diseases, and graft-host rejection
XX
SQ   Sequence 1013 BP; 220 A; 272 C; 327 G; 192 T; 0 U; 2 Other;

Alignment Scores:
Pred. No.:                2.31e-99        Length:          1013
Score:                    1151.00         Matches:         230
Percent Similarity:       86.8%           Conservative:    6
Best Local Similarity:    84.6%           Mismatches:      22
Query Match:              71.0%           Indels:          14
DB:                       2               Gaps:            4

US-10-048-116B-6 (1-306) x AAT04269 (1-1013)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCGGCTGCTGTGGTGGTGCTCATGGTGCTG 122

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              ||||||||||||||||||||||:::|||           |||   |||
Db        123 AGCAGCCCAGGGACTGAGGGCGGAGACTCC---------GAAGCTAGCTTTGAGGCTCAG 173

Qy         41 ---------------IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuVal 55
                           |||   |||      :::     ||||||   |||
Db        174 GGTGCACTGGCCAACATTGCTGTCGACAAGGCTGGAGGTGGTGGATCCGGTGGA------ 227

Qy         56 ProArgGlySerGlyGlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGlu 75
              |||||||||||||||||||||||||||||||||||||   ||||||   ||||||
Db        228 ---GGGGGAAGTGGAGGTGGAGGGTCTGAAAGGCATTTCGTGTACCAGTTCATGGGCGAG 284

Qy         76 CysTyrTyrThrAsnGlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArg 95
              ||||||:::|||||||||||||||||||||||||   |||||||||||||||||||||||
Db        285 TGCTACTTCACCAACGGGACGCAGCGCATACGATATGTGACCAGATACATCTACAACCGG 344

Qy         96 GluGluTyrValArgTyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGly 115
              ||||||||||||||||||||||||||||||:::|||||||||||||||||||||||||||
Db        345 GAGGAGTACGTGCGCTACGACAGCGACGTGGGCGAGCACCGCGCGGTGACCGAGCTGGGG 404

Qy        116 ArgProAspAlaGluTyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGlu 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 CGGCCAGACGCCGAGTACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAG 464

Qy        136 ValAspThrAlaCysArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArg 155
              |||||||||   ||||||||||||||||||||||||||||||   ||||||||||||||||
Db        465 GTGGACACGGTGTGCAGACACAACTACGAGGGGCCGGAGACCCACACCTCCCTGCGGCGG 524

Qy        156 LeuGluGlnProAsnValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsn 175
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        525 CTTGAACAGCCCAATGTCGTCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAAC 584

Qy        176 ThrLeuValCysSerValThrAspPheTyrProAlaLysIleLysValArgTrpPheArg 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACTCTGGTCTGCTCAGTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCCGG 644

Qy        196 AsnGlyGlnGluGluThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrp 215
              ||||||||||||||||||||||||:::|||||||||||||||||||||||||||||||||
Db        645 AATGGCCAGGAGGAGACGGTGGGGCTCTCATCCACACAGCTTATTAGGAATGGGGACTGG 704

Qy        216 ThrPheGlnValLeuValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCys 235
              ||||||||||||||||||||||||||||||||||   :::|||||||||||||||||||
Db        705 ACCTTCCAGGTCCTGGTCATGCTGGAGATGACCCCTCGGCGGGGAGAGGTCTAYACCTGT 764

Qy        236 HisValGluHisProSerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGlu 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        765 CACGTGGAGCATCCCAGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCTGAG 824

Qy        256 SerAlaArgSerLys---------GlyGlyGlyGly 264
              ||||||   ||||||         |||   ||||||
Db        825 TCTGCCTGGAGCAAGATGTTGAGCGGCATCGGGGGC 860

RESULT 7
AAT17588
ID   AAT17588 standard; DNA; 1382 BP.
XX
AC   AAT17588;
XX
DT   26-SEP-1996  (first entry)
XX
DE   Vector SCE1-derived single chain gene encoding MHC fusion complex.
XX
KW   MHC; major histocompatibility complex; PCR; polymerase chain reaction;
KW   T cell activity modulator; antagonist; immune disorder; allergy;
KW   multiple sclerosis; insulin-dependent diabetes mellitus;
KW   rheumatoid arthritis; myasthenia gravis; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             6. .1382
FT                   /*tag=  a
FT   sig_peptide     6. .86
FT                   /*tag=  b
FT                   /label= I-Ad_beta_chain_leader
FT                   /note= "murine MHC class II I-Ad gene beta chain leader
FT                   sequence"
FT   misc_feature    87. .137
FT                   /*tag=  c
FT                   /label= OVA_323-339
FT                   /note= "chicken ovalbumin residues 323-339"
FT   misc_feature    138. .167
FT                   /*tag=  d
FT                   /note= "10 residue linker peptide"
FT   misc_feature    168. .452
FT                   /*tag=  e
FT                   /label= I-Ad_beta1
FT                   /note= "murine MHC class II I-Ad gene beta-1 domain"
FT   misc_feature    453. .734
FT                   /*tag=  f
FT                   /label= I-Ad_beta2
FT                   /note= "murine MHC class II I-Ad gene beta-2 domain"
FT   misc_feature    735. .806
FT                   /*tag=  g
FT                   /note= "24 residue peptide linker"
FT   misc_feature    807. .1067
FT                   /*tag=  h
FT                   /label= I-Ad_alpha1
FT                   /note= "murine MHC class II I-Ad gene alpha-2 domain"
FT   misc_feature    1068. .1352
FT                   /*tag=  i
FT                   /label= I-Ad_alpha2
FT                   /note= "murine MHC class II I-Ad gene alpha-2 domain"
FT   misc_feature    1353. .1379
FT                   /*tag=  j
FT                   /note= "EE tag"
```

```
XX
PN   WO9604314-A1.
XX
PD   15-FEB-1996.
XX
PF   31-JUL-1995;   95WO-US009816.
XX
PR   29-JUL-1994;   94US-00283302.
PR   01-FEB-1995;   95US-00382454.
XX
PA   (DADE-) DADE INT INC.
XX
PI   Wong HC,  Rhode PR,  Weidanz JA,  Grammer S,  Edwards AC;
PI   Chavaillaz P,  Jiao J;
XX
DR   WPI; 1996-129343/13.
DR   P-PSDB; AAR98907.
XX
PT   Major histocompatability complex fusion complex for modulating T cell
PT   activity - used in the treatment of immune disorders, e.g. multiple
PT   sclerosis, IDDM and rheumatoid arthritis.
XX
PS   Example 17; Fig 29; 210pp; English.
XX
CC   AAT17588 encodes a murine MHC fusion complex capable of modulating T cell
CC   activity encoded by the vector SCE1. The MHC fusion complex comprises at
CC   least one MHC molecule containing a peptide-binding groove and a
CC   presenting peptide covalently linked to the MHC molecule and opt. a
CC   transmembrane domain. DNA encoding a MHC fusion complex may be cloned
CC   into a host cell to express the complex. The transformed cells may then
CC   be used to identify peptides that modulate, pref. antagonise, T cell
CC   activity. DNA encoding a MHC fusion complex or a single chain fusion
CC   molecule may be used to vaccinate a mammal against a targeted disorder.
CC   The fusion complexes may be used to suppress an immune response in an
CC   animal suffering from an immune disorder e.g. multiple sclerosis, insulin
CC   -dependent diabetes mellitus, rheumatoid arthritis, myasthenia gravis or
CC   chronic allergies. The complexes may also be used in the treatment of
CC   livestock and pets such as cats and dogs. The MHC fusion complexes can be
CC   produced such that they contain a single antigenic peptide including one
CC   of known structure, additionally a wide range of peptides can be
CC   presented for T cell interaction
XX
SQ   Sequence 1382 BP; 320 A; 374 C; 404 G; 284 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.3e-98       Length:         1382
Score:                  1145.00       Matches:        227
Percent Similarity:     87.2%         Conservative:   4
Best Local Similarity:  85.7%         Mismatches:     24
Query Match:            70.7%         Indels:         10
DB:                     2             Gaps:           3

US-10-048-116B-6 (1-306) x AAT17588 (1-1382)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              |||||||||   |||         :::           :::         |||
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              |||      :::|||         ||||||||||||||                 |||
Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC---------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTCGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              |||||||||||||||||||||||||||||||||          :::
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy        261 GlyGlyGlyGlySer 265
              |||||||||||||||
Db        756 GGCGGTGGTGGTTCC 770

RESULT 8
AAT86989
ID   AAT86989 standard; DNA; 1382 BP.
XX
AC   AAT86989;
XX
DT   27-MAR-1998  (first entry)
XX
DE   SCE1 single chain gene.
XX
KW   Construction; major histocompatibility complex; MHC; fusion complex;
KW   SCE1 single chain gene; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             6. .1382
FT                   /*tag=  a
XX
PN   WO9728191-A1.
XX
PD   07-AUG-1997.
XX
PF   30-JAN-1997;   97WO-US001617.
XX
PR   31-JAN-1996;   96US-00596387.
XX
PA   (DADE-) DADE INT INC.
XX
PI   Rhode PR,  Jiao J,  Burkhardt M,  Wong HC;
XX
DR   WPI; 1997-402555/37.
DR   P-PSDB; AAW29214.
XX
PT   Single chain major histocompatibility complex comprising linked alpha and
PT   beta chains - useful for suppressing an immune response to an auto:immune
```

```
PT   disease, e.g. multiple sclerosis, rheumatoid arthritis, diabetes
PT   mellitus, etc.
XX
PS   Example 17; Page 140-141; 217pp; English.
XX
CC   The present sequence was used in the construction of major
CC   histocompatibility complex (MHC) fusion complexes
XX
SQ   Sequence 1382 BP; 320 A; 373 C; 405 G; 284 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.3e-98       Length:         1382
Score:                  1145.00       Matches:        227
Percent Similarity:     87.2%         Conservative:   4
Best Local Similarity:  85.7%         Mismatches:     24
Query Match:            70.7%         Indels:         10
DB:                     2             Gaps:           3

US-10-048-116B-6 (1-306) x AAT86989 (1-1382)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              ||||||||  |||      :::      :::      |||
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              |||      :::|||         ||||||||||||||                 |||
Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC--------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              ||||||||||||||||||||||||||||||||  :::
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy        261 GlyGlyGlyGlySer 265
```

```
              ||||||||||||||||
Db        756 GGCGGTGGTGGTTCC 770

RESULT 9
ACA60744
ID   ACA60744 standard; DNA; 1382 BP.
XX
AC   ACA60744;
XX
DT   16-JUN-2003  (first entry)
XX
DE   Mouse MHC I-Ad/Ova 323-339 synthetic gene SCE1.
XX
KW   MHC; major histocompatibility complex; gene therapy; fusion complex;
KW   peptide-binding groove; T cell modulation; class II MHC; vaccine;
KW   autoimmune disorder; multiple sclerosis; rheumatoid arthritis;
KW   insulin-dependent diabetes mellitus; myasthenia gravis; immunogen;
KW   chronic allergy; mouse; ds; I-Ad; gene.
XX
OS   Mus sp.
OS   Synthetic.
XX
PN   US2002198144-A1.
XX
PD   26-DEC-2002.
XX
PF   06-JUL-2001; 2001US-00900379.
XX
PR   29-JUL-1994;   94US-00283302.
PR   01-FEB-1995;   95US-00382454.
PR   17-JAN-1997;   97US-00776084.
XX
PA   (DADE-) DADE INT INC.
XX
PI   Wong HC,  Rhode PR,  Weidanz JA,  Grammer S,  Edwards AC;
PI   Chavaillaz P,  Jiao JJJ;
XX
DR   WPI; 2003-341126/32.
DR   P-PSDB; ABU72108.
XX
PT   Novel major histocompatibility complex fusion complex having presenting
PT   peptide covalently linked to MHC molecule containing peptide-binding
PT   groove, used for suppressing immune response in multiple sclerosis,
PT   allergies.
XX
PS   Example 17; Fig 29; 126pp; English.
XX
CC   The invention relates to a major histocompatibility complex (MHC) fusion
CC   complex (I) comprising an MHC molecule that contains a peptide-binding
CC   groove, and a presenting peptide covalently (e.g. an antigenic peptide)
CC   linked to the MHC molecule, where (I) is capable of modulating the
CC   activity of a T cell. Also included are a DNA construct coding for the
CC   complex, where the MHC molecule is a class II MHC (e.g. mouse I-Ad or I-
CC   As, or human HLA-DR1 (human leukocyte antigen-DR1)), a multivalent MHC
CC   fusion complex comprising two or more linked complexes, identifying a
CC   peptide that can modulate the activity of T cells (involving introducing
CC   into host cells cloning vectors that each contain the fusion complex DNA,
CC   culturing the host cells under conditions suitable for expression of the
CC   MHC fusion complex, and selecting host cells that express MHC fusion
CC   complex that modulate the activity of T cells), a single recombinant
CC   expression vector comprising DNA that codes for the alpha and beta chains
CC   of the fusion complex MHC protein, a single recombinant expression vector
CC   comprising DNA that codes for a T cell costimulatory factor and the alpha
CC   and beta chains of the MHC fusion complex. The DNA constructs can contain
CC   heterologous leader peptide sequences and Kozak sequence for efficient
CC   expression of the fusion complex. Also included are inducing an immune
CC   response in a mammal (including vaccinating a mammal against a targeted
CC   disorder, by administering DNA sequence comprising a fusion complex, or
CC   DNA sequence coding for a fusion complex which is a single chain fusion
CC   molecule) and suppressing an immune response in a mammal by administering
CC   to the mammal a DNA sequence comprising an expression vector, encoding a
CC   full length MHC molecule that contains a transmembrane domain, and a
CC   presenting peptide that is a T cell receptor (TCR) antagonist or partial
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CC   agonist and is covalently linked to the MHC protein, or DNA sequence
CC   coding for the fusion complex which is a single chain fusion molecule.
CC   The methods are useful for identifying a peptide that can modulate the
CC   activity of T cells, inducing an immune response in a mammal (including
CC   vaccinating a mammal against a targeted disorder) and for suppressing an
CC   immune response in a mammal. The disorders include an autoimmune disorder
CC   such as multiple sclerosis, insulin-dependent diabetes mellitus,
CC   rheumatoid arthritis, myasthenia gravis or chronic allergies. The present
CC   sequence encodes a mouse MHC class II I-Ad fusion complex of the
CC   invention
XX
SQ   Sequence 1382 BP; 320 A; 373 C; 405 G; 284 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.3e-98       Length:          1382
Score:                  1145.00       Matches:         227
Percent Similarity:     87.2%         Conservative:    4
Best Local Similarity:  85.7%         Mismatches:      24
Query Match:            70.7%         Indels:          10
DB:                     8             Gaps:            3

US-10-048-116B-6 (1-306) x ACA60744 (1-1382)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              |||||||||   |||         :::           :::          |||
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              |||      :::|||          ||||||||||||||                  |||
Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC--------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              ||||||||||||||||||||||||||||||||          :::
```

```
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy        261 GlyGlyGlyGlySer 265
              |||||||||||||||
Db        756 GGCGGTGGTGGTTCC 770

RESULT 10
AAT17586
ID   AAT17586 standard; DNA; 1385 BP.
XX
AC   AAT17586;
XX
DT   26-SEP-1996  (first entry)
XX
DE   Vector SSC1-derived single chain gene encoding MHC fusion complex.
XX
KW   MHC; major histocompatibility complex; PCR; polymerase chain reaction;
KW   T cell activity modulator; antagonist; immune disorder; allergy;
KW   multiple sclerosis; insulin-dependent diabetes mellitus;
KW   rheumatoid arthritis; myasthenia gravis; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             6. .1385
FT                   /*tag=  a
FT   sig_peptide     6. .86
FT                   /*tag=  b
FT                   /label= I-Ad_beta_chain_leader
FT                   /note= "murine MHC class II I-Ad gene beta chain leader
FT                   sequence"
FT   misc_feature    87. .137
FT                   /*tag=  c
FT                   /label= OVA_323-339
FT                   /note= "chicken ovalbumin residues 323-339"
FT   misc_feature    138. .167
FT                   /*tag=  d
FT                   /note= "10 residue linker peptide"
FT   misc_feature    168. .452
FT                   /*tag=  e
FT                   /label= I-Ad_beta1
FT                   /note= "murine MHC class II I-Ad gene beta-1 domain"
FT   misc_feature    453. .734
FT                   /*tag=  f
FT                   /label= I-Ad_beta2
FT                   /note= "murine MHC class II I-Ad gene beta-2 domain"
FT   misc_feature    735. .806
FT                   /*tag=  g
FT                   /note= "24 residue peptide linker"
FT   misc_feature    807. .1067
FT                   /*tag=  h
FT                   /label= I-Ad_alpha1
FT                   /note= "murine MHC class II I-Ad gene alpha-2 domain"
FT   misc_feature    1068. .1352
FT                   /*tag=  i
FT                   /label= I-Ad_alpha2
FT                   /note= "murine MHC class II I-Ad gene alpha-2 domain"
FT   misc_feature    1353. .1382
FT                   /*tag=  j
FT                   /note= "6xHis tag"
XX
PN   WO9604314-A1.
XX
PD   15-FEB-1996.
XX
PF   31-JUL-1995;   95WO-US009816.
XX
PR   29-JUL-1994;   94US-00283302.
PR   01-FEB-1995;   95US-00382454.
XX
PA   (DADE-) DADE INT INC.
XX
PI   Wong HC,  Rhode PR,  Weidanz JA,  Grammer S,  Edwards AC;
```

```
PI   Chavaillaz P,  Jiao J;
XX
DR   WPI; 1996-129343/13.
DR   P-PSDB; AAR98905.
XX
PT   Major histocompatability complex fusion complex for modulating T cell
PT   activity - used in the treatment of immune disorders, e.g. multiple
PT   sclerosis, IDDM and rheumatoid arthritis.
XX
PS   Example 17; Fig 27; 210pp; English.
XX
CC   AAT17586 encodes a murine MHC fusion complex capable of modulating T cell
CC   activity encoded by the vector SSC1. The MHC fusion complex comprises at
CC   least one MHC molecule containing a peptide-binding groove and a
CC   presenting peptide covalently linked to the MHC molecule and opt. a
CC   transmembrane domain. DNA encoding a MHC fusion complex may be cloned
CC   into a host cell to express the complex. The transformed cells may then
CC   be used to identify peptides that modulate, pref. antagonise, T cell
CC   activity. DNA encoding a MHC fusion complex or a single chain fusion
CC   molecule may be used to vaccinate a mammal against a targeted disorder.
CC   The fusion complexes may be used to suppress an immune response in an
CC   animal suffering from an immune disorder e.g. multiple sclerosis, insulin
CC   -dependent diabetes mellitus, rheumatoid arthritis, myasthenia gravis or
CC   chronic allergies. The complexes may also be used in the treatment of
CC   livestock and pets such as cats and dogs. The MHC fusion complexes can be
CC   produced such that they contain a single antigenic peptide including one
CC   of known structure, additionally a wide range of peptides can be
CC   presented for T cell interaction
XX
SQ   Sequence 1385 BP; 316 A; 384 C; 398 G; 287 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.3e-98       Length:         1385
Score:                  1145.00       Matches:        227
Percent Similarity:     87.2%         Conservative:   4
Best Local Similarity:  85.7%         Mismatches:     24
Query Match:            70.7%         Indels:         10
DB:                     2             Gaps:           3

US-10-048-116B-6 (1-306) x AAT17586 (1-1385)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              |||||||||   |||         :::         :::         |||
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              |||      :::|||         ||||||||||||||                 |||
Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC--------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTCGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              ||||||||||||||||||||||||||||||||          :::
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy        261 GlyGlyGlyGlySer 265
              |||||||||||||||
Db        756 GGCGGTGGTGGTTCC 770

RESULT 11
AAT86987
ID   AAT86987 standard; DNA; 1385 BP.
XX
AC   AAT86987;
XX
DT   27-MAR-1998  (first entry)
XX
DE   SSC1 single chain gene.
XX
KW   Construction; major histocompatibility complex; MHC; fusion complex;
KW   SSC1 single chain gene; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             6. .1385
FT                   /*tag=  a
XX
PN   WO9728191-A1.
XX
PD   07-AUG-1997.
XX
PF   30-JAN-1997;   97WO-US001617.
XX
PR   31-JAN-1996;   96US-00596387.
XX
PA   (DADE-) DADE INT INC.
XX
PI   Rhode PR,  Jiao J,  Burkhardt M,  Wong HC;
XX
DR   WPI; 1997-402555/37.
DR   P-PSDB; AAW29212.
XX
PT   Single chain major histocompatibility complex comprising linked alpha and
PT   beta chains - useful for suppressing an immune response to an auto:immune
PT   disease, e.g. multiple sclerosis, rheumatoid arthritis, diabetes
PT   mellitus, etc.
XX
PS   Example 17; Page 135-137; 217pp; English.
XX
CC   The present sequence was used in the construction of major
CC   histocompatibility complex (MHC) fusion complexes
XX
SQ   Sequence 1385 BP; 316 A; 383 C; 399 G; 287 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.3e-98       Length:         1385
Score:                  1145.00       Matches:        227
```

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Percent Similarity:     87.2%          Conservative:  4
Best Local Similarity:  85.7%          Mismatches:    24
Query Match:            70.7%          Indels:        10
DB:                     2              Gaps:          3

US-10-048-116B-6 (1-306) x AAT86987 (1-1385)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              |||||||||   |||         :::           :::          |||
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              |||      :::|||          ||||||||||||||                  |||
Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC--------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              ||||||||||||||||||||||||||||||  :::
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy        261 GlyGlyGlyGlySer 265
              |||||||||||||||
Db        756 GGCGGTGGTGGTTCC 770

RESULT 12
ACA60742
ID   ACA60742 standard; DNA; 1385 BP.
XX
AC   ACA60742;
XX
DT   16-JUN-2003  (first entry)
XX
DE   Mouse MHC I-Ad/Ova 323-339 synthetic gene SSC1.
XX
KW   MHC; major histocompatibility complex; gene therapy; fusion complex;
KW   peptide-binding groove; T cell modulation; class II MHC; vaccine;
KW   autoimmune disorder; multiple sclerosis; rheumatoid arthritis;
KW   insulin-dependent diabetes mellitus; myasthenia gravis; immunogen;
KW   chronic allergy; mouse; ds; I-Ad; gene.
XX
OS   Mus sp.
OS   Synthetic.
XX
PN   US2002198144-A1.
XX
PD   26-DEC-2002.
XX
PF   06-JUL-2001; 2001US-00900379.
XX
PR   29-JUL-1994;   94US-00283302.
PR   01-FEB-1995;   95US-00382454.
PR   17-JAN-1997;   97US-00776084.
XX
PA   (DADE-) DADE INT INC.
XX
PI   Wong HC,  Rhode PR,  Weidanz JA,  Grammer S,  Edwards AC;
PI   Chavaillaz P,  Jiao JJJ;
XX
DR   WPI; 2003-341126/32.
DR   P-PSDB; ABU72106.
XX
PT   Novel major histocompatibility complex fusion complex having presenting
PT   peptide covalently linked to MHC molecule containing peptide-binding
PT   groove, used for suppressing immune response in multiple sclerosis,
PT   allergies.
XX
PS   Example 17; Fig 27; 126pp; English.
XX
CC   The invention relates to a major histocompatibility complex (MHC) fusion
CC   complex (I) comprising an MHC molecule that contains a peptide-binding
CC   groove, and a presenting peptide covalently (e.g. an antigenic peptide)
CC   linked to the MHC molecule, where (I) is capable of modulating the
CC   activity of a T cell. Also included are a DNA construct coding for the
CC   complex, where the MHC molecule is a class II MHC (e.g. mouse I-Ad or I-
CC   As, or human HLA-DR1 (human leukocyte antigen-DR1)), a multivalent MHC
CC   fusion complex comprising two or more linked complexes, identifying a
CC   peptide that can modulate the activity of T cells (involving introducing
CC   into host cells cloning vectors that each contain the fusion complex DNA,
CC   culturing the host cells under conditions suitable for expression of the
CC   MHC fusion complex, and selecting host cells that express MHC fusion
CC   complex that modulate the activity of T cells), a single recombinant
CC   expression vector comprising DNA that codes for the alpha and beta chains
CC   of the fusion complex MHC protein, a single recombinant expression vector
CC   comprising DNA that codes for a T cell costimulatory factor and the alpha
CC   and beta chains of the MHC fusion complex. The DNA constructs can contain
CC   heterologous leader peptide sequences and Kozak sequence for efficient
CC   expression of the fusion complex. Also included are inducing an immune
CC   response in a mammal (including vaccinating a mammal against a targeted
CC   disorder, by administering DNA sequence comprising a fusion complex, or
CC   DNA sequence coding for a fusion complex which is a single chain fusion
CC   molecule) and suppressing an immune response in a mammal by administering
CC   to the mammal a DNA sequence comprising an expression vector, encoding a
CC   full length MHC molecule that contains a transmembrane domain, and a
CC   presenting peptide that is a T cell receptor (TCR) antagonist or partial
CC   agonist and is covalently linked to the MHC protein, or DNA sequence
CC   coding for the fusion complex which is a single chain fusion molecule.
CC   The methods are useful for identifying a peptide that can modulate the
CC   activity of T cells, inducing an immune response in a mammal (including
CC   vaccinating a mammal against a targeted disorder) and for suppressing an
CC   immune response in a mammal. The disorders include an autoimmune disorder
CC   such as multiple sclerosis, insulin-dependent diabetes mellitus,
CC   rheumatoid arthritis, myasthenia gravis or chronic allergies. The present
CC   sequence encodes a mouse MHC class II I-Ad fusion complex of the
CC   invention
XX
SQ   Sequence 1385 BP; 316 A; 383 C; 399 G; 287 T; 0 U; 0 Other;
```

```
Alignment Scores:
Pred. No.:                1.3e-98        Length:          1385
Score:                    1145.00        Matches:          227
Percent Similarity:       87.2%          Conservative:       4
Best Local Similarity:    85.7%          Mismatches:        24
Query Match:              70.7%          Indels:            10
DB:                       8              Gaps:               3

US-10-048-116B-6 (1-306) x ACA60742 (1-1385)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              |||||||||   |||         :::             :::          |||
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              |||      :::|||           ||||||||||||||                 |||
Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC--------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              |||||||||||||||||||||||||||||||         :::
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy        261 GlyGlyGlyGlySer 265
              |||||||||||||||
Db        756 GGCGGTGGTGGTTCC 770

RESULT 13
AAT17587
ID   AAT17587 standard; DNA; 1508 BP.
XX
AC   AAT17587;
XX
DT   26-SEP-1996  (first entry)
XX
DE   Vector SCT1-derived single chain gene encoding MHC fusion complex.
XX
KW   MHC; major histocompatibility complex; PCR; polymerase chain reaction;
KW   T cell activity modulator; antagonist; immune disorder; allergy;
KW   multiple sclerosis; insulin-dependent diabetes mellitus;
KW   rheumatoid arthritis; myasthenia gravis; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             6. .1508
FT                   /*tag=  a
FT   sig_peptide     6. .86
FT                   /*tag=  b
FT                   /label= I-Ad_beta_chain_leader
FT                   /note= "murine MHC class II I-Ad gene beta chain leader
FT                   sequence"
FT   misc_feature    87. .137
FT                   /*tag=  c
FT                   /label= OVA_323-339
FT                   /note= "chicken ovalbumin residues 323-339"
FT   misc_feature    138. .167
FT                   /*tag=  d
FT                   /note= "10 residue linker peptide"
FT   misc_feature    168. .452
FT                   /*tag=  e
FT                   /label= I-Ad_beta1
FT                   /note= "murine MHC class II I-Ad gene beta-1 domain"
FT   misc_feature    453. .734
FT                   /*tag=  f
FT                   /label= I-Ad_beta2
FT                   /note= "murine MHC class II I-Ad gene beta-2 domain"
FT   misc_feature    735. .806
FT                   /*tag=  g
FT                   /note= "24 residue peptide linker"
FT   misc_feature    807. .1067
FT                   /*tag=  h
FT                   /label= I-Ad_alpha1
FT                   /note= "murine MHC class II I-Ad gene alpha-2 domain"
FT   misc_feature    1068. .1352
FT                   /*tag=  i
FT                   /label= I-Ad_alpha2
FT                   /note= "murine MHC class II I-Ad gene alpha-2 domain"
FT   misc_feature    1353. .1505
FT                   /*tag=  j
FT                   /label= I-Ad_alpha-TM
FT                   /note= "murine MHC class II I-Ad gene alpha-transmembrane
FT                   domain"
XX
PN   WO9604314-A1.
XX
PD   15-FEB-1996.
XX
PF   31-JUL-1995;   95WO-US009816.
XX
PR   29-JUL-1994;   94US-00283302.
PR   01-FEB-1995;   95US-00382454.
XX
PA   (DADE-) DADE INT INC.
XX
PI   Wong HC,  Rhode PR,  Weidanz JA,  Grammer S,  Edwards AC;
PI   Chavaillaz P,  Jiao J;
XX
DR   WPI; 1996-129343/13.
DR   P-PSDB; AAR98906.
XX
PT   Major histocompatability complex fusion complex for modulating T cell
PT   activity - used in the treatment of immune disorders, e.g. multiple
PT   sclerosis, IDDM and rheumatoid arthritis.
XX
PS   Example 17; Fig 28; 210pp; English.
XX
```

```
CC   AAT17587 encodes a murine MHC fusion complex capable of modulating T cell
CC   activity encoded by the vector SCT1. The MHC fusion complex comprises at
CC   least one MHC molecule containing a peptide-binding groove and a
CC   presenting peptide covalently linked to the MHC molecule and opt. a
CC   transmembrane domain. DNA encoding a MHC fusion complex may be cloned
CC   into a host cell to express the complex. The transformed cells may then
CC   be used to identify peptides that modulate, pref. antagonise, T cell
CC   activity. DNA encoding a MHC fusion complex or a single chain fusion
CC   molecule may be used to vaccinate a mammal against a targeted disorder.
CC   The fusion complexes may be used to suppress an immune response in an
CC   animal suffering from an immune disorder e.g. multiple sclerosis, insulin
CC   -dependent diabetes mellitus, rheumatoid arthritis, myasthenia gravis or
CC   chronic allergies. The complexes may also be used in the treatment of
CC   livestock and pets such as cats and dogs. The MHC fusion complexes can be
CC   produced such that they contain a single antigenic peptide including one
CC   of known structure, additionally a wide range of peptides can be
CC   presented for T cell interaction
XX
SQ   Sequence 1508 BP; 337 A; 414 C; 440 G; 317 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.46e-98        Length:         1508
Score:                  1145.00         Matches:        227
Percent Similarity:     87.2%           Conservative:   4
Best Local Similarity:  85.7%           Mismatches:     24
Query Match:            70.7%           Indels:         10
DB:                     2               Gaps:           3

US-10-048-116B-6 (1-306) x AAT17587 (1-1508)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              |||||||||   |||        :::            :::         |||
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              |||      :::|||         ||||||||||||||                 |||
Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC---------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
              |||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTCGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              ||||||||||||||||||||||||||||||||          :::
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy        261 GlyGlyGlyGlySer 265
              |||||||||||||||
Db        756 GGCGGTGGTGGTTCC 770

RESULT 14
AAT86988
ID   AAT86988 standard; DNA; 1508 BP.
XX
AC   AAT86988;
XX
DT   27-MAR-1998  (first entry)
XX
DE   SCT1 single chain gene.
XX
KW   Construction; major histocompatibility complex; MHC; fusion complex;
KW   SCT1 single chain gene; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             6. .1508
FT                   /*tag=  a
XX
PN   WO9728191-A1.
XX
PD   07-AUG-1997.
XX
PF   30-JAN-1997;   97WO-US001617.
XX
PR   31-JAN-1996;   96US-00596387.
XX
PA   (DADE-) DADE INT INC.
XX
PI   Rhode PR,  Jiao J,  Burkhardt M,  Wong HC;
XX
DR   WPI; 1997-402555/37.
DR   P-PSDB; AAW29213.
XX
PT   Single chain major histocompatibility complex comprising linked alpha and
PT   beta chains - useful for suppressing an immune response to an auto:immune
PT   disease, e.g. multiple sclerosis, rheumatoid arthritis, diabetes
PT   mellitus, etc.
XX
PS   Example 17; Page 137-139; 217pp; English.
XX
CC   The present sequence was used in the construction of major
CC   histocompatibility complex (MHC) fusion complexes
XX
SQ   Sequence 1508 BP; 337 A; 413 C; 441 G; 317 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.46e-98        Length:         1508
Score:                  1145.00         Matches:        227
Percent Similarity:     87.2%           Conservative:   4
Best Local Similarity:  85.7%           Mismatches:     24
Query Match:            70.7%           Indels:         10
DB:                     2               Gaps:           3

US-10-048-116B-6 (1-306) x AAT86988 (1-1508)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65
```

```
Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              |||||||||   |||         :::         :::         |||
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              |||       :::|||           ||||||||||||||                 |||
Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC---------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              ||||||||||||||||||||||||||||||||           :::
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy        261 GlyGlyGlyGlySer 265
              |||||||||||||||
Db        756 GGCGGTGGTGGTTCC 770
```

RESULT 15
AAX89069
ID AAX89069 standard; DNA; 1508 BP.
XX
AC AAX89069;
XX
DT 14-SEP-1999 (first entry)
XX
DE Single chain IAd/OVA 323-229 MHC fusion protein encoding DNA.
XX
KW Major histocompatibility complex; MHC; single chain MHC; sc-MHC; Ig;
KW peptide binding groove; immunoglobulin; T cell receptor; immune response;
KW immune-related disorder; antigenic peptide; fusion protein; ss.
XX
OS Synthetic.
XX
PN WO9921572-A1.
XX
PD 06-MAY-1999.
XX
PF 13-OCT-1998; 98WO-US021520.
XX
PR 29-OCT-1997; 97US-00960190.
XX
PA (SUNO-) SUNOL MOLECULAR CORP.
XX
PI Rhode PR, Acevedo J, Burkhardt M, Jiao J, Wong HC;
XX
DR WPI; 1999-418411/35.
DR P-PSDB; AAY27111.
XX
PT Single chain major histocompatibility complex class I complexes.
XX
PS Example 1; Fig 1; 148pp; English.
XX
CC The invention relates to new single chain major histocompatibility
CC complex (sc-MHC) class II complexes that comprise a peptide binding
CC groove, and a modified class II beta 2 chain or covalently linked
CC immunoglobulin (Ig) light chain constant (C1) region. The MHC complexes
CC are useful for detection and analysis of peptide ligands, pathogenic T-
CC cells, for functional, cellular and molecular assays. They can be used to
CC identify and isolate T cell receptor and/or MHC agonists and antagonists.
CC They can be used in vivo to compete with pathogenic antigen presenting
CC cells involved in immune-related disorders. They can also be used to
CC raise antibodies and to screen immune cells. It is also use in a method
CC of suppressing an immune response in mammals. The sc-MHC complexes
CC comprising modified class II beta 2 chains and/or Ig-C1 regions are
CC soluble and provide enhanced yield. These MHC complexes also can contain
CC single antigenic peptides readily isolated from expressing cells in
CC significant quantities. The polyspecific MHC complexes also provide a
CC means to detect cells expressing multiple target structures with a single
CC complex. The present sequence represents a DNA encoding a single chain
CC IAd/OVA 323-229 MHC fusion protein
XX
SQ Sequence 1508 BP; 337 A; 413 C; 441 G; 317 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.46e-98	Length:	1508
Score:	1145.00	Matches:	227
Percent Similarity:	87.2%	Conservative:	4
Best Local Similarity:	85.7%	Mismatches:	24
Query Match:	70.7%	Indels:	10
DB:	2	Gaps:	3

US-10-048-116B-6 (1-306) x AAX89069 (1-1508)

```
Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              |||||||||   |||         :::         :::         |||
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              |||       :::|||           ||||||||||||||                 |||
Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC---------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404
```

```
Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              ||||||||||||||||||||||||||||||         :::
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy        261 GlyGlyGlyGlySer 265
              |||||||||||||||
Db        756 GGCGGTGGTGGTTCC 770
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Job time : 539.723 secs

GenCore version 5.1.9

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 30, 2006, 01:28:47 ; Search time 6366.34 Seconds
(without alignments)
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Title: US-10-048-116B-6_COPY_1_300
Perfect score: 1572
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Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/abss/ABSSWEB_spool/US10048116/runat_29062006_093311_10139/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss07
-USER=US10048116_@CGN_1_1_7274_@runat_29062006_093311_10139 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1572	100.0	921	2	AX081281	AX081281 Sequence
2	1255.5	79.9	893	2	AR047947	AR047947 Sequence
3	1161.5	73.9	4724	2	AR199666	AR199666 Sequence
4	1154	73.4	1013	2	AR047957	AR047957 Sequence
5	1145	72.8	1382	2	AR033964	AR033964 Sequence
6	1145	72.8	1382	2	AR175097	AR175097 Sequence
7	1145	72.8	1382	2	CS079301	CS079301 Sequence
8	1145	72.8	1382	2	AX032545	AX032545 Sequence
9	1145	72.8	1385	2	AR033962	AR033962 Sequence
10	1145	72.8	1385	2	AR175095	AR175095 Sequence
11	1145	72.8	1385	2	CS079299	CS079299 Sequence
12	1145	72.8	1385	2	AX032543	AX032543 Sequence
13	1145	72.8	1508	2	AR033963	AR033963 Sequence
14	1145	72.8	1508	2	AR152030	AR152030 Sequence
15	1145	72.8	1508	2	AR175096	AR175096 Sequence
16	1145	72.8	1508	2	CS079300	CS079300 Sequence
17	1145	72.8	1508	2	AX032544	AX032544 Sequence
18	1136	72.3	1508	2	BD138632	BD138632 Soluble M
19	1131.5	72.0	1251	6	BC010322	BC010322 Mus muscu
20	1102.5	70.1	798	6	MUSMHIABQ	M13537 Mouse MHC c
21	1096.5	69.8	798	2	CQ777552	CQ777552 Sequence
22	1054.5	67.1	888	6	MUSMHABNO	M15848 Mouse MHC c
23	1054.5	67.1	1204	6	BC008168	BC008168 Mus muscu
24	1050.5	66.8	792	6	AY452202	AY452202 Mus muscu
25	1042.5	66.3	777	6	AF065913	AF065913 Mus muscu
26	1042.5	66.3	792	6	AF293060	AF293060 Mus muscu
27	1042.5	66.3	792	6	MUSMHIH2	M66213 Mouse MHC c
28	1042.5	66.3	1162	6	BC057998	BC057998 Mus muscu
29	1041.5	66.3	792	6	MUSMHIABS	M13540 Mouse MHC c
30	1036.5	65.9	792	6	AF119251	AF119251 Mus muscu
31	1036.5	65.9	792	6	AF119252	AF119252 Mus muscu
32	1033.5	65.7	750	6	AF065912	AF065912 Mus muscu
33	1030.5	65.6	1078	6	AF293061	AF293061 Mus muscu
34	1028.5	65.4	792	6	MUSMHIABK	M13538 Mouse MHC c
35	1016.5	64.7	792	6	MUSMHIABU	M13539 Mouse MHC c
36	998.5	63.5	1070	6	AF015280	AF015280 Mus muscu
37	993.5	63.2	760	6	MUSMHIABF	M13541 Mouse MHC c
38	979.5	62.3	702	2	AR106257	AR106257 Sequence
39	979.5	62.3	702	2	AR229609	AR229609 Sequence
40	979.5	62.3	702	2	AR363024	AR363024 Sequence
41	972	61.8	575	6	AY303785	AY303785 Mus muscu
42	972	61.8	578	6	AY303784	AY303784 Mus muscu
43	972	61.8	1243	2	AX490802	AX490802 Sequence
44	964.5	61.4	792	6	AY626181	AY626181 Rattus no
45	964.5	61.4	792	6	AY626184	AY626184 Rattus no

ALIGNMENTS

RESULT 1
AX081281
LOCUS AX081281 921 bp DNA linear PAT 27-FEB-2001
DEFINITION Sequence 2 from Patent WO0109194.
ACCESSION AX081281
VERSION AX081281.1 GI:13170131
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Glaichenhaus,N. and Malherbe,L.
TITLE Recombinant proteins and molecular complexes derived therefrom, analogous to molecules involved in immune responses
JOURNAL Patent: WO 0109194-A 2 08-FEB-2001;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
FEATURES Location/Qualifiers
source 1. .921
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Ligation de fragments d'ADNc"
CDS 1. .921
/note="unnamed protein product"
/codon_start=1
/transl_table=11
/protein_id="CAC33123.1"

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                     /db_xref="GI:13170132"
                     /translation="MALQIPSLLLSAAVVVLMVLSSPGTEGGNSICFSPSLEHPIVVS
                     GSWDGGGGSLVPRGSGGGGSERHFVVQFKGECYYTNGTQRIRLVTRYIYNREEYVRYD
                     SDVGEYRAVTELGRPDAEYWNSQPEILERTRAEVDTACRHNYEGPETSTSLRRLEQPN
                     VAISLSRTEALNHHNTLVCSVTDFYPAKIKVRWFRNGQEETVGVSSTQLIRNGDWTFQ
                     VLVMLEMTPHQGEVYTCHVEHPSLKSPITVEWRAQSESARSKGGGGSTTAPSAQLKKK
                     LQALKKKNAQLKWKLQALKKKLAQHHHHHH"
ORIGIN

Alignment Scores:
Pred. No.:              4.86e-156       Length:         921
Score:                  1572.00         Matches:        300
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     2               Gaps:           0

US-10-048-116B-6_COPY_1_300 (1-300) x AX081281 (1-921)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 60

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 180

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 240

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 300

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 360

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 420

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 480

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 540

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 600

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 660

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 720

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCCGAGTCTGCCCGGAGCAAG 780

Qy        261 GlyGlyGlyGlySerThrThrAlaProSerAlaGlnLeuLysLysLysLeuGlnAlaLeu 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        781 GGAGGTGGAGGATCCACTACAGCTCCATCAGCTCAGTTGAAAAAGAAATTGCAAGCACTG 840

Qy        281 LysLysLysAsnAlaGlnLeuLysTrpLysLeuGlnAlaLeuLysLysLysLeuAlaGln 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAAAAAGAACGCTCAGCTGAAGTGGAAACTTCAAGCCCTCAAGAAGAAACTCGCCCAG 900

RESULT 2
AR047947
LOCUS       AR047947                893 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 25 from patent US 5820866.
ACCESSION   AR047947
VERSION     AR047947.1  GI:5970290
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 893)
  AUTHORS   Kappler,J.W. and Marrack,P.
  TITLE     Product and process for T cell regulation
  JOURNAL   Patent: US 5820866-A 25 13-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .893
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.35e-122       Length:         893
Score:                  1255.50         Matches:        242
Percent Similarity:     95.4%           Conservative:   6
Best Local Similarity:  93.1%           Mismatches:     7
Query Match:            79.9%           Indels:         5
DB:                     2               Gaps:           1

US-10-048-116B-6_COPY_1_300 (1-300) x AR047947 (1-893)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 120

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              ||||||||||||||||||||||||||||||:::     :::   :::
Db        121 AGCAGCCCCGGGACTGAGGGCGGAAACTCCGTACATGCTGCCCATGCT---------- 168

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
                    ::::::   :::      ||||||||||||||||||||||||||||||||||||||
Db        169 ---GAGATCAATGAGGCTGGCAGAGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 225

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 285

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
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Db        286 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 345

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 405

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 465

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 525

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
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Db        526 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 585

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
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Db        586 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 645

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 705

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        706 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 765

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        766 AGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCCGAGTCTGCCCGGAGCAAG 825

RESULT 3
AR199666
LOCUS       AR199666                4724 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 8 from patent US 6355479.
ACCESSION   AR199666
VERSION     AR199666.1  GI:20249740
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4724)
  AUTHORS   Webb,S.R., Winqvist,O., Karlsson,L., Jackson,M.R. and Peterson,P.A.
  TITLE     MHC class II antigen-presenting systems and methods for activating
            CD4+ T cells
  JOURNAL   Patent: US 6355479-A 8 12-MAR-2002;
FEATURES             Location/Qualifiers
     source          1. .4724
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              9.66e-112       Length:         4724
Score:                  1161.50         Matches:        228
Percent Similarity:     85.8%           Conservative:   1
Best Local Similarity:  85.4%           Mismatches:     1
Query Match:            73.9%           Indels:         37
DB:                     2               Gaps:           2

US-10-048-116B-6_COPY_1_300 (1-300) x AR199666 (1-4724)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 510

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              ||||||||||||||||||||||||||||
Db        511 AGCAGCCCAGGGACTGAGGGCGGAAAC------------------------------ 537

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60

Db        537 ------------------------------------------------------------ 537

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
                         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 ---------TCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 588

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
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Db        589 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 648

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        649 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 708

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        709 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 768

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        769 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 828

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              :::||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        829 ATCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 888

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        889 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 948

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        949 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 1008

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1009 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 1068

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1069 AGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCCGAGTCTGCCCGGAGCAAG 1128

Qy        261 ---------GlyGlyGlyGly 264
                       |||   |||||
Db       1129 ATGTTGAGCGGCATCGGGGGC 1149

RESULT 4
AR047957
LOCUS       AR047957                1013 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 38 from patent US 5820866.
ACCESSION   AR047957
VERSION     AR047957.1  GI:5970300
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1013)
  AUTHORS   Kappler,J.W. and Marrack,P.
  TITLE     Product and process for T cell regulation
  JOURNAL   Patent: US 5820866-A 38 13-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .1013
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              8.51e-112       Length:         1013
Score:                  1154.00         Matches:        231
Percent Similarity:     86.8%           Conservative:   5
Best Local Similarity:  84.9%           Mismatches:     22
Query Match:            73.4%           Indels:         14
DB:                     2               Gaps:           4

US-10-048-116B-6_COPY_1_300 (1-300) x AR047957 (1-1013)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCGGCTGCTGTGGTGGTGCTGATGGTGCTG 122

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              ||||||||||||||||||||||||:::|||           |||   |||
Db        123 AGCAGCCCAGGGACTGAGGGCGGAGACTCC---------GAAGCTAGCTTTGAGGCTCAG 173

Qy         41 --------------IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuVal 55
                           |||   |||      :::     ||||||   |||
Db        174 GGTGCACTGGCCAACATTGCTGTCGACAAGGCTGGAGGTGGTGGATCCGGTGGA------ 227

Qy         56 ProArgGlySerGlyGlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGlu 75
                     ||||||||||||||||||||||||||||||||||   ||||||   ||||||
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Db        228 ---GGGGGAAGTGGAGGTGGAGGGTCTGAAAGGCATTTCGTGTACCAGTTCATGGGCGAG 284

Qy         76 CysTyrTyrThrAsnGlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArg 95
              ||||||:::||||||||||||||||||||||||   ||||||||||||||||||||||||
Db        285 TGCTACTTCACCAACGGGACGCAGCGCATACGATATGTGACCAGATACATCTACAACCGG 344

Qy         96 GluGluTyrValArgTyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGly 115
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||||
Db        345 GAGGAGTACGTGCGCTACGACAGCGACGTGGGCGAGCACCGCGCGGTGACCGAGCTGGGG 404

Qy        116 ArgProAspAlaGluTyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGlu 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 CGGCCAGACGCCGAGTACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAG 464

Qy        136 ValAspThrAlaCysArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArg 155
              |||||||||   ||||||||||||||||||||||||||||   ||||||||||||||||
Db        465 GTGGACACGGTGTGCAGACACAACTACGAGGGGCCGGAGACCCACACCTCCCTGCGGCGG 524

Qy        156 LeuGluGlnProAsnValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsn 175
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        525 CTTGAACAGCCCAATGTCGTCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAAC 584

Qy        176 ThrLeuValCysSerValThrAspPheTyrProAlaLysIleLysValArgTrpPheArg 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACTCTGGTCTGCTCAGTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCCGG 644

Qy        196 AsnGlyGlnGluGluThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrp 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 AATGGCCAGGAGGAGACGGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGG 704

Qy        216 ThrPheGlnValLeuValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCys 235
              ||||||||||||||||||||||||||||||||||   :::||||||||||||||||||||
Db        705 ACCTTCCAGGTCCTGGTCATGCTGGAGATGACCCCTCGGCGGGGAGAGGTCTACACCTGT 764

Qy        236 HisValGluHisProSerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGlu 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        765 CACGTGGAGCATCCCAGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCTGAG 824

Qy        256 SerAlaArgSerLys---------GlyGlyGlyGly 264
              ||||||   ||||||         |||   ||||||
Db        825 TCTGCCTGGAGCAAGATGTTGAGCGGCATCGGGGGC 860

RESULT 5
AR033964
LOCUS       AR033964               1382 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 123 from patent US 5869270.
ACCESSION   AR033964
VERSION     AR033964.1  GI:5949569
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1382)
  AUTHORS   Rhode,P.R., Jiao,J.-A., Burkhardt,M. and Wong,H.C.
  TITLE     Single chain MHC complexes and uses thereof
  JOURNAL   Patent: US 5869270-A 123 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .1382
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.13e-110      Length:         1382
Score:                  1145.00        Matches:        227
Percent Similarity:     87.2%          Conservative:   4
Best Local Similarity:  85.7%          Mismatches:     24
Query Match:            72.8%          Indels:         10
DB:                     2              Gaps:           3

US-10-048-116B-6_COPY_1_300 (1-300) x AR033964 (1-1382)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              |||||||||   |||          :::          :::          |||
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              |||      :::|||          ||||||||||||||                  |||
Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC--------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              ||||||||||||||||||||||||||||||||         :::
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy        261 GlyGlyGlyGlySer 265
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Db        756 GGCGGTGGTGGTTCC 770

RESULT 6
AR175097
LOCUS       AR175097               1382 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 123 from patent US 6309645.
ACCESSION   AR175097
VERSION     AR175097.1  GI:17916396
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1382)
  AUTHORS   Rhode,P.R., Jiao,J.-A., Burkhardt,M. and Wong,H.C.
  TITLE     MHC molecules and uses thereof
  JOURNAL   Patent: US 6309645-A 123 30-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .1382
                     /organism="unknown"
                     /mol_type="unassigned DNA"
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ORIGIN

Alignment Scores:
Pred. No.:                1.13e-110       Length:          1382
Score:                    1145.00         Matches:         227
Percent Similarity:       87.2%           Conservative:    4
Best Local Similarity:    85.7%           Mismatches:      24
Query Match:              72.8%           Indels:          10
DB:                       2               Gaps:            3

US-10-048-116B-6_COPY_1_300 (1-300) x AR175097 (1-1382)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              |||||||||   |||         :::         :::         |||
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              |||      :::|||          ||||||||||||||                  |||
Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC--------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              ||||||||||||||||||||||||||||||||          :::
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy        261 GlyGlyGlyGlySer 265
              |||||||||||||||
Db        756 GGCGGTGGTGGTTCC 770

RESULT 7
CS079301
LOCUS       CS079301               1382 bp    DNA     linear   PAT 06-MAY-2005
DEFINITION  Sequence 123 from Patent EP1526141.
ACCESSION   CS079301
VERSION     CS079301.1  GI:63093743
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1
  AUTHORS   Rhode,P.R., Jiao,J.A., Burkhardt,M. and Wong,H.C.
  TITLE     MHC complexes and uses thereof
  JOURNAL   Patent: EP 1526141-A 123 27-APR-2005;
            Altor BioScience Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .1382
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:                1.13e-110       Length:          1382
Score:                    1145.00         Matches:         227
Percent Similarity:       87.2%           Conservative:    4
Best Local Similarity:    85.7%           Mismatches:      24
Query Match:              72.8%           Indels:          10
DB:                       2               Gaps:            3

US-10-048-116B-6_COPY_1_300 (1-300) x CS079301 (1-1382)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              |||||||||   |||         :::         :::         |||
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              |||      :::|||          ||||||||||||||                  |||
Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC--------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              ||||||||||||||||||||||||||||||||          :::
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy        261 GlyGlyGlyGlySer 265
              |||||||||||||||
Db        756 GGCGGTGGTGGTTCC 770

RESULT 8
AX032545
LOCUS       AX032545               1382 bp    DNA     linear   PAT 20-SEP-2000
DEFINITION  Sequence 123 from Patent EP0997477.
ACCESSION   AX032545
VERSION     AX032545.1  GI:10279486
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1
  AUTHORS   Chavaillaz,P.A., Edwards,A.C., Grammer,S., Jiao,J.A., Rhode,P.R.,
            Weidanz,J.A. and Wong,H.C.
  TITLE     Mhc complexes and uses thereof
  JOURNAL   Patent: EP 0997477-A 123 03-MAY-2000;
            SUNOL MOLECULAR CORP (US)
FEATURES             Location/Qualifiers
     source          1. .1382
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:              1.13e-110      Length:         1382
Score:                  1145.00        Matches:        227
Percent Similarity:     87.2%          Conservative:   4
Best Local Similarity:  85.7%          Mismatches:     24
Query Match:            72.8%          Indels:         10
DB:                     2              Gaps:           3

US-10-048-116B-6_COPY_1_300 (1-300) x AX032545 (1-1382)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              |||||||||   |||       :::         :::         |||
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              |||      :::|||          ||||||||||||||||                 |||
Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC---------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              ||||||||||||||||||||||||||||||||          :::
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy        261 GlyGlyGlyGlySer 265
              |||||||||||||||
Db        756 GGCGGTGGTGGTTCC 770

RESULT 9
AR033962
LOCUS       AR033962               1385 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 121 from patent US 5869270.
ACCESSION   AR033962
VERSION     AR033962.1  GI:5949567
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1385)
  AUTHORS   Rhode,P.R., Jiao,J.-A., Burkhardt,M. and Wong,H.C.
  TITLE     Single chain MHC complexes and uses thereof
  JOURNAL   Patent: US 5869270-A 121 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .1385
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.13e-110      Length:         1385
Score:                  1145.00        Matches:        227
Percent Similarity:     87.2%          Conservative:   4
Best Local Similarity:  85.7%          Mismatches:     24
Query Match:            72.8%          Indels:         10
DB:                     2              Gaps:           3

US-10-048-116B-6_COPY_1_300 (1-300) x AR033962 (1-1385)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              |||||||||   |||       :::         :::         |||
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              |||      :::|||          ||||||||||||||||                 |||
Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC---------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
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Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
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Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120

Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140

Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160

Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180

Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200

Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220

Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240

Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260

Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy        261 GlyGlyGlyGlySer 265

Db        756 GGCGGTGGTGGTTCC 770

RESULT 10
AR175095
LOCUS       AR175095               1385 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 121 from patent US 6309645.
ACCESSION   AR175095
VERSION     AR175095.1  GI:17916394
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1385)
  AUTHORS   Rhode,P.R., Jiao,J.-A., Burkhardt,M. and Wong,H.C.
  TITLE     MHC molecules and uses thereof
  JOURNAL   Patent: US 6309645-A 121 30-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .1385
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.13e-110       Length:         1385
Score:                  1145.00         Matches:        227
Percent Similarity:     87.2%           Conservative:   4
Best Local Similarity:  85.7%           Mismatches:     24
Query Match:            72.8%           Indels:         10
DB:                     2               Gaps:           3

US-10-048-116B-6_COPY_1_300 (1-300) x AR175095 (1-1385)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20

Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40

Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60

Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC--------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80

Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100

Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120

Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140

Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160

Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180

Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200

Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220

Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240

Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260

Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy        261 GlyGlyGlyGlySer 265

Db        756 GGCGGTGGTGGTTCC 770

RESULT 11
CS079299
LOCUS       CS079299               1385 bp    DNA     linear   PAT 06-MAY-2005
DEFINITION  Sequence 121 from Patent EP1526141.
ACCESSION   CS079299
VERSION     CS079299.1  GI:63093741
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1
  AUTHORS   Rhode,P.R., Jiao,J.A., Burkhardt,M. and Wong,H.C.
  TITLE     MHC complexes and uses thereof
  JOURNAL   Patent: EP 1526141-A 121 27-APR-2005;
            Altor BioScience Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .1385
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
ORIGIN
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Alignment Scores:
Pred. No.:                1.13e-110       Length:         1385
Score:                    1145.00         Matches:        227
Percent Similarity:       87.2%           Conservative:   4
Best Local Similarity:    85.7%           Mismatches:     24
Query Match:              72.8%           Indels:         10
DB:                       2               Gaps:           3

US-10-048-116B-6_COPY_1_300 (1-300) x CS079299 (1-1385)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              |||||||||   |||         :::           :::          |||
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              |||      :::|||          ||||||||||||||                  |||
Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC--------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              ||||||||||||||||||||||||||||||          :::
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy        261 GlyGlyGlyGlySer 265
              |||||||||||||||
Db        756 GGCGGTGGTGGTTCC 770

RESULT 12
AX032543
LOCUS       AX032543               1385 bp    DNA     linear   PAT 20-SEP-2000
DEFINITION  Sequence 121 from Patent EP0997477.
ACCESSION   AX032543
VERSION     AX032543.1  GI:10279484
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1
  AUTHORS   Chavaillaz,P.A., Edwards,A.C., Grammer,S., Jiao,J.A., Rhode,P.R.,
            Weidanz,J.A. and Wong,H.C.
  TITLE     Mhc complexes and uses thereof
  JOURNAL   Patent: EP 0997477-A 121 03-MAY-2000;
            SUNOL MOLECULAR CORP (US)
FEATURES             Location/Qualifiers
     source          1. .1385
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:                1.13e-110       Length:         1385
Score:                    1145.00         Matches:        227
Percent Similarity:       87.2%           Conservative:   4
Best Local Similarity:    85.7%           Mismatches:     24
Query Match:              72.8%           Indels:         10
DB:                       2               Gaps:           3

US-10-048-116B-6_COPY_1_300 (1-300) x AX032543 (1-1385)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              |||||||||   |||         :::           :::          |||
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              |||      :::|||          ||||||||||||||                  |||
Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC--------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              ||||||||||||||||||||||||||||||||          :::
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy        261 GlyGlyGlyGlySer 265
              |||||||||||||||
Db        756 GGCGGTGGTGGTTCC 770

RESULT 13
AR033963
LOCUS       AR033963               1508 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 122 from patent US 5869270.
ACCESSION   AR033963
VERSION     AR033963.1  GI:5949568
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1508)
  AUTHORS   Rhode,P.R., Jiao,J.-A., Burkhardt,M. and Wong,H.C.
  TITLE     Single chain MHC complexes and uses thereof
  JOURNAL   Patent: US 5869270-A 122 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .1508
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.26e-110      Length:         1508
Score:                  1145.00        Matches:        227
Percent Similarity:     87.2%          Conservative:   4
Best Local Similarity:  85.7%          Mismatches:     24
Query Match:            72.8%          Indels:         10
DB:                     2              Gaps:           3

US-10-048-116B-6_COPY_1_300 (1-300) x AR033963 (1-1508)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              |||||||||   |||          :::          :::          |||
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              |||       :::|||           ||||||||||||||                  |||
Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC---------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGGCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
              ||||||||||||||||||||||||||||||||          :::
Db        705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG---------ACTAGTGGTGGCGGTGGCAGC 755

Qy        261 GlyGlyGlyGlySer 265
              |||||||||||||||
Db        756 GGCGGTGGTGGTTCC 770

RESULT 14
AR152030
LOCUS       AR152030               1508 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 24 from patent US 6232445.
ACCESSION   AR152030
VERSION     AR152030.1  GI:15118080
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1508)
  AUTHORS   Rhode,P.R., Acevedo,J., Burkhardt,M., Jiao,J.-a. and Wong,H.C.
  TITLE     Soluble MHC complexes and methods of use thereof
  JOURNAL   Patent: US 6232445-A 24 15-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .1508
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.26e-110      Length:         1508
Score:                  1145.00        Matches:        227
Percent Similarity:     87.2%          Conservative:   4
Best Local Similarity:  85.7%          Mismatches:     24
Query Match:            72.8%          Indels:         10
DB:                     2              Gaps:           3

US-10-048-116B-6_COPY_1_300 (1-300) x AR152030 (1-1508)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
              |||||||||   |||          :::          :::          |||
Db         66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA------ 119

Qy         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
              |||       :::|||           ||||||||||||||                  |||
Db        120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC---------------GGCGGA 164

Qy         61 GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 80
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224

Qy         81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284
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Qy        101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 344

Qy        121 TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 404

Qy        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 464

Qy        161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG 524

Qy        181 ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 584

Qy        201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644

Qy        221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704

Qy        241 SerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
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AR175096
LOCUS       AR175096               1508 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 122 from patent US 6309645.
ACCESSION   AR175096
VERSION     AR175096.1  GI:17916395
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1508)
  AUTHORS   Rhode,P.R., Jiao,J.-A., Burkhardt,M. and Wong,H.C.
  TITLE     MHC molecules and uses thereof
  JOURNAL   Patent: US 6309645-A 122 30-OCT-2001;
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.26e-110      Length:         1508
Score:                  1145.00        Matches:        227
Percent Similarity:     87.2%          Conservative:   4
Best Local Similarity:  85.7%          Mismatches:     24
Query Match:            72.8%          Indels:         10
DB:                     2              Gaps:           3

US-10-048-116B-6_COPY_1_300 (1-300) x AR175096 (1-1508)

Qy          1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 20
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Db          6 ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG 65

Qy         21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
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